

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 11:54:40 ; Search time 147.676 Seconds
(without alignments)
861.643 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHHLWLLCLQIWPENAA.....KASTQDSKPPGTSSEIVIX 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1695	99.9	328	5 AAB47878	Aab47878 SCZ/CD84.
2	1695	99.9	328	5 AAE26238	Aae26238 Human CD8
3	1695	99.9	328	8 ADL82907	Adl82907 Human PRO
4	1695	99.9	328	8 ADO05708	Ado05708 Human leu
5	1695	99.9	328	8 ADQ19067	Adq19067 Human sof
6	1695	99.9	328	8 ADP23943	Adp23943 PRO polyp
7	1695	99.9	329	2 AAW74891	Aaw74891 Human sec
8	1695	99.9	329	5 ABG95343	Abg95343 Human nov
9	1695	99.9	329	6 ABO34537	Ab034537 Region of
10	1695	99.9	329	7 ADI23198	Adi23198 Novel hum
11	1695	99.9	329	8 ADH74200	Adh74200 Human sec
12	411	24.2	79	2 AAY12524	Aay12524 Human 5'
13	382.5	22.6	551	5 ABG96270	Abg96270 Human imm
14	382.5	22.6	565	8 ADK98560	Adk98560 Human imm
15	382.5	22.6	610	5 AAU74425	Aau74425 Human PRO
16	378.5	22.3	526	8 ADL57243	Adl57243 Human NOV
17	378.5	22.3	526	8 ADL57105	Adl57105 Human NOV
18	378.5	22.3	615	8 ADL57103	Adl57103 Human NOV
19	374	22.1	654	8 ADO63782	Ado63782 Human Ly-
20	374	22.1	654	8 ADO78174	Ado78174 Human Ly-
21	373	22.0	289	4 AAE12078	Aae12078 Dendritic
22	373	22.0	289	5 AAE26243	Aae26243 Human CD2
23	373	22.0	289	5 ABP65110	Abp65110 Hypoxia-1
24	373	22.0	289	7 ABW01823	Abw01823 Human CD2
25	370	21.8	289	5 AAE26250	Aae26250 Human CD2

ALIGNMENTS

RESULT 1

AAB47878
ID AAB47878 standard; protein; 328 AA.
XX
AC AAB47878;
XX
DT 02-MAY-2002 (first entry)
XX
DE SCZ/CD84.
XX
KW SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele;
KW polymorphic marker; chromosome 1q22.
XX Homo sapiens.
XX
PN WO200202054-A2.
XX
PD 10-JAN-2002.
XX
PF 23-APR-2001; 2001WO-US013040.
XX
PR 21-APR-2000; 2000US-0198873P.
XX
(RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Brzustowicz LM, Bassett AS;
XX
DR WPI; 2002-171605/22.
DR N-PSDB; AAI72383.
XX
PT Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by
PT determining presence or absence of an allele of a linked polymorphic
PT marker present on chromosome 1q22, were the marker is linked to a variant
PT form of the SCZ gene.
XX
PS Example 6; Page 70; 82pp; English.
XX
CC This sequence is encoded by the SCZ gene which was isolated using the
CC method of the invention. The SCZ gene has been previously identified as
CC CD84, GenBank Accession No: NM_003874. CD84 is a 73 kDa antigen present
CC on platelets, monocytes and circulating B cells. This protein may be
CC involved in the processes by which the brain responds to biological
CC stimuli. Therefore they may provide targets for therapeutic intervention
CC in the treatment of schizophrenia. The SCZ sequence may be used in a new
CC method of diagnosing schizophrenia. The SCZ sequence may be used in a new
CC method of diagnosing susceptibility to schizophrenia in a patient. The
CC method comprises determining the presence or absence of an allele of a
CC linked polymorphic marker in the DNA of the patient. The polymorphic
CC marker is present in chromosome 1q22 and is linked to a gene (SCZ) having

CC a variant form associated with a phenotype of schizophrenia
XX
SQ Sequence 328 AA;

Query Match 99.9%; Score 1695; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 8e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTWPAAAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60

QY 61 AYVTPGDSAPVVTVTHRNYYERIHAGLPNNYLVISDLRMDAGYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVVTVTHRNYYERIHAGLPNNYLVISDLRMDAGYKADINTQADPYTT 120

QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQI 180
DB 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVIL 240

QY 241 SSVFLRFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPTNTVYS 300
DB 241 SSVFLRFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPTNTVYS 300

QY 301 EVQFADKMGKASTQDSKPPGTSSEYI 328
DB 301 EVQFADKMGKASTQDSKPPGTSSEYI 328

RESULT 2
AAE26238
ID AAE26238 standard; protein; 328 AA.
XX
AC AAE26238;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human CD84 protein.
XX
KW Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein;
KW immune proliferative disorder; immune disorder; rheumatoid arthritis;
KW Carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease;
KW Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic;
KW osteoarthritis; allergic inflammatory disorder; viral infection; asthma;
KW psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis;
KW diabetes mellitus; septic shock; chronic obstructive pulmonary disease;
KW emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis;
KW acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic;
KW immunosuppressive; neuroprotective; antiinflammatory; Crohn's disease;
KW osteopathic; antibacterial; immunomodulator; inflammatory bowel disease;
KW jaundice; dermatological; ulcerative colitis; AIDS; CD84.
XX
OS Homo sapiens.
XX
PN EP1223218-A1.
XX
PD 17-JUL-2002.
XX
PF 02-NOV-2001; 2001EP-00309339.
XX
PR 03-NOV-2000; 2000US-00706167.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Fraser CC;
XX
WPI: 2002-620680/67.
DR N-PSDB; AAD43563.
XX

PT Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
PT like domains and SLAM associated protein, termed CD2000 or CD2001, useful
PT for treating immune, inflammatory, or hepatic circulatory disorders.
XX
XX Disclosure; Page 76-77; 138pp; English.
XX
XX The invention relates to nucleic acid molecule, designated CD2000 which
XX encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains
XX and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is
XX useful for treating disorder such as immune proliferative disorders,
XX immune disorders (e.g. carcinoma), viral infection, autoimmune disorders
XX (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's
XX disease), T cell disorder (e.g. acquired immune deficiency syndrome
XX (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative
XX colitis), inflammatory disorders (e.g. rheumatoid arthritis and
XX osteoarthritis), allergic inflammatory disorders (e.g. asthma and
XX psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and
XX insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,
XX chronic obstructive pulmonary disease (e.g. emphysema), bronchitis,
XX cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis,
XX acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in
XX gene therapy. CD2000 DNA is useful in screening assays, detection assays
XX (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
XX medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
XX trials and pharmacogenomics), and in methods of treatment (e.g.
XX therapeutic and prophylactic). The present sequence is human CD84 protein
XX used in the invention
SQ Sequence 328 AA;

Query Match 99.9%; Score 1695; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 8e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTWPAAAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60

QY 61 AYVTPGDSAPVVTVTHRNYYERIHAGLPNNYLVISDLRMDAGYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVVTVTHRNYYERIHAGLPNNYLVISDLRMDAGYKADINTQADPYTT 120

QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQI 180
DB 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVIL 240

QY 241 SSVFLRFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPTNTVYS 300
DB 241 SSVFLRFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPTNTVYS 300

QY 301 EVQFADKMGKASTQDSKPPGTSSEYI 328
DB 301 EVQFADKMGKASTQDSKPPGTSSEYI 328

RESULT 3
ADL82907
ID ADL82907 standard; protein; 328 AA.
XX
AC ADL82907;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human PRO24934, SEQ ID 109.
XX
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.

XX Homo sapiens.
OS WO2004024097-A2.
XX PD 25-MAR-2004.
XX 15-SEP-2003; 2003WO-US029097.
XX 16-SEP-2002; 2002US-0411392P.
XX (GETH) GENENTECH INC.
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX WPI; 2004-329389/30.
DR N-PSDB; ADL82906.
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX Claim 10; Fig 109; 695pp; English.
XX The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IGA deficiency, selective IGM
CC deficiency, selective deficiency of IGC subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knock-out animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX SQ Sequence 328 AA;
Query Match 99.9%; Score 1695; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 8e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHLLWILLCLQTWPEAGKDSFTVNGILGESVTFPVNIOEPRQVKIIAWTSKTSV 60
Db 1 MAQHLLWILLCLQTWPEAGKDSFTVNGILGESVTFPVNIOEPRQVKIIAWTSKTSV 60
QY 61 AYVTPGDSETAPVVTVTHRNYERIHALGPNYLVISDLRMEADGDKADINTQADPYTT 120
Db 61 AYVTPGDSETAPVVTVTHRNYERIHALGPNYLVISDLRMEADGDKADINTQADPYTT 120
QY 121 TKRYNLIQYRRLGPKITQSLMASVNSTCNVTLTCSVEKEKRVNWNPSLGEENVLQI 190
Db 121 TKRYNLIQYRRLGPKITQSLMASVNSTCNVTLTCSVEKEKRVNWNPSLGEENVLQI 190
QY 181 FQTPEDQELTYTCTAQNPNVNSDSISAROLCADIAMGPRTHHTGLLSVLAMFLLVLIL 240
Db 181 FQTPEDQELTYTCTAQNPNVNSDSISAROLCADIAMGPRTHHTGLLSVLAMFLLVLIL 240
QY 241 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEPNTVYS 300
Db 241 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEPNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 4
ADO05708
ID ADO05708 standard; protein; 328 AA.
XX AC ADO05708;
XX 15-JUL-2004 (first entry)
XX Human leukocyte differentiation antigen CD84.
XX T cell; antiallergic; immunosuppressive; virucide; antibacterial;
KW antiparasitic; cytostatic; gene therapy; human; CD83;
KW leukocyte differentiation antigen.
XX OS Homo sapiens.
XX WO2004032867-A2.
XX 22-APR-2004.
XX 09-OCT-2003; 2003WO-US032065.
XX 09-OCT-2002; 2002US-0417102P.
XX 09-OCT-2002; 2002US-0417103P.
XX 18-OCT-2002; 2002US-0417243P.
XX 08-NOV-2002; 2002US-0419575P.
XX 08-NOV-2002; 2002US-0424777P.
XX 08-NOV-2002; 2002US-0424881P.
XX (TOLE-) TOLERRX INC.
XX Rao P, Szymanska G;
XX WPI; 2004-340801/31.
XX N-PSDB; ADO05707.
XX GENBANK; 6650105.
XX Treating a condition that benefits from modulating regulatory or effector
PT T cell function comprises administering an agent that modulates the
PT expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbeta1,
PT Jagged-1 or GPR-32).
XX Example; SEQ ID NO 8; 161pp; English.
XX The invention relates to treating a subject having a condition that
CC benefits from modulating the balance of regulatory T cell function
CC relative to effector T cell function, or vice versa, in a subject. The
CC method involves administering an agent that modulates the expression or
CC activity of a molecule selected from PTGER2 and TGFbeta1, or Jagged-1,
CC GPR-32, CD84, CD89, serotonin R, BY55, serotonin R2C, GPR63,
CC histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-
CC 3-related kinase to the subject, such that treatment occurs. The methods
CC are useful for diagnosing, preventing or treating conditions
CC characterized by a too-vigorous or weak effector T cell or regulatory T
CC cell response to antigens associated with the condition, such as in an
CC allergic response, an autoimmune disorder, a viral infection, a microbial
CC infection, a parasitic infection or a tumour. The present sequence
CC represents a human leukocyte differentiation CD84 antigen, preferentially
CC expressed in regulatory T cells.
XX SQ Sequence 328 AA;
Query Match 99.9%; Score 1695; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 8e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHLLWILLCLQTWPEAGKDSFTVNGILGESVTFPVNIOEPRQVKIIAWTSKTSV 60
Db 1 MAQHLLWILLCLQTWPEAGKDSFTVNGILGESVTFPVNIOEPRQVKIIAWTSKTSV 60
QY 61 AYVTPGDSETAPVVTVTHRNYERIHALGPNYLVISDLRMEADGDKADINTQADPYTT 120
Db 61 AYVTPGDSETAPVVTVTHRNYERIHALGPNYLVISDLRMEADGDKADINTQADPYTT 120

QY	121	TKRYNLQIYRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLEEGNVLQI	180
Db	121	TKRYNLQIYRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLEEGNVLQI	180
QY	181	FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL	240
Db	181	FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL	240
QY	241	SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS	300
Db	241	SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS	300
QY	301	EVQFADKMGKASTQDSKPPGTSSYEIVI	328
Db	301	EVQFADKMGKASTQDSKPPGTSSYEIVI	328
RESULT 5			
ID	ADQ19067	standard; protein; 328 AA.	
XX	AC	ADQ19067;	
XX	DT	26-AUG-2004 (first entry)	
XX	DE	Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.	
XX	KW	soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.	
XX	OS	Homo sapiens.	
XX	PN	WO2004048938-A2.	
XX	PD	10-JUN-2004.	
XX	PF	26-NOV-2003; 2003WO-US038193.	
XX	PR	26-NOV-2002; 2002US-0429739P.	
XX	PA	(PROT-) PROTEIN DESIGN LABS INC.	
XX	PI	Aziz N, Ginsburg WM, Zlotnik A;	
XX	DR	WPI; 2004-441208/41.	
XX	PT	Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.	
XX	PS	Example 2; SEQ ID NO 1886; 210pp; English.	
XX	CC	The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.	
XX	SQ	Sequence 328 AA;	
Query Match			
Best Local Similarity 99.9%; Score 1695; DB 8; Length 328;			
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY	1	MAQHLLWILLCLQTPWPAAGKDEIFTVNGILGESVTPFPVNIQEPQVKIIAWTSKTSV	60
Db	1	MAQHLLWILLCLQTPWPAAGKDEIFTVNGILGESVTPFPVNIQEPQVKIIAWTSKTSV	60
QY	61	AYVTPGDSETPAVVTVTHRNYERIHALGPNYNLVIDSLRMEADAGDYKADINTQADPYTT	120
Db	61	AYVTPGDSETPAVVTVTHRNYERIHALGPNYNLVIDSLRMEADAGDYKADINTQADPYTT	120
QY	121	TKRYNLQIYRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLEEGNVLQI	180
Db	121	TKRYNLQIYRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLEEGNVLQI	180
QY	181	FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL	240
Db	181	FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL	240
QY	241	SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS	300
Db	241	SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS	300
QY	301	EVQFADKMGKASTQDSKPPGTSSYEIVI	328
Db	301	EVQFADKMGKASTQDSKPPGTSSYEIVI	328
RESULT 6			
ID	ADP23943	standard; protein; 328 AA.	
XX	AC	ADP23943;	
XX	DT	18-NOV-2004 (first entry)	
XX	DE	PRO polypeptide SEQ ID NO:1121.	
XX	KW	PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.	
XX	OS	Unidentified.	
XX	PN	WO2004041170-A2.	
XX	PD	21-MAY-2004.	
XX	PF	30-OCT-2003; 2003WO-US034312.	
XX	PR	01-NOV-2002; 2002US-0423394P.	
XX	PA	(GETH) GENENTECH INC.	
XX	PI	Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;	
XX	DR	WPI; 2004-419628/39.	
XX	CC	The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,	

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.

XX
SQ Sequence 328 AA;

Query Match 99.9%; Score 1695; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 9e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTWPEAAGKDSIFVTNGILGESVTFPVNIQEPQVKIITAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPEAAGKDSIFVTNGILGESVTFPVNIQEPQVKIITAWTSKTSV 60
QY 61 AVYTPGDSAPVVTTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
DB 61 AVYTPGDSAPVVTTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPLEEGNVLOI 180
DB 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPLEEGNVLOI 180
QY 181 FQTPEDQELTYCTAQNPNVSNNSDSISARQLCADIAMGERTHTGLSVLAMPFLVLIL 240
DB 181 FQTPEDQELTYCTAQNPNVSNNSDSISARQLCADIAMGERTHTGLSVLAMPFLVLIL 240
QY 241 SSVFLPRLFKRRDAAASKTIITYIMASRNTQPAESRIYDEILQSKVLPSKEPNTVYS 300
DB 241 SSVFLPRLFKRRDAAASKTIITYIMASRNTQPAESRIYDEILQSKVLPSKEPNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
DB 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 7
AAW74891
ID AAW74891 standard; protein; 329 AA.

XX AC AAW74891;
XX XX
XX DT 25-JAN-1999 (first entry)
XX DE Human secreted protein encoded by gene 164 clone HSAWF26.
XX KW Human; secreted protein; testis; tumour; foetal brain tissue;
XX KW fusion protein; cancer; central nervous system; seizure; diagnosis;
XX KW neurodegenerative disease.
XX OS Homo sapiens.
XX OS
XX PH Key Location/Qualifiers
XX FT Misc-difference 329 /label= unknown
XX FT
XX XX WO9839448-A2.
XX XX
PD 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004493.
PF
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040628P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0048974P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.

```
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 12-OCT-1997; 97US-0061060P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI: 1998-506364/43.
XX N-PSDB; AAV59674.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 641-642; 721pp; English.
XX
XX This sequence represents a secreted human protein encoded by the nucleic
CC acid molecule designated Gene 164 from the human cDNA clone HSAWF26
CC (deposited as clone ATCC 97903 and ATCC 209049). The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
XX Sequence 329 AA;
SQ
Query Match 99.9%; Score 1695; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAQHLWILLCLQWPEAAGKDSIFVTNGILGESVTFPNIOEPROVKIIAWTSKTSV 60
DB 1 MAQHLWILLCLQWPEAAGKDSIFVTNGILGESVTFPNIOEPROVKIIAWTSKTSV 60
```

```
OY 61 AAVTPGDSFAPVVTVTHRNYYERIHAGLPNNLVISDLRMEDAGDYKADINTQADPYTT 120
DB 61 AAVTPGDSFAPVVTVTHRNYYERIHAGLPNNLVISDLRMEDAGDYKADINTQADPYTT 120
OY 121 TKRYNLQIYRRLGPKIKTQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPGEEGNVLQI 180
DB 121 TKRYNLQIYRRLGPKIKTQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPGEEGNVLQI 180
OY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMPFLVLIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMPFLVLIL 240
OY 241 SSVFLFRLFKRRQDAASKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPPVNTVYS 300
DB 241 SSVFLFRLFKRRQDAASKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPPVNTVYS 300
OY 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
DB 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
RESULT 8
ABG95343
ID ABG95343 standard; protein; 329 AA.
XX
XX AC ABG95343;
XX
XX DT 15-JAN-2003 (first entry)
XX
XX DE Human novel secreted protein #164.
XX
XX KW Human; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasia cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
XX OS Homo sapiens.
XX
XX PN US6420526-B1.
XX
XX PD 16-JUL-2002.
XX
XX PF 08-SEP-1998; 98US-00149476.
XX
XX PR 07-MAR-1997; 97US-0038621P.
XX PR 07-MAR-1997; 97US-0040161P.
XX PR 07-MAR-1997; 97US-0040162P.
XX PR 07-MAR-1997; 97US-0040163P.
XX PR 07-MAR-1997; 97US-0040333P.
XX PR 07-MAR-1997; 97US-0040334P.
XX PR 07-MAR-1997; 97US-0040336P.
XX PR 07-MAR-1997; 97US-0040626P.
XX PR 11-APR-1997; 97US-0043311P.
XX PR 11-APR-1997; 97US-0043312P.
XX PR 11-APR-1997; 97US-0043313P.
XX PR 11-APR-1997; 97US-0043314P.
XX PR 11-APR-1997; 97US-0043315P.
XX PR 11-APR-1997; 97US-0043568P.
XX PR 11-APR-1997; 97US-0043569P.
XX PR 11-APR-1997; 97US-0043576P.
XX PR 11-APR-1997; 97US-0043578P.
XX PR 11-APR-1997; 97US-0043580P.
XX PR 11-APR-1997; 97US-0043669P.
XX PR 11-APR-1997; 97US-0043670P.
XX PR 11-APR-1997; 97US-0043671P.
XX PR 11-APR-1997; 97US-0043672P.
XX PR 11-APR-1997; 97US-0043674P.
XX PR 23-MAY-1997; 97US-0047492P.
XX PR 23-MAY-1997; 97US-0047500P.
```


RESULT 9
ABO34537
ID ABO34537 standard; protein; 329 AA.
XX AC ABO34537;
XX AC
XX DT 22-SEP-2003 (first entry)
XX DE
XX DE Region of human secreted protein encoded by cDNA sequence #164.
XX
KW Human; secreted protein; hyperproliferative disorder; leukaemia;
KW breast cancer; wound; reproductive disorder; blood-related disorder;
KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;
KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;
KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;
KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;
KW angina pectoris; cerebral ischaemia; congenital heart defect;
KW respiratory disorder; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;
KW immunosuppressive; antibacterial; haemostatic; thrombolytic;
KW anticoagulant; neuroprotective; thyromimetic; antiallergic;
KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;
KW cerebroprotective; cardiant; nootropic; antiparkinsonian;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
XX US2003049619-A1.
XX
XX 13-MAR-2003.
XX
XX 16-MAR-2001; 2001US-00809391.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048966P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057659P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJU/) NI J.

```
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREN/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHI/) SHI Y.
PA (LAFU/) LAFLEUR D W.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI: 2003-521800/49.
DR N-PSDB; ACD82804.
DR
XX
XX New genes and its encoded prostate cancer antigen proteins, useful for
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
PT ischemia.
XX
XX Claim 3; SEQ ID NO 483; 260pp; English.
XX
XX The present invention relates to the isolation of novel human secreted
CC proteins and the polynucleotide sequences encoding them. The invention
CC also discloses vectors, host cells, antibodies, and recombinant methods
CC for producing human secreted proteins. The polypeptide and polynucleotide
CC sequences for the secreted proteins are useful for preventing, treating,
CC ameliorating or diagnosing medical conditions such as hyperproliferative
CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive
CC disorders, blood-related disorders (e.g. haemophilia or
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory
CC disorders, neurological disorders (e.g. Alzheimer's disease or
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.
CC ABO34374-ABO34815 represent human secreted proteins or their fragments.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
XX Sequence 329 AA;
SQ
Query Match 99.9%; Score 1695; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1e-138;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHLLWILLCLQWPEAAGKDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQWPEAAGKDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
QY 61 AYTTPGDSAPVVTVTHRYNRYERIHAGFNYNLIVISDLRMEDAGDYKADINTQADPYTT 120
DB 61 AYTTPGDSAPVVTVTHRYNRYERIHAGFNYNLIVISDLRMEDAGDYKADINTQADPYTT 120
QY 121 TKRYNLQIYRRLGPKPKITQSLMASVNSTCNVTLTCSVEKEKNVYNNWSPIGBEGNVLQI 180
DB 121 TKRYNLQIYRRLGPKPKITQSLMASVNSTCNVTLTCSVEKEKNVYNNWSPIGBEGNVLQI 180
```

```
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0057859P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIUJ/) NI J.
PA (FENG/) FENG P.

PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (ERNE/) EENER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, BednariK DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PR, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
WPI; 2003-898535/82.
N-PSDB; ADI22889.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
PS Claim 11; SEQ ID NO 483; 256bp; English.
CC
CC The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a
CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The is the amino acid sequence of a novel human
CC secreted protein of the invention.
XX
SQ Sequence 329 AA;
Query Match 99.9%; Score 1695; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1e-138; Mismatches 0; Indels 0; Gaps 0;
Matches 328; Conservative 0;
QY 1 MAQHLLWILLCLQTWPEAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAMTSKTSV 60
DB 1 MAQHLLWILLCLQTWPEAGKDSIEFTVNGILGESVTFPVNIQEPQVKIIAMTSKTSV 60
QY 61 AYVTPGDSAPVTVVTHRNYYERIHAGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVTVVTHRNYYERIHAGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
QY 121 TKRYNLQIYRELGPKITQSLMASVNSCNVLTCSVEKEKKNVTYNSPLGEGSNVLQI 180
DB 121 TKRYNLQIYRELGPKITQSLMASVNSCNVLTCSVEKEKKNVTYNSPLGEGSNVLQI 180
QY 181 FQTPEDQELITYCTAQNPNVSNNSDISARQLCADIAMGFRTHHTGLLSVLAFFLLVLIL 240
DB 181 FQTPEDQELITYCTAQNPNVSNNSDISARQLCADIAMGFRTHHTGLLSVLAFFLLVLIL 240
QY 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDILQSKVLPSKEEPVNTVYS 300
DB 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDILQSKVLPSKEEPVNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSSEYIEVI 328
DB 301 EVQFADKMGKASTQDSKPPGTSSEYIEVI 328
```


RESULT 11
ADH74200
ID ADH74200 standard; protein; 329 AA.
XX
AC ADH74200;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human secreted protein #164.
XX
KW human; secreted protein; cancer; haematopoietic disorder;
KW endocrine disorder; immune system disease; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN US2003225248-A1.
XX
PD 04-DEC-2003.
XX
PF 10-JUN-2002; 2002US-00164861.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043356P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047616P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047619P.
PR 23-MAY-1997; 97US-0047620P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057661P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2004-131264/13.
XX N-PSDB; ADH73891.
XX
XX Isolated nucleic acid molecules encoding human secreted proteins, useful
PT for preventing, diagnosing and treating disorders associated with
PT aberrant expression and activity.
XX
XX Claim 11; SEQ ID NO 483; 142pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and the human
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,
CC endocrine disorders, diseases of the immune system, inflammatory
CC disorders and many others. Full details of disorders that may be

CC prevented, diagnosed and/or treated by the above methods are given in the
CC specification. The nucleic acid molecules may be used to produce their
CC proteins. The nucleic acid and its complementary sequences may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The SpE may also be used
CC as antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of SP expression and activity. The anti-SP
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-SP antibodies may also be used as diagnostic
CC agents for detecting the presence of the proteins in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents the amino acid sequence of a human secreted protein.
XX
SQ Sequence 329 AA;

Query Match 99.9%; Score 1695; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1e-138;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTWPAAAGKDSIFVTNGILGESVTFPVNIOEPQVQKIIAMTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSIFVTNGILGESVTFPVNIOEPQVQKIIAMTSKTSV 60
QY 61 AVTTPGDSAPVVTTHRYERHALGPNVNLVLSLRMEDAGDYKADINTQADPYTT 120
DB 61 AVTTPGDSAPVVTTHRYERHALGPNVNLVLSLRMEDAGDYKADINTQADPYTT 120
QY 121 TKRYNLQIYRLRGKPKITQSLMASVNSTCNVLTCSVEKEKNVYNSPLGEGNVLQI 180
DB 121 TKRYNLQIYRLRGKPKITQSLMASVNSTCNVLTCSVEKEKNVYNSPLGEGNVLQI 180
QY 181 FQTPEDQELTYTCTAQPNVSNNSDISARQLCADIAMGFRTHTGLLSVLAMFLLVLIL 240
DB 181 FQTPEDQELTYTCTAQPNVSNNSDISARQLCADIAMGFRTHTGLLSVLAMFLLVLIL 240
QY 241 SSVFLFRFLFKRQDAASKKTIYTYMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 300
DB 241 SSVFLFRFLFKRQDAASKKTIYTYMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSSYBIV 328
DB 301 EVQFADKMGKASTQDSKPPGTSSYBIV 328

RESULT 12
AAV12524
ID AAV12524 standard; protein; 79 AA.

XX AAV12524;
XX
DT 22-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID NO: 189 from WO 9906553.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; antiinflammatory; tumour inhibition; antitumour.

OS Homo sapiens.

XX WO9906553-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-1B001237.

PR 01-AUG-1997; 97US-00905051.

XX (GDSST) GENSET.

XX
PI

Dumas Milne Edwards J, Duclert A, Lacroix B;

WPI; 1999-153783/13.

N-PSDB; AAX41382.

XX New nucleic acids encoding human secreted proteins - obtained from cDNA
libraries derived from umbilical cord, lymph ganglia, lymphocytes and
placental tissue.

Claim 34; Page 323; 411pp; English.

XX AAX41379 to AAX41526 represent 5' expressed sequence tags (ESTs) for
human secreted proteins, and encode the proteins given in AAX12521 to
AAX12668, respectively. The proteins given represent the signal peptide
and an N-terminal fragment of a secreted protein. The nucleic acid
sequences can be used for producing secreted human gene products. They
can also be used to develop products for diagnosis and therapy. The
proteins obtained may have cytokine activity, cell
proliferation/differentiation activity, haematopoiesis regulating
activity, tissue growth regulating activity, reproductive hormone
regulating activity, chemotactic/chemokinetic activity, haemostatic and
thrombolytic activity, receptor/ligand activity, antiinflammatory
activity, tumour inhibition activity or other activities. The products
can be used in forensic, gene therapy and chromosome mapping procedures.
The sequences can also be used for obtaining corresponding promoter
sequences. The nucleic acids encoding the signal peptide can be used for
directing extracellular secretion of a polypeptide or the insertion of a
polypeptide into a membrane, or importing a polypeptide into a cell
Sequence 79 AA;

Query Match 24.2%; Score 411; DB 2; Length 79;

Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTWPAAAGKDSIFVTNGILGESVTFPVNIOEPQVQKIIAMTSKTSV 60

DB 1 MAQHLLWILLCLQTWPAAAGKDSIFVTNGILGESVTFPVNIOEPQVQKIIAMTSKTSV 60

QY 61 AVTTPGDSAPVVTTH 78

DB 61 AVTTPGDSAPVVTTH 78

RESULT 13
ABG96270
ID ABG96270 standard; protein; 551 AA.

XX ABG96270;

XX 11-DEC-2002 (first entry)

XX Human immunoglobulin superfamily protein IGSFP-8.

XX Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder;
KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;
KW paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;
KW primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma;
KW autoimmune disorder; inflammatory disorder;
KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; asthma;
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease;
KW diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout;
KW Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;
KW multiple sclerosis; rheumatoid arthritis; osteoporosis; pancreatitis;
KW Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis;
KW trauma; viral infection; bacterial infection; fungal infection;
KW parasitic infection; protozoal infection; helminthic infection;
KW gene therapy; human.

XX Homo sapiens.

XX WO200272794-A2.

XX PD 19-SEP-2002.
 XX PF 12-MAR-2002; 2002WO-US009052.
 XX PR 12-MAR-2001; 2001US-0275249P.
 PR 31-AUG-2001; 2001US-0316810P.
 PR 21-SEP-2001; 2001US-0323977P.
 PR 26-OCT-2001; 2001US-0348447P.
 PR 02-NOV-2001; 2001US-0343880P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Yue H, Xu Y, Thangavelu K, Warren BA, Tang YT, Duggan BM;
 PI Tran UK, Baughn MR, Honchell CD, Burford N, Forsythe LJ, Yang J;
 PI Mason PM;
 XX WPI: 2002-723340/78.
 DR N-PSDB; ABS76363.
 XX New human immunoglobulin superfamily proteins and polynucleotides, useful
 PT for diagnosing, treating or preventing disorders with aberrant IGSFP
 PT expression, such as autoimmune, inflammatory or cell proliferative
 PT diseases.
 XX Claim 1; Page 129-130; 145pp; English.
 XX The present invention relates to new immunoglobulin superfamily proteins
 CC (IGSFP). The polypeptides, polynucleotides, agonists and antagonists are
 CC useful for diagnosing, treating or preventing disorders associated with
 CC aberrant expression of IGSFP, particularly cell proliferative, e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancers including leukaemia, lymphoma, sarcoma or
 CC myeloma, and autoimmune or inflammatory disorders, e.g. acquired
 CC immunodeficiency syndrome (AIDS), allergies, anaemia, asthma, autoimmune
 CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
 CC glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,
 CC Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis,
 CC osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid
 CC arthritis, Sjogren's syndrome, uveitis, trauma, or viral, bacterial,
 CC fungal, parasitic, protozoal or helminthic infections. They are also
 CC useful in the assessment of the effects of exogenous compounds on the
 CC expression of nucleic acid and amino acid sequences of IGSFP. The present
 CC amino acid sequence represents a human IGSFP protein of the invention
 XX Sequence 551 AA;
 SQ
 Query Match 22.6%; Score 382.5; DB 5; Length 551;
 Best Local Similarity 33.9%; Pred. No. 4.2e-24;
 Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;
 QY 3 QHLLWILLCLQTPWPAAGKDSIFTVNGILGSGVTFPPVNIQBPPOVKIIAWTS-KTSVA 61
 DB 33 QTSLLFLMLGLR-----ASGKDSAPTGVSGILGSGVTLPLNISVDTEIENWIGPKNALA 88
 QY 62 YVTPGSETAPVTVTHRNYYERHAGLPNNLVISDLRMDAGDYKADINTQADPYTTT 121
 DB 89 FARPKEN-----VTIMVKSYLGRDITKWSYLSICISNLTLNDAGSKAQINQNFVETTE 143
 QY 122 KRYNIQYRLGPKLT-QSLMASVNSTCNVLTCSVEKEKNVTYNSPL-----GEE 174
 DB 144 EEFTLFVYEQBPQVTKSVKSENFCNITLMCSVKGAESVLSWTPREPHASENSG 203
 QY 175 GNVLIQFQTPEDQELTYCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
 DB 204 GSILTVSRFTCDPLPCTIAQNPVSQSSLPVHVGFQCTDPCASRGTTGET-VGVGLG 262
 QY 232 MFFLLVILLS-----VFLFR---LFRKQDQASKKITYTYIMASRNTQPAESRIY 279
 DB 263 EPVTLPLALPACRDTKQVWVLFNTSIISKEREAAATADPLI-----KSRDPYKNRYW 314

RESULT 14

ADK98560
 ID ADK98560 standard; protein; 565 AA.
 XX AC ADK98560;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human immune response associated protein IRAP-23 protein.
 XX KW immune response associated protein; IRAP; antiarteriosclerotic;
 KW cytotatic; neuroprotective; antiparkinsonian; hepatotropic;
 KW cerebroprotective; antiinflammatory; neurotropic; vasotrophic;
 KW arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease;
 KW Parkinson's; Crohn's; gene therapy; human.
 XX OS Homo sapiens.
 XX WO2004020593-A2.
 XX PN 11-MAR-2004.
 XX PD 26-AUG-2003; 2003WO-US026988.
 XX PF 30-AUG-2002; 2002US-0407561P.
 XX PR 11-SEP-2002; 2002US-0410178P.
 PR 13-SEP-2002; 2002US-0410571P.
 PR 18-OCT-2002; 2002US-041906P.
 PR 25-OCT-2002; 2002US-0421445P.
 XX (INCY-) INCYTE CORP.
 XX Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;
 PI Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;
 XX WPI: 2004-239178/22.
 DR N-PSDB; ADK98595.
 XX New isolated immune response associated proteins (IRAP) polypeptide and
 PT polynucleotide, useful for diagnosing and/or treating disorders with
 PT aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
 PT and stroke.
 XX Claim 1; SEQ ID NO 23; 207pp; English.
 XX The invention relates to a novel isolated immune response associated
 CC protein (IRAP) comprising any of 35 fully defined sequences given in the
 CC specification. The polypeptide of the invention demonstrates
 CC antiarteriosclerotic, cytotatic, neuroprotective, antiparkinsonian,
 CC hepatotropic, cerebroprotective, antiinflammatory, neurotropic and
 CC vasotrophic activities and may be useful for treating a disease or
 CC condition associated with decreased expression or overexpression of
 CC functional immune response associated proteins, while the antibody is
 CC useful for diagnosing a condition or disease associated with the
 CC expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke,
 CC Alzheimer's disease, Parkinson's disease and Crohn's disease.
 CC Furthermore, the molecules of the invention may be utilised during gene
 CC therapy procedures. The current sequence is that of a human IRAP protein
 CC of the invention.
 XX SQ Sequence 565 AA;
 Query Match 22.6%; Score 382.5; DB 8; Length 565;
 Best Local Similarity 33.9%; Pred. No. 4.4e-24;
 Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;
 QY 3 QHLLWILLCLQTPWPAAGKDSIFTVNGILGSGVTFPPVNIQBPPOVKIIAWTS-KTSVA 61
 DB 33 QTSLLFLMLGLR-----ASGKDSAPTGVSGILGSGVTLPLNISVDTEIENWIGPKNALA 88
 QY 62 YVTPGSETAPVTVTHRNYYERHAGLPNNLVISDLRMDAGDYKADINTQADPYTTT 121
 DB 89 FARPKEN-----VTIMVKSYLGRDITKWSYLSICISNLTLNDAGSKAQINQNFVETTE 143

[illegible]

RESULT 15

AAU74425
ID AAU74425 standard; protein: 610 AA

AAU74425:

23-APR-2002 (first entry)

DE Human protein sequence #3, related to isolation of genes within SLE-1B.

Human; systemic lupus erythematosus 1B; SLE-1B; dermatological; antiinflammatory; immunosuppressive; systemic autoimmune disorder; signalling lymphocyte activation molecule; SLAM; lymphocyte antigen 9; Ly-9; 2B4; natural killer cell receptor; CD48; CD84; LY108; CS1; DEDD; NIT1; upstream transcription factor 1; USF 1; GOLGA4; immune tolerance.

OS Homo sapiens.

AA WO200188200-A2

22-NOV-2001

17-MAY-2001: 2001WO-IIS016051.

XX
PB
17-MAY-2000 2000US-0204963P

PK	17-MAY-2000; 2000US-0204963P.
PR	21-SEP-2000; 2000US-0234457P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Wakeland EK, Wandstrat A, Morel L:

WPI; 2002-066695/09.

DR N-PSDB; AAS20420.

Screening for susceptibility to systemic autoimmune disorder by screening PT for a mutation within the systemic lupus erythematosus-1B loci.

PS Disclosure; Page 118-120; 128pp; English;

The present invention relates to a new method for screening for susceptibility to a systemic autoimmune disorder. The method comprises screening for at least one mutation within the systemic lupus erythematosus (SLE)-1B loci. Screening for susceptibility to autoimmune disorders such as systemic lupus erythematosus involves screening for at least one mutation in a gene or genes with the SLE-1B loci such as a gene encoding signalling lymphocyte activation molecule (SLAM), lymphocyte antigen (Lyt)-9, 2B4 (a natural killer cell receptor), CD48, CD84, LY108, CS1, DRD9, NTR1, upstream transcription factor (USF1), GOLA4. The method of the invention is useful for treating SLE and involves administering a construct comprising a wild-type sequence encoding any one of the above mentioned genes. Gene therapy also involves the use of antisense constructs or ribozymes directed against the above mentioned genes for treating SLE. Note: The present protein sequence represents a human protein of the invention that relates to the isolation of genes within SLE-1B that mediate a break in immune tolerance. This sequence is shown in the sequence listing but is not further defined in the specification

Sequence 610 AA;

Query Match	22.6%	Score	382.5	DB	5	Length	610
Best Local Similarity	33.9%	Pred. No.	4.9e-24				
Matches	101	Conservative	60	Mismatches	100	Indels	37
Gaps	11						
Qy	3	QHHLWILLLLCLQWPEAAGKDSBIFTVNGILGSGVTFPPVNIQBPQVKIIAWTs-KTSVA	61				
Db	2	QTSLLFLMLGR---	ASGRKDSAPT	VVSGILGSGVTLP	PLNISVDTEI	ENVIWIGPKNALA	57
Qy	62	YVTFGDSAPVTVTHRNRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPVT	121				
Db	58	FARPKEN-----	VTIMVKSYLGLDITKWSYSLCISNLTNDAGSKYKAOINQRNFVETTE	112			
Qy	122	KRYNLQYIRLRLGPKKIT-QSLMASVNSTCNVTITSCSEKEKNVTYNWSPL-----	GEE	174			
Db	113	EEFTLPVYEQLQSPQVTKSVKVSSENFSCNITLMCSVKGAEKSVLYSWT	PREPHASESNG	172			
Qy	175	GNVLQIFQTPEDQELVITCTAONPVSNNSD-SISARQLCAD--	JAMGFRTHGLLSVLA	231			
Db	173	GSILITVSRITPCDPLPYICTAONPVSORSLPVHVGFCTDPCASRGTTGET--	VVGVLG	231			
Qy	232	MFLLVLILSS-----	VELFR--	LFKRRODAASKTITYVIMASRNTQPAESRIY	279		
Db	232	EPVTLPLALPACDRDTEKVMVLFNTSIISKEREBAATDPLI-----	KSRDPPKYNRW	283			

Search completed: February 4, 2005, 12:11:02

Job time : 151.676 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 12:04:15 ; Search time 38.0095 Seconds
(without alignments)
646.143 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQWPEAA.....KASTQSKPGTSSYEIVIX 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	99.9	328	4	US-09-949-016-6428 Sequence 6428, Ap
2	1695	99.9	329	4	US-09-149-476-483 Sequence 483, App
3	1695	99.9	332	4	US-09-949-016-7327 Sequence 7327, App
4	227	13.4	365	4	US-09-949-016-6907 Sequence 6907, Ap
5	227	13.4	391	4	US-09-949-016-7325 Sequence 7325, Ap
6	194	11.4	307	1	US-08-348-792-8 Sequence 8, Appli
7	194	11.4	307	2	US-08-462-738-8 Sequence 8, Appli
8	194	11.4	307	3	US-09-199-955-8 Sequence 8, Appli
9	194	11.4	307	3	US-08-880-875-8 Sequence 8, Appli
10	194	11.4	335	1	US-08-348-792-2 Sequence 2, Appli
11	194	11.4	335	2	US-08-462-738-2 Sequence 2, Appli
12	194	11.4	335	3	US-09-199-955-2 Sequence 2, Appli
13	194	11.4	335	3	US-08-880-875-2 Sequence 2, Appli
14	194	11.4	335	4	US-09-369-248A-3 Sequence 3, Appli
15	193	11.4	143	3	US-09-227-357-192 Sequence 192, App
16	187.5	11.1	298	1	US-08-348-792-4 Sequence 4, Appli
17	187.5	11.1	298	2	US-08-462-738-4 Sequence 4, Appli
18	187.5	11.1	298	3	US-09-199-955-4 Sequence 4, Appli
19	187.5	11.1	298	3	US-08-880-875-4 Sequence 4, Appli
20	186.5	11.0	343	1	US-08-348-792-10 Sequence 10, Appl
21	186.5	11.0	343	2	US-08-462-738-10 Sequence 10, Appl
22	186.5	11.0	343	3	US-09-199-955-10 Sequence 10, Appl
23	186.5	11.0	343	3	US-08-880-875-10 Sequence 10, Appl
24	173	10.2	305	1	US-08-348-792-6 Sequence 6, Appli
25	173	10.2	305	2	US-08-462-738-6 Sequence 6, Appli
26	173	10.2	305	3	US-09-199-955-6 Sequence 6, Appli
27	173	10.2	305	3	US-08-880-875-6 Sequence 6, Appli

28	166.5	9.8	285	4	US-09-369-248A-2	Sequence 2, Appli
29	165.5	9.8	329	1	US-08-348-792-12	Sequence 12, Appl
30	165.5	9.8	329	2	US-08-462-738-12	Sequence 12, Appl
31	165.5	9.8	329	3	US-09-199-955-12	Sequence 12, Appl
32	165.5	9.8	329	3	US-08-880-875-12	Sequence 12, Appl
33	161	9.5	144	4	US-09-513-999C-4353	Sequence 4353, Ap
34	140.5	8.3	458	4	US-09-435-956A-1	Sequence 1, Appli
35	138	8.1	450	4	US-09-907-794A-320	Sequence 320, App
36	138	8.1	450	4	US-09-905-125A-320	Sequence 320, App
37	138	8.1	450	4	US-09-902-775A-320	Sequence 320, App
38	138	8.1	450	4	US-09-906-700-320	Sequence 320, App
39	138	8.1	450	4	US-09-903-603A-320	Sequence 320, App
40	138	8.1	450	4	US-09-904-920A-320	Sequence 320, App
41	138	8.1	450	4	US-09-909-064-320	Sequence 320, App
42	138	8.1	450	4	US-09-905-381A-320	Sequence 320, App
43	138	8.1	450	4	US-09-906-618-320	Sequence 320, App
44	137.5	8.1	518	4	US-09-919-172-20	Sequence 20, Appl
45	137	8.1	351	3	US-08-466-465-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6428

Query Match	99.9%	Score 1695;	DB 4;	Length 328;
Best Local Similarity	100.0%;	Pred. No. 3.5e-166;		
Matches 328;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAQHLLWILLCLQWPEAGKDS	EFTVNGILGESVTPVNTQEP	ROVKIIAWTSKTSV 60
Db	1	MAQHLLWILLCLQWPEAGKDS	EFTVNGILGESVTPVNTQEP	ROVKIIAWTSKTSV 60
QY	61	AVYTPGDS	ETAPVVTTHRYNRYERIH	ALGPNVNLVSLRMDAGDYKADINTQADPYTT 120
Db	61	AVYTPGDS	ETAPVVTTHRYNRYERIH	ALGPNVNLVSLRMDAGDYKADINTQADPYTT 120
QY	121	TKRYNLQIYRRLGKPKITQSL	MAVSNSTCNVLTCSVEKEEK	NVTNWSPLGSEGNVLOI 180
Db	121	TKRYNLQIYRRLGKPKITQSL	MAVSNSTCNVLTCSVEKEEK	NVTNWSPLGSEGNVLOI 180
QY	181	FQTPEDQELTYTCTAQNPSV	NNSDSISARQLCADIAMG	FTHHTGLLSVLAMFLLVLIL 240
Db	181	FQTPEDQELTYTCTAQNPSV	NNSDSISARQLCADIAMG	FTHHTGLLSVLAMFLLVLIL 240
QY	241	SSVFLFLFKRRDAAASKKTI	YTIYIMASRNTQPAESRI	YDEILQSKVLPKSEKPPVNTVYS 300
Db	241	SSVFLFLFKRRDAAASKKTI	YTIYIMASRNTQPAESRI	YDEILQSKVLPKSEKPPVNTVYS 300
QY	301	EVQFADKMGKASTQDSKPG	CTSSYEIVI 328	

Db 301 EVQFADRMKGKASTQDSKPGTSSVEIVI 328

RESULT 2

US-09-149-476-483

; Sequence 483, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: P2002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; EARLIER APPLICATION NUMBER: FCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,618

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,503

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,592

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,581

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,584

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,500

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,492

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,598

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,613

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,582

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,596

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,612

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,632

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,601

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/043,580

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,568

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,314

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,569

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,311

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,671

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,674

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,669

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,312

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,313

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,672

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,315

; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/048,974

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/056,886

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,877

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,893

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,630

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,878

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,662

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,872

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,882

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,637

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,903

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,888

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,879

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,880

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,894

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,911

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,636

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,874

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,910

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,864

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,631

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,845

; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,892

; EARLIER FILING DATE: 1997-08-22

;; EARLIER APPLICATION NUMBER: 60/057,761
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/047,595
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,599
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,588
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,585
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,586
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,590
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,594
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,589
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,593
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,614
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,578
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,576
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/047,501
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,670
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/056,632
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,664
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,876
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,881
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,909
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,875
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,862
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,887
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,908
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/057,650
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/056,884
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/057,669
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/049,610
;; EARLIER FILING DATE: 1997-06-13
;; EARLIER APPLICATION NUMBER: 60/061,060
;; EARLIER FILING DATE: 1997-10-02

Query Match 99.9%; Score 1695; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.5e-166;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQWTWPEAAAGKDSFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60
Db 1 MAQHLLWILLCLQWTWPEAAAGKDSFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60
QY 61 AYTTPGDSETAPVVTVTHRYNYYERIHAGPNYNLVISDLRMEADAGYKADINTQADPYTT 120
Db 61 AYTTPGDSETAPVVTVTHRYNYYERIHAGPNYNLVISDLRMEADAGYKADINTQADPYTT 120

QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTVYNWSPGEGNVLOI 180
Db 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTVYNWSPGEGNVLOI 180
QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
Db 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
QY 241 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 300
Db 241 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 3

US-09-949-016-7327
; Sequence 7327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7327
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7327

Query Match 99.9%; Score 1695; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.6e-166;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQWTWPEAAAGKDSFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 60
Db 5 MAQHLLWILLCLQWTWPEAAAGKDSFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSV 64
QY 61 AYTTPGDSETAPVVTVTHRYNYYERIHAGPNYNLVISDLRMEADAGYKADINTQADPYTT 120
Db 65 AYTTPGDSETAPVVTVTHRYNYYERIHAGPNYNLVISDLRMEADAGYKADINTQADPYTT 124
QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTVYNWSPGEGNVLOI 180
Db 125 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTVYNWSPGEGNVLOI 184
QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
Db 185 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 244
QY 241 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 300
Db 245 SSVFLFLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSPKEPNTVYS 304
QY 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 305 EVQFADKMGKASTQDSKPPGTSSYEIVI 332

RESULT 4

US-09-949-016-6907

```
; Sequence 6907, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6907
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6907

Query Match      13.4%; Score 227; DB 4; Length 365;
Best Local Similarity 23.6%; Pred. No. 1e-14;
Matches 85; Conservative 65; Mismatches 142; Indels 68; Gaps 15;

Qy 8 ILLCLQW--PEAGKDSIFTVNGILGESVTPVNIQEQ---PROVKIIAW-----TSKT 58
Db 9 ILLLLKVVYQKCGSGADHVVISGV-----PLQLPNSIQTKVDSIAWKLLPSQN 61
Qy 59 SVAVYTPGDSAPVTVTHRYERIHAGNPNVNLVSLRMDAGDYKADINTQADPY 118
Db 62 GFHILKWENGLSPNTSN-----DRFSFIVKNSLLIKAAQOQDSGLYCLEV-TSISGK 115
Qy 119 TTKRYNLQIYRRLGKPKITQSLMASVNSTCNVLTCTSCVEKEKNVTYNW---SPLGEE 174
Db 116 VQTATFQVFDKVEKPRLOQGGKILDRGCOVALSCLVSR-DGNVSYAWYRGSKLIQTA 174
Qy 175 GNVLQIFQTPEDQEL-----TYTCTAQNPNVNSNDSISARQLCADIAMGFRTHHTGLLS 228
Db 175 GNLTYL-----DEVDINGTHTYTCNVSNPVSWESHTLNLTQDCQNAHQEFR----- 221
Qy 229 VLAMFLLVLILSSVFLRFLP-----KRRQDAASK--TIYTVI--MASRNTQPA 274
Db 222 -FWPFLVIIVLSALFLGTACFCVWRRKRKEKQSETSPKEFLTIEDVKDKLTKRNHEQ 280
Qy 275 E-----SRIYDEILQSKVLPSKEEPPVNTVYSEVQADKMGKASTQDKPKPGTSSYEV 327
Db 281 EQTFPGGSGTYSMIQSSSAPTSQEPAYTLYSLIQSRKSGSRKRNHSPSFNSTIYEV 340

RESULT 5
US-09-949-016-7325
; Sequence 7325, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7325
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7325

Query Match      13.4%; Score 227; DB 4; Length 391;
Best Local Similarity 23.6%; Pred. No. 1e-14;
Matches 85; Conservative 65; Mismatches 142; Indels 68; Gaps 15;

Qy 8 ILLCLQW--PEAGKDSIFTVNGILGESVTPVNIQEQ---PROVKIIAW-----TSKT 58
Db 35 ILLLLKVVYQKCGSGADHVVISGV-----PLQLPNSIQTKVDSIAWKLLPSQN 87
Qy 59 SVAVYTPGDSAPVTVTHRYERIHAGNPNVNLVSLRMDAGDYKADINTQADPY 118
Db 88 GFHILKWENGLSPNTSN-----DRFSFIVKNSLLIKAAQOQDSGLYCLEV-TSISGK 141
Qy 119 TTKRYNLQIYRRLGKPKITQSLMASVNSTCNVLTCTSCVEKEKNVTYNW---SPLGEE 174
Db 142 VQTATFQVFDKVEKPRLOQGGKILDRGCOVALSCLVSR-DGNVSYAWYRGSKLIQTA 200
Qy 175 GNVLQIFQTPEDQEL-----TYTCTAQNPNVNSNDSISARQLCADIAMGFRTHHTGLLS 228
Db 201 GNLTYL-----DEVDINGTHTYTCNVSNPVSWESHTLNLTQDCQNAHQEFR----- 247
Qy 229 VLAMFLLVLILSSVFLRFLP-----KRRQDAASK--TIYTVI--MASRNTQPA 274
Db 248 -FWPFLVIIVLSALFLGTACFCVWRRKRKEKQSETSPKEFLTIEDVKDKLTKRNHEQ 306
Qy 275 E-----SRIYDEILQSKVLPSKEEPPVNTVYSEVQADKMGKASTQDKPKPGTSSYEV 327
Db 307 EQTFPGGSGTYSMIQSSSAPTSQEPAYTLYSLIQSRKSGSRKRNHSPSFNSTIYEV 366

RESULT 6
US-08-348-792-8
; Sequence 8, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```



```

; MOLECULE TYPE: protein
US-08-348-792-8

Query Match      11.4%; Score 194; DB 1; Length 307;
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

QY 33 LGESTVTFP-----VNIQEPQVKIIATWSKT-----SVAVYTPGDSSTAPVVTVTHRN 80
DB 11 LGSKVLLPLTYBRINKSMNKSIIHVVTWAKSLSENSVENKIVSLDPSEAGPPRYLGDRIKF 70
QY 81 YVERIHALGPNVNLVSLDRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKKIT 138
DB 71 YLE-----NUTLGIRESRKEDEGWYMTL-----EKNVSVQVFCQLRLYEQVSTPEIK 119
QY 139 QSLMASVNSTCMTVITCSVEKEEKVNTYNS-----PL--GEGNVLOIFOTPEDELT 190
DB 120 VLNKQENGCTLLILGCTVEKGD-HVAYSWSKAGTHPLNPANSSHLLSLTLGPQHADNI 178
QY 191 YTCTAQNPNVNSDSISARQLCADIAMGPRTH-----HTGLLSVLAMFLLVLILS 241
DB 179 YICTVSNPISNNSQTFSPWPGC-----RTPSETKPMWVYAGLGGVIMILIMVILQ 231
QY 242 SVFLRFLFKRR-----QDAASKTIYTYIMASR-----NTOPAE---SRIYDEILQ 284
DB 232 -----LRRGKTNHYQTTVEKKSITIYAQVKPGPLQKLDSPAPDPCCTIY--VAA 282
QY 285 SKVLPKSEEPVN--TVYSEV 302
DB 283 TEPVPESVQETNSITVYASV 302
```

```

RESULT 7
US-08-462-738-8
; Sequence 8, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; NUMBER OF INVENTIONS: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-738-8

Query Match      11.4%; Score 194; DB 2; Length 307;
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

QY 33 LGESTVTFP-----VNIQEPQVKIIATWSKT-----SVAVYTPGDSSTAPVVTVTHRN 80
DB 11 LGSKVLLPLTYBRINKSMNKSIIHVVTWAKSLSENSVENKIVSLDPSEAGPPRYLGDRIKF 70
QY 81 YVERIHALGPNVNLVSLDRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKKIT 138
DB 71 YLE-----NUTLGIRESRKEDEGWYMTL-----EKNVSVQVFCQLRLYEQVSTPEIK 119
QY 139 QSLMASVNSTCMTVITCSVEKEEKVNTYNS-----PL--GEGNVLOIFOTPEDELT 190
DB 120 VLNKQENGCTLLILGCTVEKGD-HVAYSWSKAGTHPLNPANSSHLLSLTLGPQHADNI 178
QY 191 YTCTAQNPNVNSDSISARQLCADIAMGPRTH-----HTGLLSVLAMFLLVLILS 241
DB 179 YICTVSNPISNNSQTFSPWPGC-----RTPSETKPMWVYAGLGGVIMILIMVILQ 231
QY 242 SVFLRFLFKRR-----QDAASKTIYTYIMASR-----NTOPAE---SRIYDEILQ 284
DB 232 -----LRRGKTNHYQTTVEKKSITIYAQVKPGPLQKLDSPAPDPCCTIY--VAA 282
QY 285 SKVLPKSEEPVN--TVYSEV 302
DB 283 TEPVPESVQETNSITVYASV 302
```

```

RESULT 8
US-09-199-955-8
; Sequence 8, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; NUMBER OF INVENTIONS: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,473
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
```

```

; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-199-955-8

Query Match 11.4%; Score 194; DB 3; Length 307;
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

Qy 33 LGESVTFP-----VNIQEPQVKIIAWTSKT-----SVAYVTPGDSAPVVTVTHRN 80
Db 11 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDYKF 70
Qy 81 YYERIHAGPNYNIIVISDLRMDAGDYKADINTQADPVTTKRYNLO--IYRRLGPKKIT 138
Db 71 YLE-----NLTGIRSRKDEGWYMTL-----EKNVSQVRFCLQLRYEQVSTPEIK 119
Qy 139 QSLMASVNSTCNVTLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 190
Db 120 VLNKTQENGCTLILGCTVEKGD-HVAYSWEKAGTHPLNPANGSHLLSLTLGPHADNI 178
Qy 191 YTCTAQNPNVNSDISARQICADIAMGRTH-----HTGLLSVLAMFFLLVLILS 241
Db 179 YICTVSNPISNNSQTFSPWPGC-----RTDPSKTPWAVYAGLLGVIMILIMVILQ 231
Qy 242 SVFLFRLFKR-----ODAASKTIYTYIMASR-----NTQPAB---SRIYDEILQ 284
Db 232 -----LRRGKTNHYQTTVEKKSLLTYAQVQKPGPLQKLDSPADPCCTIY--VAA 282
Qy 285 SKVLPSKEEPPV--TVYSEV 302
Db 283 TEPVPSVQETNSITVYASV 302

RESULT 9
US-08-880-875-8
; Sequence 8, Application US/08880875
; Patent No. 6399065
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,777
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.

; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-199-955-8

Query Match 11.4%; Score 194; DB 3; Length 307;
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

Qy 33 LGESVTFP-----VNIQEPQVKIIAWTSKT-----SVAYVTPGDSAPVVTVTHRN 80
Db 11 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDYKF 70
Qy 81 YYERIHAGPNYNIIVISDLRMDAGDYKADINTQADPVTTKRYNLO--IYRRLGPKKIT 138
Db 71 YLE-----NLTGIRSRKDEGWYMTL-----EKNVSQVRFCLQLRYEQVSTPEIK 119
Qy 139 QSLMASVNSTCNVTLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 190
Db 120 VLNKTQENGCTLILGCTVEKGD-HVAYSWEKAGTHPLNPANGSHLLSLTLGPHADNI 178
Qy 191 YTCTAQNPNVNSDISARQICADIAMGRTH-----HTGLLSVLAMFFLLVLILS 241
Db 179 YICTVSNPISNNSQTFSPWPGC-----RTDPSKTPWAVYAGLLGVIMILIMVILQ 231
Qy 242 SVFLFRLFKR-----ODAASKTIYTYIMASR-----NTQPAB---SRIYDEILQ 284
Db 232 -----LRRGKTNHYQTTVEKKSLLTYAQVQKPGPLQKLDSPADPCCTIY--VAA 282
Qy 285 SKVLPSKEEPPV--TVYSEV 302
Db 283 TEPVPSVQETNSITVYASV 302

RESULT 10
US-08-348-792-2
; Sequence 2, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
```

REFERENCE/DOCKET NUMBER: DX0436
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-792-2

Query Match 11.4%; Score 194; DB 1; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;
QY 33 LGESVTFP-----VNTQEPQVKIIAWTSKT-----SVAYVTPGDSAPVVTVTHRN 80
DB 39 LGSKVLLPLTYERINKSMNKSIHVVMTAKSLSENSVENKIVSLDPSEAGPPRYLGDYK 98
QY 81 YIERHALGPNVNLVSLRMEADAGYKADINTQADPYTTTKRYNLQ--LYRRLGPKKIT 138
DB 99 YLE-----NLTLGIRSRKDEGWYMTL-----EKNVSVQRFCLRLYEQVSTPEIK 147
QY 139 QSLMASVNSTCNVLTCSVEKEKNVTYNWS-----PL--GEEGNVLQIFOTPEDELT 190
DB 148 VLNKTEGTCITLIGCTVEKGD-HVAYSSEKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 191 YTCTAQNPNVNSDSISARQLCADIAMGRTH-----HTGLLSVLAMFLLVLIIS 241
DB 207 YICTVSNPISSNQTSPWPGC-----RTDPSEKPAWVAGLGGVIMILIMVILQ 259
QY 242 SVFLFLFKR-----QDAASKTIYTIMASR-----NTQPAE---SRIYDEILQ 284
DB 260 -----LRRGKTNHYQTVEKSLTIYAQVQKPLQKLDSPFAQDPCTTIY--VAA 310
QY 285 SKVLPSKEEPPVN--TVYSEV 302
DB 311 TEPVPESVQETNSITVYASV 330

RESULT 11
US-08-462-738-2
Sequence 2, Application US/08462738
Patent No. 5977303
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-738-2
Query Match 11.4%; Score 194; DB 2; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;
QY 33 LGESVTFP-----VNTQEPQVKIIAWTSKT-----SVAYVTPGDSAPVVTVTHRN 80
DB 39 LGSKVLLPLTYERINKSMNKSIHVVMTAKSLSENSVENKIVSLDPSEAGPPRYLGDYK 98
QY 81 YIERHALGPNVNLVSLRMEADAGYKADINTQADPYTTTKRYNLQ--LYRRLGPKKIT 138
DB 99 YLE-----NLTLGIRSRKDEGWYMTL-----EKNVSVQRFCLRLYEQVSTPEIK 147
QY 139 QSLMASVNSTCNVLTCSVEKEKNVTYNWS-----PL--GEEGNVLQIFOTPEDELT 190
DB 148 VLNKTEGTCITLIGCTVEKGD-HVAYSSEKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 191 YTCTAQNPNVNSDSISARQLCADIAMGRTH-----HTGLLSVLAMFLLVLIIS 241
DB 207 YICTVSNPISSNQTSPWPGC-----RTDPSEKPAWVAGLGGVIMILIMVILQ 259
QY 242 SVFLFLFKR-----QDAASKTIYTIMASR-----NTQPAE---SRIYDEILQ 284
DB 260 -----LRRGKTNHYQTVEKSLTIYAQVQKPLQKLDSPFAQDPCTTIY--VAA 310
QY 285 SKVLPSKEEPPVN--TVYSEV 302
DB 311 TEPVPESVQETNSITVYASV 330

RESULT 12
US-09-199-955-2
Sequence 2, Application US/09199955
Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473

```

;
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-199-955-2

Query Match 11.4%; Score 194; DB 3; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

QY 33 LGESVTFP-----VNIQEPQVKKIIAWTSKT-----SVAYVTPGDSETPAPVVTVTHRN 80
DB 39 LGSKVLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSSEAGPPRYLGDYKF 98
QY 81 YIERIHALGPNVNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQ--IYRLGKPKIT 138
DB 99 YLE-----NLTGIRESRKDEGWYMTL-----EKNVSVQRFCLQLRLYEQVSTPEIK 147
QY 139 QSLMASVNSTCNVTLTCSVEKEEKVNTYNS-----PL--GEEGNVLIQFQTPDEQLT 190
DB 148 VLNTQENGTCITLIGCTVEKGD--HVAYSWSEKAGTHPLNPANSHLLSLTLTGPHADNI 206
QY 191 YTCTAQNPVNSDSISARQLCADIAMGFRTH-----HTGLLSVLAFFLLVLILS 241
DB 207 YICTVSNPISNSQTFSPWPGC-----RTDPSEKPAWVYAGLLGGVIMILIMVILQ 259
QY 242 SVFLRFLFKR-----QDAASKKIITYYIMASR-----NTQPAE---SRIYDEILQ 284
DB 260 -----LRRGKTNHYQTTVEKSLTIYAQVKPGLQKLDSPFADQDCTTIY--VAA 310
QY 285 SKVLPSKEEPPVN--TVYSEV 302
DB 311 TEPVPESVQETNSITVYASV 330

RESULT 13
US-08-880-875-2
; Sequence 2, Application US/08880875
; Patent No. 6399065
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875

;
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-199-955-2

Query Match 11.4%; Score 194; DB 3; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

QY 33 LGESVTFP-----VNIQEPQVKKIIAWTSKT-----SVAYVTPGDSETPAPVVTVTHRN 80
DB 39 LGSKVLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSSEAGPPRYLGDYKF 98
QY 81 YIERIHALGPNVNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQ--IYRLGKPKIT 138
DB 99 YLE-----NLTGIRESRKDEGWYMTL-----EKNVSVQRFCLQLRLYEQVSTPEIK 147
QY 139 QSLMASVNSTCNVTLTCSVEKEEKVNTYNS-----PL--GEEGNVLIQFQTPDEQLT 190
DB 148 VLNTQENGTCITLIGCTVEKGD--HVAYSWSEKAGTHPLNPANSHLLSLTLTGPHADNI 206
QY 191 YTCTAQNPVNSDSISARQLCADIAMGFRTH-----HTGLLSVLAFFLLVLILS 241
DB 207 YICTVSNPISNSQTFSPWPGC-----RTDPSEKPAWVYAGLLGGVIMILIMVILQ 259
QY 242 SVFLRFLFKR-----QDAASKKIITYYIMASR-----NTQPAE---SRIYDEILQ 284
DB 260 -----LRRGKTNHYQTTVEKSLTIYAQVKPGLQKLDSPFADQDCTTIY--VAA 310
QY 285 SKVLPSKEEPPVN--TVYSEV 302
DB 311 TEPVPESVQETNSITVYASV 330

RESULT 14
US-09-369-248A-3
; Sequence 3, Application US/09369248A
; Patent No. 6620912
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation
; TITLE OF INVENTION: Molecule
; FILE REFERENCE: PF448P1
; CURRENT APPLICATION NUMBER: US/09/369,248A
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/073,962
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 60/078,572
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-09-369-248A-3:
Query Match      11.4%; Score 194; DB 4; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels 78; Gaps 16;

QY 33 LGESVTFF-----VNIQEPQVKIATWTSK-----SVAVTPGDSAPVVTVTHRN 80
DB 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVLSDSEAGPPYILGDRYKF 98
QY 81 YVERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
DB 99 YLE-----NLTLGIRSKEDGWLMTL---EKNVSQRFCLQLRLYEQVSTPEIK 147
QY 139 QSLMASVNSTCNVTLTCSVEKEKNVTYWS-----PL--GEEGNVLOIFQTPDOELT 190
DB 148 VLNKTOENGCTCTILGCTVEKGD-HVAYSWSKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 191 YCTAONPVSNNSDSISARQLCADIAMGRTH-----HTGLLSVLAMFFLLVLILS 241
DB 207 YICTVSNPISSNSQTFSPWPGC-----RTDPSKPMWAVAGLLGGVIMILIWVILQ 259
QY 242 SVFLPLFKRR-----QDAASKTIYTYIMASR-----NTQPAE---SRIYDEILQ 284
DB 260 -----LRRGKTNHYQTVTEKKSITIYAQVQKPGLOKCLDSFPAQDPCTIY--VAA 310
QY 285 SKVLPSKEPYN--TYSEV 302
DB 311 TEPVPESVQETNSITVYASV 330

RESULT 15
US-09-227-357-192
; Sequence 192, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 192
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (92)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-227-357-192

Query Match      11.4%; Score 193; DB 3; Length 143;
Best Local Similarity 32.6%; Pred. No. 7.3e-12;
Matches 44; Conservative 28; Mismatches 51; Indels 12; Gaps 2;

QY 7 WILLICL-----QWPEAAGKDSIFTVNGILGESVTFPPVNIQEPQVKIATWTSKTS 59
DB 6 WLLLLLQEGSQRRRLRWCGSEE-----VVAVLQESISLFLPEIPDDEEVENIWSHKS 60
QY 60 VAVVTPGDSAPVVTVTHRNYYVERIHALGPNYNLVISDLRMDAGDYKADINTQADPYT 119
DB 61 LATVVPKEGHGHPATVWTPNPHYQGVSFDPDXYSLSHLSNLWSWEDSGLYQAQVNLRTSQIS 120
QY 120 TTKRYNLQIYRRLGK 134
DB 121 TMOQYNLCVYRWLSE 135
```

Search completed: February 4, 2005, 12:17:03
Job time : 39.0095 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 12:15:12 ; Search time 108.42 Seconds
(without alignments)
986.338 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQTWPEAA.....KASTQDSKPGTSSYEIVIX 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	99.9	328	14	US-10-104-943-4
2	1695	99.9	328	14	US-10-436-523-30
3	1695	99.9	329	10	US-09-809-191-483
4	1695	99.9	329	10	US-09-882-171-483
5	1695	99.9	329	15	US-10-164-861-483
6	382.5	22.6	551	15	US-10-471-449-8
7	382.5	22.6	610	10	US-09-860-836B-11
8	374	22.1	654	14	US-10-104-943-7
9	374	22.1	654	16	US-10-310-612-2
10	374	22.1	654	16	US-10-328-538-2
11	373	22.0	289	14	US-10-220-946-18
12	373	22.0	289	14	US-10-436-523-76
13	373	22.0	289	15	US-10-170-385-131
					Sequence 4, Appli
					Sequence 30, Appl
					Sequence 483, App
					Sequence 483, App
					Sequence 483, App
					Sequence 8, Appli
					Sequence 11, Appl
					Sequence 7, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 18, Appl
					Sequence 76, Appl
					Sequence 131, App

14	370	21.8	289	14	US-10-436-523-88	Sequence 88, Appl
15	370	21.8	289	14	US-10-436-523-89	Sequence 89, Appl
16	370	21.8	289	14	US-10-436-523-90	Sequence 90, Appl
17	369	21.8	289	14	US-10-436-523-91	Sequence 91, Appl
18	367	21.6	285	14	US-10-436-523-100	Sequence 100, App
19	363.5	21.4	346	15	US-10-257-174-33	Sequence 33, Appl
20	363.5	21.4	335	9	US-09-732-524-2	Sequence 2, Appli
21	362.5	21.4	335	9	US-09-989-722-253	Sequence 253, App
22	362.5	21.4	335	9	US-09-989-723-253	Sequence 253, App
23	362.5	21.4	335	9	US-09-989-729-253	Sequence 253, App
24	362.5	21.4	335	9	US-09-989-727-253	Sequence 253, App
25	362.5	21.4	335	9	US-09-989-731-253	Sequence 253, App
26	362.5	21.4	335	9	US-09-989-732-253	Sequence 253, App
27	362.5	21.4	335	9	US-09-745-605-4	Sequence 4, Appli
28	362.5	21.4	335	9	US-09-991-073-253	Sequence 253, App
29	362.5	21.4	335	9	US-09-990-442-253	Sequence 253, App
30	362.5	21.4	335	9	US-09-991-163-253	Sequence 253, App
31	362.5	21.4	335	9	US-09-993-604-253	Sequence 253, App
32	362.5	21.4	335	9	US-09-990-456-253	Sequence 253, App
33	362.5	21.4	335	9	US-09-989-721-253	Sequence 253, App
34	362.5	21.4	335	9	US-09-992-598-253	Sequence 253, App
35	362.5	21.4	335	9	US-09-989-293A-253	Sequence 253, App
36	362.5	21.4	335	9	US-09-989-735-253	Sequence 253, App
37	362.5	21.4	335	9	US-09-990-444-253	Sequence 253, App
38	362.5	21.4	335	9	US-09-991-181-253	Sequence 253, App
39	362.5	21.4	335	9	US-09-989-730-253	Sequence 253, App
40	362.5	21.4	335	9	US-09-990-436-253	Sequence 253, App
41	362.5	21.4	335	9	US-09-993-687-253	Sequence 253, App
42	362.5	21.4	335	10	US-09-989-734-253	Sequence 253, App
43	362.5	21.4	335	10	US-09-997-653-253	Sequence 253, App
44	362.5	21.4	335	10	US-09-989-724-253	Sequence 253, App
45	362.5	21.4	335	10	US-09-989-728-253	Sequence 253, App

ALIGNMENTS

RESULT 1

US-10-104-943-4
; Sequence 4, Application US/10104943
; Publication No. US20030092017A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL IMMUNOGLOBULIN SUPERFAMILY MEMBE
; TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0135 NP
; CURRENT APPLICATION NUMBER: US/10/104,943
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,037
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/281,223
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-943-4

Query Match	99.9%	Score 1695;	DB 14;	Length 328;
Best Local Similarity	100.0%	Pred. No. 2e-144;		
Matches 328;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MAQHLLWILLCLQTWPEAAKDSEIFTVNGILGESVTPVNIQEPQVKIIAWTSTSV	60	
Db	1	MAQHLLWILLCLQTWPEAAKDSEIFTVNGILGESVTPVNIQEPQVKIIAWTSTSV	60	
QY	61	AYVTPGDSAPVVTTHRYERIHALGNVNLVSLRMEADAGYKADINTQADPYTT	120	
Db	61	AYVTPGDSAPVVTTHRYERIHALGNVNLVSLRMEADAGYKADINTQADPYTT	120	
QY	121	TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEKKNVTYNNWSPLGEGNVLQI	180	

Db 121 TKRYNLQIYRRLGPKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQI 180
Qy 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Db 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Qy 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Db 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Qy 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 2
US-10-436-523-30
; Sequence 30, Application US/10436523
; Publication No. US20030180988A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 30
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-30

Query Match 99.9%; Score 1695; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 2e-144;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQHLLWILLCLQTPWPEAAAGKDSIEFTVNGILGESVTFPVNIQEPQVQKIIAWTSKTSV 60
Db 1 MAQHLLWILLCLQTPWPEAAAGKDSIEFTVNGILGESVTFPVNIQEPQVQKIIAWTSKTSV 60
Qy 61 AYVTPGDSCTAPVVTVTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
Db 61 AYVTPGDSCTAPVVTVTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
Qy 121 TKRYNLQIYRRLGPKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQI 180
Db 121 TKRYNLQIYRRLGPKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQI 180
Qy 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Db 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Qy 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Db 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Qy 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 3
US-09-809-391-483
; Sequence 483, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 483
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-483

Query Match 99.9%; Score 1695; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.1e-144;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQHLLWILLCLQTPWPEAAAGKDSIEFTVNGILGESVTFPVNIQEPQVQKIIAWTSKTSV 60
Db 1 MAQHLLWILLCLQTPWPEAAAGKDSIEFTVNGILGESVTFPVNIQEPQVQKIIAWTSKTSV 60
Qy 61 AYVTPGDSCTAPVVTVTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
Db 61 AYVTPGDSCTAPVVTVTHRYNRYERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
Qy 121 TKRYNLQIYRRLGPKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQI 180
Db 121 TKRYNLQIYRRLGPKITQSLMASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQI 180
Qy 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Db 181 FQTPEDQELTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFLLVLIL 240
Qy 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Db 241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILOSKVLPSKEEPPVNTVYS 300
Qy 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328
Db 301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

RESULT 4
US-09-882-171-483
; Sequence 483, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336

Mon Feb 7 10:55:04 2005

[illegible]

```
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
```

```
Query Match          99.9%; Score 1695; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.1e-144;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAQHLLWILLCLQWPEAAGKDSIFVTNGILGESVTFPPVNIQBPQVQKIIAMTSKTSV 60
DB 1 MAQHLLWILLCLQWPEAAGKDSIFVTNGILGESVTFPPVNIQBPQVQKIIAMTSKTSV 60

QY 61 AYVTPGDSAPVVTTHRYNRYERIHALGPNYLVISDLRMDAGDYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVVTTHRYNRYERIHALGPNYLVISDLRMDAGDYKADINTQADPYTT 120

QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTYNNWSPGLGEGNVLOI 180
DB 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTYNNWSPGLGEGNVLOI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240

QY 241 SSVFLFRLPKRRQDAASKKTIYTIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS 300
DB 241 SSVFLFRLPKRRQDAASKKTIYTIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS 300

QY 301 EVQFADKMGKASTQDSKPGTSSYEIVI 328
DB 301 EVQFADKMGKASTQDSKPGTSSYEIVI 328
```

```
RESULT 5
US-10-164-861-483
; Sequence 483, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
```

```
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 483
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-483
```

```
Query Match          99.9%; Score 1695; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.1e-144;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQWPEAAGKDSIFVTNGILGESVTFPPVNIQBPQVQKIIAMTSKTSV 60
DB 1 MAQHLLWILLCLQWPEAAGKDSIFVTNGILGESVTFPPVNIQBPQVQKIIAMTSKTSV 60

QY 61 AYVTPGDSAPVVTTHRYNRYERIHALGPNYLVISDLRMDAGDYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVVTTHRYNRYERIHALGPNYLVISDLRMDAGDYKADINTQADPYTT 120

QY 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTYNNWSPGLGEGNVLOI 180
DB 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEEKNTYNNWSPGLGEGNVLOI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240

QY 241 SSVFLFRLPKRRQDAASKKTIYTIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS 300
DB 241 SSVFLFRLPKRRQDAASKKTIYTIMASRNTQPAESRIYDEILQSKVLPKEEPVNTVYS 300

QY 301 EVQFADKMGKASTQDSKPGTSSYEIVI 328
DB 301 EVQFADKMGKASTQDSKPGTSSYEIVI 328
```

```
RESULT 6
US-10-471-449-8
; Sequence 8, Application US/10471449
; Publication No. US2004009771A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry; XU, Yuming;
; APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
; APPLICANT: TANG, Y. Tom; DUGGAN, Brendan M.;
; APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
; APPLICANT: HONCHELL, Cynthia D.; BURFORD, Neil;
; APPLICANT: FORSYTHE, Ian J.; YANG, Juming;
; APPLICANT: MASON, Patricia M.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0925 USN
; CURRENT APPLICATION NUMBER: US/10/471,449
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US02/09052
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/275,249
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/316,810
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/323,977
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/348,447
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/343,880
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 551
```

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7500099CD1
US-10-471-449-8

Query Match 22.6%; Score 382.5; DB 15; Length 551;
Best Local Similarity 33.9%; Pred. No. 1.3e-25;
Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 33 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 88
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 89 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 143
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 174
Db 144 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 203
Qy 175 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 231
Db 204 GSILTVSRTPCDPLPYICTAQNVPVSQRSSLPVHVGFQCTDPCASRGGTGTGET-VVGVLG 262
Qy 232 MFLLVLILSS-----VFLFR---LFKRRQDAASKTIITYIMASRNTQPAESRIY 279
Db 263 EPVTLPLALPACRDTKRVWLFNTSIISKEREAAADPLI-----KSRDPYKNRVW 314

RESULT 7
US-09-860-836B-11
Query Match 22.6%; Score 382.5; DB 10; Length 610;
Best Local Similarity 33.9%; Pred. No. 1.5e-25;
Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 2 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 57
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 58 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 112
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 174
Db 113 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 172
Qy 175 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 231

Query Match 22.6%; Score 382.5; DB 10; Length 610;
Best Local Similarity 33.9%; Pred. No. 1.5e-25;
Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 2 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 57
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 58 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 112
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 174
Db 113 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 172
Qy 175 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 231

Db 173 GSILTVSRTPCDPLPYICTAQNVPVSQRSSLPVHVGFQCTDPCASRGGTGTGET-VVGVLG 231
Qy 232 MFLLVLILSS-----VFLFR---LFKRRQDAASKTIITYIMASRNTQPAESRIY 279
Db 232 EPVTLPLALPACRDTKRVWLFNTSIISKEREAAADPLI-----KSRDPYKNRVW 283

RESULT 8
US-10-104-943-7
Query Match 22.1%; Score 374; DB 14; Length 654;
Best Local Similarity 33.0%; Pred. No. 9.9e-25;
Matches 98; Conservative 59; Mismatches 104; Indels 36; Gaps 10;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 33 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 88
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 89 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 143
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 175
Db 144 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 203
Qy 176 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 232
Db 204 GSILTVSRTPCDPLPYICTAQNVPVSQRSSLPVHVGFQCTDPCASRGGTGTGET-VVGVLG 262
Qy 233 PFLLVLILSS-----VFLFR---LFKRRQDAASKTIITYIMASRNTQPAESRIY 279
Db 263 EPVTLPLALPACRDTKRVWLFNTSIISKEREAAADPLI-----KSRDPYKNRVW 313

Query Match 22.1%; Score 374; DB 14; Length 654;
Best Local Similarity 33.0%; Pred. No. 9.9e-25;
Matches 98; Conservative 59; Mismatches 104; Indels 36; Gaps 10;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 33 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 88
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 89 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 143
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 175
Db 144 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 203
Qy 176 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 232
Db 204 GSILTVSRTPCDPLPYICTAQNVPVSQRSSLPVHVGFQCTDPCASRGGTGTGET-VVGVLG 262
Qy 233 PFLLVLILSS-----VFLFR---LFKRRQDAASKTIITYIMASRNTQPAESRIY 279
Db 263 EPVTLPLALPACRDTKRVWLFNTSIISKEREAAADPLI-----KSRDPYKNRVW 313

RESULT 9
US-10-310-612-2
Query Match 22.1%; Score 374; DB 14; Length 654;
Best Local Similarity 33.0%; Pred. No. 9.9e-25;
Matches 98; Conservative 59; Mismatches 104; Indels 36; Gaps 10;

Qy 3 QHLLWILLCLQWPEAAGKSEIFTVNGILGESVTFPVNIQEPQVQKIIA WTS-KTSVA 61
Db 33 QTSLLFLMLGLR-----ASGKDSAPTVVSGILGSGVTLPLNISVDTEIENVIWGPKNALA 88
Qy 62 YVTPGDSAPVTVTHRYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTT 121
Db 89 FARPKEN-----VTIMVKSYLGRDLITKWSYSLCISNLTLDNDAGSYKAQINQNFVTTT 143
Qy 122 KRYNLOIYRRLGPKKIT-QSLMASVNSTCNVTLTCSVEKEEKVNTYNSPL-----GEE 175
Db 144 EFTLVFVYEQLEQPOVTMKSVMKSVKSENFCNITLMCSVKAESVLYSWTPREP HASESNG 203
Qy 176 GNVLIQIFQTPEDQELTYTCTAQNVPVNSND-SISARQLCAD--IANGFRTHHTGLLSVLA 232
Db 204 GSILTVSRTPCDPLPYICTAQNVPVSQRSSLPVHVGFQCTDPCASRGGTGTGET-VVGVLG 262
Qy 233 PFLLVLILSS-----VFLFR---LFKRRQDAASKTIITYIMASRNTQPAESRIY 279
Db 263 EPVTLPLALPACRDTKRVWLFNTSIISKEREAAADPLI-----KSRDPYKNRVW 313

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 12:03:57 ; Search time 31.7784 Seconds
(without alignments)
996.126 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQTPWAAA.....KASTQDSKPPGTSSYEIVIX 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	19.8	629	A46500	Ly-9.2 antigen - m
2	194	11.4	335	S58832	signaling lymphocy
3	180	10.6	240	S01299	OK-45 membrane gly
4	179.5	10.6	240	JL0143	antigen BCM1 precu
5	164	9.7	398	J49443	gene 2B4 protein -
6	143.5	8.5	521	S34338	biliary glycoprote
7	142.5	8.4	458	1 WMSR1	biliary glycoprote
8	142.5	8.4	521	JC1508	biliary glycoprote
9	141.5	8.3	347	S41638	T-cell surface gly
10	139.5	8.2	458	JC1509	biliary glycoprote
11	137.5	8.1	518	JC4024	poliovirus recepto
12	137	8.1	351	1 RWHUC2	T-cell surface gly
13	135.5	8.0	702	A36319	carcinoembryonic a
14	134.5	7.9	417	1 RWHUPA	poliovirus recepto
15	131.5	7.8	344	A27681	nonspecific cross-
16	127.5	7.5	344	B28967	T-cell surface gly
17	127.5	7.5	392	1 RWHUPD	poliovirus recepto
18	125	7.4	338	JC4776	limbic-system-asso
19	124.5	7.3	519	A44783	ecto-ATPase precu
20	123.5	7.3	417	A44194	poliovirus recepto
21	122.5	7.2	321	JH0395	biliary glycoprote
22	122.5	7.2	351	JH0396	biliary glycoprote
23	122.5	7.2	417	JH0394	biliary glycoprote
24	122.5	7.2	464	2 C30127	transmembrane carc
25	122.5	7.2	526	1 A32164	biliary glycoprote
26	121.5	7.2	338	2 JC1238	opioid-binding pro
27	121.5	7.2	344	2 J49585	CD2 antigen protei
28	121.5	7.2	345	2 S03199	opioid-binding pro
29	121.5	7.2	345	2 JC1239	opioid-binding pro

ALIGNMENTS

RESULT 1

A46500

Ly-9.2 antigen - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A46500

R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.

J. Immunol. 149, 1636-1641, 1992

A;Title: Isolation and characterization of cDNA clones for mouse Ly-9.

A;Reference number: A46500; MUID:92373005; PMID:1506686

A;Accession: A46500

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-629 <S>

A;Cross-references: GB:M84412; NID:gl98931; PIDN:AAA39468.1; PID:gl98932

A;Experimental source: C57BL/6

A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)

C;Keywords: transmembrane protein

Query Match 19.8%; Score 336; DB 2; Length 629;

Best Local Similarity 24.7%; Pred. No. 3.4e-19;

Matches 100; Conservative 55; Mismatches 136; Indels 114; Gaps 7;

QY	19	AAGKGSEIFTVNGILGESVTFPVNIQBPQVKIIAMTSTKTSVAYVTPGDSETAPVVTWTH	78
DB	230	AAGK-----TVGILGEPTVLPLEFRATRAKNNVWVNLNTSVISQERRGAATADSRKPK	284
QY	79	RNYIERIHALGPNYNLIVSLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGKPKIT	138
DB	285	GSEERRVTSDDQSLKISQLKMDAGPVHAYVCSEASRDPVSRHFHTLLVYKRLEKPSVT	344
QY	139	QSLMASVNSTCNTLTCSVEKEKNYTNWSPIGEES-----NVLIQIFQTPEDQELTYT	192
DB	345	KSPVHMNGICEVVLTCSDVGGNNVTYTWPLQNKAVMSQGKSHLNVSWESGHLNFT	404
QY	193	CTAQNPNVNSDSISARQLCADIAMGPRHTHTGLLSVLAMFFLLVILSSVFLRFLKR-	251
DB	405	CTAHNPVNSNSSQFSSGTCISGPE---RNKRFWLLLLLVL---LLLMLIGGYFILRKKQC	459
QY	252	-----RODAASKTIYTYMAS-----	268
DB	460	SSLATRYRAEVPFAEIPPTGHHQGFVLSQRYEKLDMSAKTRRHQPTPTSDTSESSAT	519
QY	269	-----RNTQPAESRIYDEILQSKV-----	287
DB	520	TEEDDEKTRMHSTANSRNQLYDLVTHQDIAHALAYEGQVEYEAITPVYKVDGSMDEMDA	579
QY	288	-----LPSKEEVPNTVYSEVQFADKMGKASTQDSKPP	319
DB	580	YIQVSLNVQGETPLPQKKEDSNITYCSVQKPKTKTAQTTPQDDAESP	624

Qy	9	LLCLQTWPAAAGKDSFTVNGILGESVTFFPNIQEPQVKIIAW---TSKTSVAYVIP	65
		: : : :	
Db	15	LLSLVT----GFDDQSPVNNAITGTSNVTLTILKHPLASYORLTWLHTNTOKILEYFPN	70
		: : : :	

Qy

Query Match 10.6%; Score 179.5; DB 2; Length 240;
Best Local Similarity 23.6%; Pred. NO. 4.3e-07;
Matches 58; Conservative 47; Mismatches 120; Indels 21; Gaps 7
Qy 7 WILLCLQTWPEAAG-KOSEFTVNGILGESVTFFPVNIQFPROVKIATWSKVAVYTP 65

Db

8

WCLVLELLPLGTGFGQHSIPDINATGNSVTLKIHKDPLGPKRITWLTKNQKILEY 67

QY

66

GDSFAPVTVTHRYRERHALGPNYNLVISDLRMDAGDYKADINTQADPVTTKRYN 125

Db

68

NYNSTK---TIPSEFKGRVLEENNGALHISNVRKEDKGTVMRVLRETE---NELKIT 121

QY

126

LQIYRRLGPKIKTQSLMASVNSTCNVTLTCSVEKEKNVTYNW-----SPLGEENVLQ 179

Db

122

LEVDPVPKPSIEINKTEASTDCHLRLECEV--KQHDVDTWYESSGPPPKSPGVLD 179

QY

180

IFQTPDEQLTYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLI 239

Db

180

LIVTPQNKSTFYTCQVSNPNVSSKNDTVYFTLPC-DLA-----RSSGVCWTATLWLVVTLLI 233

QY

240

LSSVFL 245

Db

234

IHRILL 239

RESULT 5

I49443

gene 2B4 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49443

R:Mathew, P.A.; Garni-Wagner, B.A.; Land, K.; Takashima, A.; Stoneman, E.; Bennett, M.; J. Immunol. 151, 5328-5337, 1993

A:Title: Cloning and characterization of the 2B4 gene encoding a molecule associated with

A:Reference number: I49443; MUID:94044757; PMID:8228228

A:Accession: I49443

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-398 <RES>

A:Cross-references: UNIPROT:Q07763; GB:L19057; NID:G309076; PIDN:AAA16353.1; PID:G309077

C:Genetics:

A:Gene: 2B4

Query Match 9.78; Score 164; DB 2; Length 398;

Best Local Similarity 22.38; Pred. No. 1.5e-05;

Matches 83; Conservative 49; Mismatches 139; Indels 102; Gaps 13;

QY

29

VNGILGESVTF-PVNIQEPQVKIIAWTSKTSVAYVTPGDSETAPVTVTHRYRYEIIHA 87

Db

29

VVGSGKPVQLRPSNIQ-----TKDVSQW-----KKTEQSGSHRKIEI 66

QY

88

L-----GPNY-NLVISDL-----RMDAGDYKADINTQADPVTTKRYNL 126

Db

67

LWNYNDGPNVSNVFSFDIYGFDFALSISAKLQDSGHYLLBI-TNTGKVCNKNFOL 125

QY

127

QIYRRLGPKIKTQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPLGEGNVLOIFQTPED 186

Db

126

LILDHVTENLKAQMKPWTGTQCLFUSCLVTKDD-NVSAFATRGTLISNQNSHTWE 184

QY

187

QEL-----TYTCTAQNPNVNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLI 240

Db

185

NQIDASSLHYTCNVSNRASWANTLNFTHGCSQVPSNFRPLPGVIIV-----LVTLFL 240

QY

241

SSVFLRFLF--KRQDAASKK---TITYINASR----- 269

Db

241

GAIICFCVTKRKLQKQFSPKEPLTIYEVKDSRSDRQGCSSRASGPSAVQBDGRQR 300

QY

270

-----NTQPAESRIYDEILQSKVLPSKEEPTVNTVYSEVQFADKMGKASTQ 314

Db

301

ELDRRVSEVLQPLQQTFFPQDRTGWTYSMIOCKPSDSTSQEKTCTVYSVVQPSRKSGSKRN 360

QY

315

DSKPPGTSSYEIV 327

Db

361

QNYSLCTVYEIV 373

RESULT 6

S34338

biliary glycoprotein A precursor - mouse

N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein

C:Species: Mus musculus (house mouse)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S34338; JCL510; A41093

R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.

A:Description: A C1p-family gene present on the lactose-protease plasmid of lactococcus

A:Reference number: S34338

A:Accession: S34338

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-521 <HUA>

A:Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:G312585; PIDN:CAA47698.1; PID:G312

R:McCuag, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993

A:Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein

A:Reference number: JCI1505; MUID:93273228; PMID:8500759

A:Accession: JCI1510

A:Molecule type: mRNA

A:Residues: 1-81,'Q','P',143-521 <MCC>

A:Cross-references: GB:X67281

R:Williams, R.K.; Jiang, G.S.; Holmes, K.V.

Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991

A:Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen

A:Reference number: A41093; MUID:91288498; PMID:1648219

A:Accession: A41093

A:Status: preliminary

A:Molecule type: protein

A:Residues: 35-59 <WIL>

C:Comment: This protein is expressed at the cell surface and plays a determinant role i

C:Genetics:

A:Gene: BgpF

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

C:Keywords: glycoprotein; receptor

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:160-219/Domain: immunoglobulin homology <IMM1>

F:254-303/Domain: immunoglobulin homology <IMM2>

F:339-396/Domain: immunoglobulin homology <IMM3>

F:87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (

Query Match 8.58; Score 143.5; DB 2; Length 521;

Best Local Similarity 23.88; Pred. No. 0.00099;

Matches 59; Conservative 36; Mismatches 94; Indels 59; Gaps 10;

QY

1

MAQHLL-----WILL-----CIQTW-----PEAAGKDSFIYVNGILGES 36

Db

3

LASAHLLKGQVFWGILLTASLASNSPPTTAETVAVPQVAEDNNVLLVHNL---- 58

QY

37

VTFPVNIQEPQVKIIAWTSKTSVAYVTPGDSETAPVTVTHRYRYEIIHA-----LGPNY 92

Db

59

-----PLALGAFAYKGNPVS-----TNAEIVHFVTGTNKTITGPAHSGRETIVSNG 105

QY

93

NLVISDLRMDAGDYKADINTQADPVTTKRYNLQIYRRLGPKIKTQSLMASVNSTCNVT 152

Db

106

SLLIQRTVTKDGTGYTIEM-TDENFRRTATVQFHVHQLLKNITNSNNPVEGDSVS 164

QY

153

LTCVSKEEKNVTYNNSPLGE-----EGN-VLQIFQTPEDQELTYTCTAQNPNVS 200

Db

165

LTDCSYTDPNIIYLLWSRNGESLSEGRDLKXLSGNRTLLNLNTRNDTPGVVCTETPNVS 224

QY

201

-NNSDSIS 207

Db

225

VNRSDFPS 232

RESULT 7

WMSR1

biliary glycoprotein A precursor - mouse

N:Alternate names: carcinoembryonic antigen mmCGM1a; murine hepatitis virus receptor

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C:Accession: JCI1505; A49006; A41563; S11625

R:McCuag, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

RESULT 9

S41638
T-cell surface glycoprotein CD2 precursor - horse
N;Alternate names: T-lymphocyte surface antigen CD2
C;Species: Equus caballus (domestic horse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41638; S31578
R;Tavernor, A.S.; Kydd, J.H.; Bodian, D.L.; Jones, E.Y.; Stuart, D.I.; Davis, S.J.; Butc
Eur. J. Biochem. 219, 969-976, 1994
A;Title: Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA. Structure-b
A;Reference number: S41638; MUID:94155904; PMID:7906650
A;Accession: S41638
A;Molecule type: mRNA
A;Residues: 1-347 <TAV>
A;Cross-references: UNIPROT:P37998; EMBL:X69884; NID:g1057; PIDN:CAA49511.1; PID:g1058
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-347/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>

Query Match 8.3%; Score 141.5; DB 2; Length 347;
Best Local Similarity 21.2%; Pred. No. 0.00084;
Matches 63; Conservative 49; Mismatches 136; Indels 49; Gaps 10;

Qy 28 TVNGILGESVTFPV-NIQEPQVKIIAWT-SKTSVAVTPGDSFAPVTVTHRNYYERI 85
Db 29 TIIGALERDNLIDIPAFQMSHEVEDIQMSKGTAKFKNGS-----MTFQKDKTYEVL 82
Qy 86 HALGPNVNLVISDLRMDAGYKADINTQADPVTTTKRYNLQIYRRLGPKKITQSLMASV 145
Db 83 ----KNGTLKIKHLRIHEGYKVDAYDSGKNVLEBTFHLSLEWVSKENISW----- 132
Qy 146 NSTCNVTLTCSVEKE---EKNVYNSPLGEGNVLIQFOTPEDQELTYTCTAQNPSVNN 202
Db 133 -SCTNTTTLTCEVTGTDFFELKYLNGRMIOKSPRKVIYKRNQIASFKCTANNIVSEE 191
Qy 203 SDSISAROLCADTAMGPRTHHTGLLSVLAMFFLLVLILSSVFLFRFKRQDAASKTIY 262
Db 192 SSSVVR-CTEKGLDIY-----LISGICGGIILFVFLALLFYISKRKKQ----- 236
Qy 263 TYIMASNTQPAESRIYDEILQSKVLPSEEPVNTVYSEVQFADKMGKASTQSKPP 319
Db 237 ---NSRRNDELEITRAHKVISEGRKPHQIPGST-----PLNPAASQPPPPP 281

RESULT 10

JC1509
biliary glycoprotein E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1509
R;McCuallig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A;Reference number: JC1505; MUID:93273228; PMID:8500759

A;Accession: JC1509
A;Molecule type: mRNA
A;Residues: 1-458 <MCC>
A;Cross-references: UNIPROT:Q61351; GB:X67280
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:

A;Gene: BgpE
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,259,290,294,304,333,375/Binding site: carbohydrate (Asn) (c

Query Match 8.2%; Score 139.5; DB 2; Length 458;
Best Local Similarity 23.8%; Pred. No. 0.0018;
Matches 59; Conservative 35; Mismatches 95; Indels 59; Gaps 10;

Qy 1 MAQHHL-----WILL-----CLOTW-----PEAAGKDSIFTVNGILGSS 36
Db 3 LASAHLHGQVWVGLLTASLASWSPPTTAETVTEAVPPQVADENNVLVHNL----- 58
Qy 37 VTFFPNVNIQEPQVKIIAWT-SKTSVAVTPGDSFAPVTVTHRNYYERIHA-----LGPNY 92
Db 59 -----PLALGAFAMVKGNPVS-----TNAEIVHQVTGTNKTGTPGASHGRETYSNG 105
Qy 93 NLVISDLRMDAGYKADINTQADPVTTTKRYNLQIYRRLGPKKITQSLMASVNSTCNVT 152
Db 106 SLTIQRTVTDGTGVVTIEM-TDENFRTEATVQFVHPLLLKPNITSNNSNPVEGDDSVS 164
Qy 153 LTCSVEKEEKVNTYNSPLGE-----EGN-VLQIFOTPEDQELTYTCTAQNPSV 200
Db 165 LTCDSYTDPDNITYLWSRNGESLSEGRDLKLGSEGNRTLLNVTNRDTPGVCETERNPVS 224
Qy 201 -NNSDSIS 207
Db 225 VNRSDFPS 232

RESULT 11

JC4024

poliovirus receptor-related protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999

C;Accession: JC4024

R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dub

Gene 155, 261-285, 1995

A;Title: Complementary DNA characterization and chromosomal localization of a human gen

A;Reference number: JC4024; MUID:95237621; PMID:7721102

A;Accession: JC4024

A;Molecule type: mRNA

A;Residues: 1-518 <LOP>

A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796

C;Genetics:

A;Gene: GDB:PVRR1

A;Cross-references: GDB:583951

A;Map position: 11q23-11q24

C;Superfamily: poliovirus receptor; immunoglobulin homology

C;Keywords: glycoprotein; transmembrane protein

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>

F;356-379/Domain: transmembrane #status predicted <TM>

F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 8.1%; Score 137.5; DB 2; Length 518;

Best Local Similarity 20.6%; Pred. No. 0.003;

Matches 93; Conservative 35; Mismatches 138; Indels 185; Gaps 19;

Qy 21 GKDSIFTVN---GILGESVTPPVNIQEP-ROVKI---IAWT-----SKTSVAVVTP--G 66

Db 27 GVHSQVVQVNDVMYGFITDVLHCSFANPLPSVKITQVTVQKSTGSKQNVAIYNPSMG 86

Qy 67 DSETAPVTVTHRNYYERIHALGPNY---NLVTSDLRMDAGY----- 107

Db 87 VSVLAP-----YREVEFLRPSFTDGTIRLSLELEDEGVVYCFATFPTGNRESQL 138

Qy 108 -----KAD 110

Db 139 NLITVMAKPTNWIEGTQAVLRAKQDDKVLVATCTSANGKPPSVVSWETRLKGEARVPGD 198

Qy 111 INTQADPVTTTKRYNLQIYRRLGPKKITQSLMASVN----- 146

Db 199 SGTPMAPVTVISIRLVPSEAHQ-----QSLACIVNHYMDRFKESLTINVQYEPVETIEG 254

Qy 147 -----STCNVTLTCSVEKEEKVNTYNSPLG-----BEGNVLIQIFOTPEDQEL--T 190

Db 255 FDGNWYIQRMDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQNRITLFFKGPINYSLAGT 314

Qy 191 YTCTAQNPSVNSDSISARQLCADIAMGPRTH-----HTGLLSVLAMFFLLVLILSSV 243

Matches 93; Conservative 35; Mismatches 138; Indels 185; Gaps 19;

Db 315 YICATNPICTRSGQEVNITEFPYTPSPPEHGRRAGVPVTAIIGGVAGSILLVLIVWGG 374
QY 244 FLRLFKRRQ-----DAASKTIY--TYIMASRNTQPAESRIYDEILQSKVLPSKEPVT 297
Db 375 IVVALRRRHTFKGDYSTKHKVYGVGYSKAG-----IPQHPP----- 412
QY 298 YISEVQFADKMGKASTQDSK---PPGTSSYE 325
Db 413 MAQNLOYPD-----DSDEKKAGPLGSSYE 438

RESULT 12
RWUUC2
T-cell surface glycoprotein CD2 precursor - human
N;Alternate names: B rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text change 09-Jul-2004
C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: A28967
A;Molecule type: DNA
A;Residues: 1-351 <DIA>
A;Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
A;Accession: A26486
A;Molecule type: mRNA
A;Residues: 1-338, 'M', 340, 'Q'QKTHCPPLPKKDRNCLFQ' <SEI>
A;Accession: B26486
A;Molecule type: protein
A;Residues: 25-46, 'X', 50 <SE2>
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
A;Accession: A28416
A;Molecule type: mRNA
A;Residues: 333-351 <SE3>
R;Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap
A;Reference number: A28023; MUID:87204137; PMID:2437578
A;Accession: A28023
A;Molecule type: mRNA
A;Residues: 1-265, 'Q', 267-351 <SEE>
A;Cross-references: GB:M16445; NID:g178668; PIDN:AAAS1738.1; PID:g178669
R;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A;Reference number: S02292; MUID:87204243; PMID:2883656
A;Accession: S02292
A;Molecule type: mRNA
A;Residues: 1-338, 'M', 340, 'Q'QKTHCPPLPKKDRNCLFQ' <SAL>
A;Cross-references: GB:M16336; NID:g180093; PIDN:AAAS1946.1; PID:g180094
A;Accession: A30430
A;Molecule type: protein
A;Residues: 25-43, 152-163 <SA2>
R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.V.; Crumpton, M.
EMBO J. 7, 1675-1682, 1988
A;Title: The structure of the human CD2 gene and its expression in transgenic mice.
A;Reference number: S00829; MUID:89005055; PMID:2901953
A;Accession: S00829
A;Molecule type: DNA
A;Residues: 1-351 <LAN>
A;Cross-references: EMBL:X08781
C;Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear
or is closely associated with, the erythrocyte receptor.
C;Genetics:

A;Gene: GDB:CD2
A;Cross-references: GDB:118735; OMIM:186990
A;Map position: ip13.1-1p13.1
A;Introns: 21/1; 128/1; 205/1; 246/1
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;25-206/Domain: extracellular #status predicted <EXT>
F;237-351/Domain: transmembrane #status predicted <TMM>
F;89,141,150/Binding site: carbohydrate (Asn) #status predicted
Query Match 8.1%; Score 137; DB 1; Length 351;
Best Local Similarity 22.6%; Pred. No. 0.002;
Matches 73; Conservative 46; Mismatches 120; Indels 84; Gaps 15;
QY 13 LQTPPEAAGKDSIEFTVNGILGESVTFPV-NIQEPQVKIIAWTSKTSVAVVTPGDSETA 71
Db 31 LETW-----GALGQDINLDIPSFQMSDDIDDKW-EKTS-----DKKKI 68
QY 72 PVVTVTHRYVER-IHALGPNVNLVISDLRMEADGDKADINTQADPVYTKRYNLQIYR 130
Db 69 AQFRKEKETFEKOTYKLFKNGTLKIKHLKTDQDIYKVSIVYDTKGNVLEKIFDLKIQE 128
QY 131 RLGPKITQSLMASVNSWC-NVTLTCSVEKEEKVYVNWSPGLBEGNVLOIFQTPEDQEL 189
Db 129 RVSFKPISW-----TCINTLTTCV-----MNGTDELNLYQDGKHLKUSQRVITHKW 176
QY 190 T-----YTCAQNPVSNNS--DSISARQLCADIAMGPRTHHTGLLSV-----LAMFFLL 236
Db 177 TTSLSAKFCTAGNKVSKESSEVPSCPEKGLDIVL-----IIGICGGSLLMVFA 228
QY 237 VLISSVFLFLFKRQDAASKKIYYIMASRNTQPAESRIYDEILQSKVLPSKEPVP 296
Db 229 LLV-----FYITRKQK-----RSRRNDELETRAHVATEERGRKPHQIPAS 271
QY 297 TVYSEVQFADKMGKASTQDSKPP 319
Db 272 T-----PONPATSQHPPPP 285

RESULT 13
A36319
carcinoembryonic antigen precursor - human
N;Alternate names: CEA; meconium antigen 100
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence, revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: A36319; A27773; A25845; S09106; S31737; A44476; I54224; I59098; A2E
R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively,
Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
A;Reference number: A36319; MUID:90258861; PMID:2342461
A;Accession: A36319
A;Molecule type: DNA
A;Residues: 1-702 <SCH>
A;Cross-references: UNIPROT:P06731; GB:M17303; NID:g178676; PIDN:AA559513.1; PID:g178677
A;Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-Thr
R;Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stammers, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A;Title: Isolation and characterization of full-length functional cDNA clones for human
A;Reference number: A27773; MUID:88038876; PMID:3670312
A;Accession: A27773
A;Molecule type: mRNA
A;Residues: 1-702 <BEA>
A;Cross-references: GB:M29540; NID:g180222; PIDN:AA51967.1; PID:g180223
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Eiting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: A31037
A;Molecule type: mRNA
A;Residues: 1-702 <BAR>

A;Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
A;Note: the authors translated the codon GTC for residue 130 as Leu
R;Oikawa, S.; Nakazato, H.; Kosaki, S.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA sequence
A;Reference number: A25845; MUID:87128144; PMID:3814146
A;Accession: A25845
A;Molecule type: mRNA
A;Residues: 5-702 <OIK>
A;Cross-references: GB:M15042; NID:g180198; PIDN:AAA51963.1; PID:g180199
R;Oikawa, S.
submitted to the EMBL Data Library, September 1989
A;Reference number: S08106
A;Accession: S08106
A;Molecule type: mRNA
A;Residues: 5-319,321-702 <OIK>
A;Cross-references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
R;Barnett, T.
submitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcinoembryonic antigen
A;Reference number: S31737
A;Accession: S31737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BA2>
A;Cross-references: EMBL:X62151
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen gene
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: A44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
R;Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
A;Reference number: I54224; MUID:91139118; PMID:2286372
A;Accession: I54224
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: GB:M60964; NID:g180215; PIDN:AAA51964.1; PID:g180217
R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryonic antigen
A;Reference number: I59098; MUID:87204247; PMID:3033671
A;Accession: I59098
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 331-702 <RE2>
A;Cross-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
R;Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 kD and 105 kD
A;Reference number: A26831; MUID:87326349; PMID:3632664
A;Accession: A26831
A;Molecule type: protein
A;Residues: 35-64 <SIE>
R;Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at the C-terminus
A;Reference number: A35490; MUID:90321257; PMID:2372297
A;Accession: A35490
A;Molecule type: protein
A;Residues: 'X', '140-151', 'X', '155-156' <THO>
A;Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer cells
C;Comment: This is a heavily glycosylated membrane protein of unknown function is a widely used marker for the C-terminus. It is anchored to the membrane
C;Genetics:
A;Gene: GDB:CEA
A;Cross-references: GDB:I19054; OMIM:114890
A;Map position: 19q13.2-19q13.2

A;Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatidylcholine
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;5-678/Product: carcinoembryonic antigen #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;338-395/Domain: immunoglobulin homology <IMM3>
F;516-573/Domain: immunoglobulin homology <IMM4>
F;608-657/Domain: immunoglobulin homology <IMM5>
F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)
Query Match 8.0%; Score 135.5; DB 2; Length 702;
Best Local Similarity 24.3%; Pred. No. 0.0066;
Matches 51; Conservative 28; Mismatches 66; Indels 65; Gaps 11;
QY 40 PWNIOEPQVKII-----AW-----TSKTSVAVV-----TPGDSAPVVT 75
DB 42 PNVAAEGKEVLLVHNLPHLFGYSYKGERVDGNRQIRIYVIGTQQATPGPA----- 94
QY 76 VTNRNYERIHALGPNYLVISDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQIY 129
DB 95 -----YSGREIYFNASLLIQNIQNDGTGFTLVHVKISDLVNEATG-----QFRVY 141
QY 130 RLRLGPKITQSLMASVNSTCNVLTCSVEKEKNYTNW-----SP-----LGEENY 177
DB 142 PLPLKPSISSNNKPFVEDKDAVATC--EPEQTATYLMWVNNQSLFVSRQLQNSGRT 199
QY 178 LOIFOTPEQELTYTCTAQNPSV--NNSDSI 206
DB 200 LTLFNVTRNDTASYKCTQNPVSARRSDSV 229
RESULT 14
RWHUPA
poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Tak
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: S12048
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA45
A;Note: 67-Ala was also found
A;Note: the gamma form has 331-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
A;Molecule type: mRNA
A;Residues: 1-66, 'A', 68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pr
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <PVR>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>

F:42-125/Domain: immunoglobulin homology <IMM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9%; Score 134.5; DB 1; Length 417;
Best Local Similarity 19.2%; Pred. No. 0.004;
Matches 86; Conservative 53; Mismatches 137; Indels 171; Gaps 17;

QY 7 WILL---LCIQWPEAAGKDSI---FTVNGILGSEVTFPVNIQSPR---OVKLIAMTS 56
DB 9 WPELLVALLVLSWPPPGTGDDVVQAPTQVPGFLGDSVILPCVLPQNVMEVTHVSQLTWTR 68
QY 57 KTSVAYVTPGDSETAPVTVTHRYNE-----RIHALGPNYNLVISDLRMEADGD 106
DB 69 H-----GESGSMVAFPHQTQPSYSESKRLEFVAARLGAELRNASLMFGLRVEDEN 120
QY 107 Y-----KADI--NTQADPYTTTKRNLQIYRLKXP----- 135
DB 121 YTLCLFVTPFGQSRVDIWLRLVLAQPNTAEVQKVL---TGEPVPMARCVSTGGRPPAQI 177
QY 136 -----KITQSLMASVNSTCNV----- 151
DB 178 TWHSDLGGMNTPSQVPGFLSGTIVTSLWLVPSQVDGKNTCKVEHSEFEPKOLLTVN 237
QY 152 -----TLTCSVEKEKNVTYNWS-----PLGEEGNVLIQI 180
DB 238 LTVYYPEVSIISGYNWNLGQNEATLTCDARSNPETGYNWSITWTGMLPPPPAQAQQL 297
QY 181 FQTPDEOELTYCTAQNPNNSDSISARQ--LCADIANGFRTHTGL-----LSLVAMFF 234
DB 298 LIRPVDKPINTL-----ICNTNALGARQOELTVQVKEGPPSEHSGMSRNAILFLVGI 352
QY 235 LVLVLSSVFLFRKRRQDAASKTIYTYIMASRNTQPAESRIYDEILQSKVLSPKKEP 294
DB 353 LVFLILLGIGIFYWSK-----CSREVLWHCHLCPSTEHASANGHVSYSAV--SRE-- 404
QY 295 VNTVYSEVQFADKMGKATQDSKPPGT 321
DB 405 -----NSSSQDPQTGT 416

RESULT 15
A27681
Nonspecific cross-reacting antigen precursor - human
N/Alternate names: NCA; TBX/NCA
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C/Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R/Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A/Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A/Reference number: A26902; MUID:87298464; PMID:3619891
A/Accession: A26902
A/Molecule type: DNA
A/Residues: 1-141 <OIK>
A/Cross-references: UNIPROT:Q13774; GB:M17082; NID:G180230; PIDN:AAA51971.1; PID:G553222
R/Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, O
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A/Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A/Reference number: A29875; MUID:87204248; PMID:3033672
A/Accession: A29875
A/Molecule type: DNA
A/Residues: 23-141 <THO>
A/Cross-references: GB:M16337
A/Note: The authors translated the codon ACT for residue 64 as Tyr
R/Tawaragi, Y.; Oikawa, S.; Matsuka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A/Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carci
A/Reference number: A27681; MUID:88106638; PMID:3337731

A/Accession: A27681
A/Molecule type: mRNA
A/Residues: 1-238, 'V', 240-344 <TAW>
A/Cross-references: GB:M18728; NID:G189084; PIDN:AAA59907.1; PID:G189085
R/Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Eiting, J.J.
Genomics 3, 59-66, 1988
A/Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A/Reference number: A31037; MUID:89122014; PMID:3220478
A/Accession: B31037
A/Molecule type: mRNA
A/Residues: 1-137, 'L', 139-344 <BAR>
A/Cross-references: GB:M29541; NID:G189103; PIDN:AAA59915.1; PID:G189104
A/Note: The authors translated the codon TTG for residue 138 as Phe
R/Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A/Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
A/Reference number: A29918; MUID:8813989; PMID:2830274
A/Accession: A29918
A/Molecule type: mRNA
A/Residues: 1-344 <NEU>
A/Cross-references: GB:M18216; GB:J03550; NID:G178690; PIDN:AAA51739.1; PID:G178691
R/Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A/Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
A/Reference number: A27709; MUID:88268882; PMID:3390172
A/Accession: A27709
A/Molecule type: protein
A/Residues: 35-95, 99-120, 123-138, 149-151, 'X', 153-162, 166, 'X', 168-172, 'X', 174-193; 231-235
R/Hetta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A/Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
A/Reference number: A36271; MUID:90256782; PMID:2341397
A/Accession: A36271
A/Molecule type: protein
A/Residues: 35-42, 44-53; 55-80; 83-134; 139-160; 166-172; 174-180; 191-194, 204-224; 233-308; 310
R/Paxton, R.J.; Mosser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A/Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A/Reference number: A26414; MUID:87147209; PMID:3469650
A/Accession: C26414
A/Molecule type: protein
A/Residues: 35-69 <PAX>
R/Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A/Title: Identification of three new genes and estimation of the size of the carcinoemb
A/Reference number: A44476; MUID:93052339; PMID:1427854
A/Accession: E44476
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 35-141 <KHA>
A/Accession: F44476
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 35-137, 'L', 139-141 <KH2>
C/Comment: This protein appears to be processed at the carboxyl terminus and anchored th
C/Genetics:
A/Genes: GDB:NCA
A/Cross-references: GDB:120221; OMIM:163980
A/Map position: 19q13.2-19q13.2
A/Introns: 22/1
A/Note: the list of introns may be incomplete
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:104, 111, 115, 152, 173, 197, 224, 256, 274, 288, 292/Binding site: carbohydrate (Asn) (covalent)
F:309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match 7.8%; Score 131.5; DB 2; Length 344;
Best Local Similarity 25.1%; Pred. No. 0.0054;
Matches 54; Conservative 29; Mismatches 67; Indels 65; Gaps 12;

QY	40	PVNIQEPQVKIIA-----W-----TSKTSVAYV-----TPGDSETPVVT	75
Db	42	PENVAEGKEVLLLAHNLQNRIQSYKGERVDGNSLIVGYVIGTQQATPGPA-----	94
QY	76	VTHRNYYERIHALGPNYNLVISDLRMEADGY-----KAD-INTQADPYTTTKRYNLQIY	129
Db	95	-----YSGRETIYPNASLLIQNVQNTDGTGFTLQVIKSDLVNEEA-----TGQFH--VI	141
QY	130	RLRGKPKITOSLWASVNSTCNVTLTCSVEKEKNVTYNNSPICE-----EGNV- 177	
Db	142	PELPKFSISNNPNVEDKDAVFTC--EPEVQNTTYLWVWVNGQSLPVSPLQLSNGNWT	199
QY	178	LQIFQTPEDQELTYTCTAQNPS--NNSDSISARQL	211
Db	200	LTLLSVKRNDAGSYECEIQNPASANRSDPVTNLNL	234

Search completed: February 4, 2005, 12:15:56
Job time : 33.7784 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 11:55:35 ; Search time 144.561 Seconds
(without alignments)
1165.422 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHHLWILLLCIQTWPERA.....KASTQDSKPGTSSYBIVIX 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues 1612378
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1695	99.9	328	2	O15430
2	1687	99.5	328	2	O6FHA8
3	1672.5	98.6	339	2	Q8W1I8
4	1669.5	98.4	345	2	Q9UIB8
5	1324.5	78.1	272	2	Q9UIB7
6	1320	77.8	280	2	O95660
7	1125	66.3	241	2	Q9UIB6
8	1029	60.7	197	2	Q9UII7
9	944.5	55.7	329	2	Q9Z1I78
10	382.5	22.6	655	1	LY9 HUMAN
11	378.5	22.3	140	2	Q8BFV0
12	376	22.2	285	2	O8VE93
13	373	22.0	289	2	Q96A28
14	368	21.7	285	2	Q8BTK0
15	367	21.6	285	2	Q9D780
16	362.5	21.4	335	2	Q9NQ25
17	361.5	21.3	332	1	SLF6 HUMAN
18	360.5	21.3	335	2	Q9NY08
19	352	20.8	645	2	O6NZB6
20	352	20.8	649	2	Q7TME7
21	352	20.8	654	1	LY9 MOUSE
22	351	20.7	544	2	Q8C2D4
23	334.5	19.7	333	2	Q8BHK6
24	330.5	19.5	83	2	O95266
25	323.5	19.1	538	2	Q8C9E4
26	321.5	19.0	335	2	Q8CJ64
27	316.5	18.7	335	2	Q8CJ65
28	315.5	18.6	335	2	Q8BT12
29	315	18.6	300	2	Q8CJ63
30	308	18.2	296	2	Q8N6V8
31	308	18.2	328	2	Q9NY23

32 307.5 18.1 294 2 Q91XA0 mus musculus
33 282.5 16.7 351 1 SLP6 MOUSE
34 256 15.1 228 2 O8ND32
35 216.5 12.8 370 1 C244 HUMAN
36 212 12.5 42 2 Q9UF04
37 197 11.6 394 2 Q9EQK9
38 194 11.4 335 1 SLAM HUMAN
39 194 11.4 335 2 Q96QR3
40 194 11.4 416 2 O8N7I3
41 194 11.4 416 2 Q67IP8
42 190.5 11.2 198 2 Q6UWGI
43 190.5 11.2 367 2 Q6ZWLA
44 189.5 11.2 399 2 Q9ESE5
45 188 11.1 211 2 Q6ZR17

ALIGNMENTS

RESULT 1
O15430
ID O15430 PRELIMINARY; PRT; 328 AA.
AC O15430; Q8W1I8;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Leukocyte antigen CD84 (Leukocyte differentiation antigen CD84 isoform CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
DE CD84c (MAX.3 cell surface antigen precursor) (CD84 antigen).
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454416; PubMed=9310491;
RA de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";
RL Blood 90:2398-2405(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Palou E., Sole J., Pirotto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86188202; PubMed=3008886;
RA Andreesen R., Bros K.J., Osterholz J., Emrich F.;
RT "Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens.";
RL Blood 67:1257-1264(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729;
RA Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.;
RT "Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with CD84.";
RL Biochem. J. 346:729-736(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymph;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapatlenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Groumou J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RC Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82988; AAB84364.1; -;
DR EMBL; AF054815; AAF21721.1; -;
DR EMBL; AJ223324; CAAL1264.1; -;
DR EMBL; BC020063; AAH20063.1; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR GO; GO:0007156; P:hemophilic cell adhesion; TAS.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG-LIKE.
DR PROSITE; PS50835; IG-LIKE; 1.
KW SIGNAL
FT CHAIN 1 21
FT CHAIN 22 328 MAX.3 cell surface antigen.
SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206A6D0344 CRC64;

Query Match 99.9%; Score 1695; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.2e-125; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0;
QY 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
QY 61 AYVTPGDSAPVTVTHRYNRYERIHALGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVTVTHRYNRYERIHALGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
QY 121 TKRYNLIQYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPGLBEGNVLQI 180
DB 121 TKRYNLIQYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPGLBEGNVLQI 180
QY 181 FQTPEDQELTYTCTAQNPNVSNDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
QY 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSEEPVNTVYS 300
DB 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSEEPVNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSYSEI 328
DB 301 EVQFADKMGKASTQDSKPPGTSYSEI 328

RESULT 2
Q6FHA8 PRELIMINARY; PRT; 328 AA.
ID Q6FHA8
AC Q6FHA8; 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE CD84 protein (Fragment).
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541847; CAG46645.1; -;
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 2 IG-LIKE.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON TER 328 328
SQ SEQUENCE 328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;
Query Match 99.5%; Score 1687; DB 2; Length 328;
Best Local Similarity 99.7%; Pred. No. 1.4e-124; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 1;
QY 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
QY 61 AYVTPGDSAPVTVTHRYNRYERIHALGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
DB 61 AYVTPGDSAPVTVTHRYNRYERIHALGPNYNLVIDSLRMEDAGDYKADINTQADPYTT 120
QY 121 TKRYNLIQYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPGLBEGNVLQI 180
DB 121 TKRYNLIQYRRLGPKKITQSLMASVNSTCNVLTCSVEKEKNVTYNWSPGLBEGNVLQI 180
QY 181 FQTPEDQELTYTCTAQNPNVSNDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
QY 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSEEPVNTVYS 300
DB 241 SSVFLFRLFKRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSEEPVNTVYS 300
QY 301 EVQFADKMGKASTQDSKPPGTSYSEI 328
DB 301 EVQFADKMGKASTQDSKPPGTSYSEI 328

RESULT 3
Q8WWI8 PRELIMINARY; PRT; 339 AA.
ID Q8WWI8
AC Q8WWI8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Leukocyte differentiation antigen CD84 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Gava A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12632; CAA73181.1; -;
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW SIGNAL
FT SIGNAL 1 21 Potential.
FT CHAIN 22 339 leukocyte differentiation antigen CD84.
SQ SEQUENCE 339 AA; 38082 MW; E78D6D5CAC8D3604 CRC64;
Query Match 98.6%; Score 1672.5; DB 2; Length 339;
Best Local Similarity 96.5%; Pred. No. 2e-123; Indels 11; Gaps 1;
Matches 327; Conservative 0; Mismatches 1;
QY 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTWPAAAGKDSSEIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSV 60

Qy	61	AVYTPGDS	EAPVVT	THRNYYER	IHALGPNYL	VISDL	RMEDAGDY	KADINTQAD	PYTT	120																													
Db	61	AVYTPGDS	EAPVVT	THRNYYER	IHALGPNYL	VISDL	RMEDAGDY	KADINTQAD	PYTT	120																													
Qy	121	TKRYNLQY	IRBLGPK	KTQS	LMASVNST	CNVTLT	CSVEKEEK	VNTVNW	SPLBEG	NVLQI	180																												
Db	121	TKRYNLQY	IRBLGPK	KTQS	LMASVNST	CNVTLT	CSVEKEEK	VNTVNW	SPLBEG	NVLQI	180																												
Qy	181	FQTPED	QELTYT	CTAQN	PVSN	SNDS	ISARQ	CADI	AMGPR	THHTG	LLSVL	AMP	FLVL	240																									
Db	181	FQTPED	QELTYT	CTAQN	PVSN	SNDS	ISARQ	CADI	AMGPR	THHTG	LLSVL	AMP	FLVL	240																									
Qy	241	SSVFL	FLR	LKRR	QD	-----	AA	S	K	K	T	I	Y	I	M	A	S	R	N	T	O	P	A	E	S	R	I	Y	D	E	I	L	O	S	K	V	L	P	289
Db	241	SSVFL	FLR	LKRR	QD	-----	AA	S	K	K	T	I	Y	I	M	A	S	R	N	T	O	P	A	E	S	R	I	Y	D	E	I	L	O	S	K	V	L	P	300
Qy	290	SKEEP	N	T	V	T	Y	G	E	V	O	F	A	D	R	M	G	K	A	S	T	O	D	S	K	P	O	G	T	S	S	E	I	V	I	328			
Db	301	SKEEP	N	T	V	T	Y	G	E	V	O	F	A	D	R	M	G	K	A	S	T	O	D	S	K	P	O	G	T	S	S	E	I	V	I	339			

RESULT	4
Q9UIB8	PRELIMINARY; PRT; 345 AA.
ID	
AC	Q9UIB8;
DC	01-WAY-2000 (TREMBLrel. 13, Created)
DT	01-WAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Leukocyte differentiation antigen CD84 isoform CD84a.
GN	Name=CD84;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	Palou E., Sole J., Pirotto F., Gaya A.;
RA	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF054816; AAF21722.1; ..
DR	Gewu; HGNC:1704; CD84.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
SO	SEQUENCE 345 AA; 38782 MW; DA06BC5A682562DE CRC64;

Query Match	98.4%; Score 1669.5; DB 2; Length 345;
Best Local Similarity	94.8%; Pred. No. 3.4e-123;
Matches 327; Conservative	0; Mismatches 1; Indels 17; Gaps 1;
QY	1 MAQHLLWILLCLQTWPEAAGKDSIEFTVNGILGESVTFPNTQEPQVKLIIAWTSKTSV 60
Db	1 MAQHLLWILLCLQTWPEAAGKDSIEFTVNGILGESVTFPNTQEPQVKLIIAWTSKTSV 60
QY	61 AYTTPGDSETAPVVVTVTHRNYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
Db	61 AYTTPGDSETAPVVVTVTHRNYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
QY	121 TKRYNQLYRRLGPKPITQSLMASVNSTCNVTLTCSVEKEEKVNTYNSPLGEGENVLQI 180
Db	121 TKRYNQLYRRLGPKPITQSLMASVNSTCNVTLTCSVEKEEKVNTYNSPLGEGENVLQI 180
QY	181 FQTPEDQELTYTCTAQNVPVNSNDSISARQLCADIANGFRTHHTGLLSVLAMFFLLVL 240
Db	181 FQTPEDQELTYTCTAQNVPVNSNDSISARQLCADIANGFRTHHTGLLSVLAMFFLLVL 240
QY	241 SSVFLFLFKRRQD-----AASKKITYTYIMASRNTQPAESRIYDEIL 283
Db	241 SSVFLFLFKRRQRIIFPEGSLNTFTKNPYAASKKITYTYIMASRNTQPAESRIYDEIL 300
QY	284 QSKVLPSPKEPFPNTVYSEVQADKQKASTQDSKPPGTSSYEIVI 328

Db 301 QSKVLPSKEFPVNTVYSEVQFADKMGKASTQDSKPGTSSYEIV 345

RESULT 5

Q9UIB7 PRELIMINARY; PRT; 272 AA.

ID Q9UIB7

AC Q9UIB7

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Leukocyte differentiation antigen CD84 isoform CD84d.

GN Name=CD84;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP Palou E., Sole J., Piroto F., Gaya A.;

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF054817; AAE21723.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS00835; IG LIKE; 1.

SQ SEQUENCE 272 AA; 30514 MW; 6A2E13AA4E22E13E CRC64;

Query Match 78.1%; Score 1324.5; DB 2; Length 272;

Best Local Similarity 95.9%; Pred. No. 3.8e-96;

Matches 256; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

Qy 1 MAQHLLWILLCLQTWPEAAGKQSEIFTVNGILGESVTFPNIOEPQVKIIAMTSKTSV 60

Db 1 MAQHLLWILLCLQTWPEAAGKQSEIFTVNGILGESVTFPNIOEPQVKIIAMTSKTSV 60

Qy 61 AYTTPGSEAPVVTVTHRYNYYERIHALGPNYNLVIISDLRMEDAGDYKADINTQADPYTT 120

Db 61 AYTTPGSEAPVVTVTHRYNYYERIHALGPNYNLVIISDLRMEDAGDYKADINTQADPYTT 120

Qy 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPIGEGNVLQI 180

Db 121 TKRYNLQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPIGEGNVLQI 180

Qy 181 FQPEDQELTYTCTAQNVPVNSDSISARQLCADIAMGFRTHTTGLLSVLAMPFLLVLL 240

Db 181 FQPEDQELTYTCTAQNVPVNSDSISARQLCADIAMGFRTHTTGLLSVLAMPFLLVLL 240

Qy 241 SSVFLFRLFKRRQDA-----ASKKTIY 262

Db 241 SSVFLFRLFKRRQASLQGRASEHSLF 267

```

RESULT 6
O95660 PRELIMINARY; PRT; 280 AA.
AC O95660;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD84.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
RN [1]
RP SEQUENCE FROM N.A.
RA Palou E., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
RL Submitted (APR-1997), to the EMBL/GenBank/DBJ databases.
DR EMBL; U96627; AAD04232.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.

```

SQ SEQUENCE 280 AA; 31651 MW; A043E048E762A718 CRC64;

Query Match 77.8%; Score 1320; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHLLWILLCLQTPWPAAGKDSIFVTNGILGESVTFPPVNIQBPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTPWPAAGKDSIFVTNGILGESVTFPPVNIQBPQVKIIAWTSKTSV 60

QY 61 AVYTPGDSAPVVTTHRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
DB 61 AVYTPGDSAPVVTTHRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTT 120

QY 121 TKRYNLOIYRRLGKPKITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOI 180
DB 121 TKRYNLOIYRRLGKPKITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAFFLLVIL 240
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAFFLLVIL 240

QY 241 SSVFLFRFKRQ 253
DB 241 SSVFLFRFKRQ 253

RESULT 7

QYUIB6 PRELIMINARY; PRT; 241 AA.

AC QYUIB6
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Leukocyte differentiation antigen CD84 isoform CD84s.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.

RA Palou E., Sole J., Piroto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF054818; AAF21724.1; --
DR InterPro; IPR003599; IG-
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 241 AA; 26902 MW; F0121BC1609B6C52 CRC64;

Query Match 66.3%; Score 1125; DB 2; Length 241;
Best Local Similarity 94.3%; Pred. No. 1.7e-80;
Matches 215; Conservative 2; Mismatches 5; Indels 6; Gaps 1;

QY 1 MAQHLLWILLCLQTPWPAAGKDSIFVTNGILGESVTFPPVNIQBPQVKIIAWTSKTSV 60
DB 1 MAQHLLWILLCLQTPWPAAGKDSIFVTNGILGESVTFPPVNIQBPQVKIIAWTSKTSV 60

QY 61 AVYTPGDSAPVVTTHRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTT 120
DB 61 AVYTPGDSAPVVTTHRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTT 120

QY 121 TKRYNLOIYRRLGKPKITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOI 180
DB 121 TKRYNLOIYRRLGKPKITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOI 180

QY 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCA-----DIAMGFRTH 222
DB 181 FQTPEDQELTYTCTAQNPNVSNNSDSISARQLCAGNQLCPSLVSLELDH 228

RESULT 8

QYUIB7 PRELIMINARY; PRT; 197 AA.

AC QYUIB7
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Leukocyte antigen CD84 (Fragment).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.

RA Palou E., Piroto F., Sole J., Freed J.H., Peral B., Villardell C.,
Vilella R., Vives J., Gaya A.;
RL "Genomic characterization of CD84 reveals the existence of five
isoforms differing in their cytoplasmic domains."
RT Tissue Antigens 55:118-127(2000).
DR EMBL: AF101031; AAF06840.1; --
DR EMBL: AF101030; AAF06840.1; JOINED.
DR InterPro; IPR003599; IG-
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 197
SQ SEQUENCE 197 AA; 21889 MW; 2B660BF5FA871D88 CRC64;

Query Match 60.7%; Score 1029; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e-73;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 PEAAKGSIEFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAYVTPGSETAPVTV 76
DB 1 PEAAKGSIEFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAYVTPGSETAPVTV 60

QY 77 THRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLOIYRRLGKPK 136
DB 61 THRNYYERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLOIYRRLGKPK 120

QY 137 ITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOIQTPEDELTCTTAQ 196
DB 121 ITQSLMASVNSTCNVLTCSVEKEEKVNTYNSPLGEEGNVLOIQTPEDELTCTTAQ 180

QY 197 NPVSNNSDSISARQLCA 213
DB 181 NPVSNNSDSISARQLCA 197

RESULT 9

QYUIB8 PRELIMINARY; PRT; 329 AA.

AC QYUIB8
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE CD84 leukocyte antigen.
GN Name=CD84; Synonyms=CD84;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.

RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
Engel P.;
RT "Molecular cloning, characterization, and chromosomal localization of
the mouse homologue of CD84, a member of the CD2 family of cell
surface molecules.";

Immunogenetics 49:249-255(1999).
RA EMBL; AF043445; AAD02273.1; -
DR MGD; MGI:1336885; Cd84.
DR InterPro; IPR003599; Ig.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS08335; IG LIKE, 1.
SQ SEQUENCE 329 AA; 37345 MW; 43BB1AA5AF1989E0 CRC64;

Query Match 55.7%; Score 944.5; DB 2; Length 329;
Best Local Similarity 57.3%; Pred. No. 4.1e-66;
Matches 192; Conservative 48; Mismatches 82; Indels 13; Gaps 5;

QY 1 MAQHLLWILLCLQOTWPEAGKDSIEFTVNGILGESVTFPVNIQEPQVQKILAIWTSKTSV 60
DB 1 MAQRHLWIFLCLQOTWSEAGKADDPVWNGILGESVTFELNLIQEPKIDNIWTSQSSV 60

QY 61 AYVTPGDSAPVTVTHRYNRYERIHALGNVNLVSDLRMEDAGYKADINTQADPYTT 120
DB 61 AFIKPGVNAE--VTITQGYKGRIBIIDQKVDLVRDLRMDAGTYKADINEE--TI 117

QY 121 TKRYNLIQVRLKPKITQSLMASVNSTCNVTLTCSVEKEKQVYTNWSPLEEGNVLIQI 180
DB 118 TKIYLIHLYRLKTPKTIQSLIASLNTCNITLTCSVEKEKQVYTNWSPFGEKSNVLIQI 177

QY 181 FQTPDEQELTYCTAQNVPVNSNDSISAROLCADIAMGPRTHRTGLSLVLMFLLVLIL 240
DB 178 VHSFMDQKLYTCTAQNVPVNSNDSVTVQPCDTPSFPHRAVLPGLAVLFLILIP 236

QY 241 SSVFLRFLKRRDQ-----ASKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEE 293
DB 237 MIAFLRFLYKRRDRIVLEADDYKKTIVYAVV--SRNAQPTESRIYDEIPQSKMLSCKD 294

QY 294 PVNTVYSEVQFADMGKASTQDSKPPGTSSYEIVI 328
DB 295 PVTIYSSVQLSEKMKETNMKDRSLPKALGNEIIV 329

RESULT 10
LY9 HUMAN STANDARD; PRT; 655 AA.
AC Q9HBG7; Q14775; Q9HAN5; Q9NQ24;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9) (CD229 antigen).
GN Name=LY9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RN Immunogenetics 51:788-793(2000).
RN [2]
RP SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).
RX MEDLINE=96128248; PubMed=8537117;
RA Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
RA McKenzie I.F.;
RT "Isolation and characterization of cDNA clones for Humly9: the human
RT homologue of mouse Ly9.";
RN Immunogenetics 43:13-19(1996).
RN [3]
RP SEQUENCE OF 1-151 FROM N.A.
RA Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,

Margolin J.F.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q9HBG7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9HBG7-2; Sequence=VSP_002525;
CC Name=3;
CC IsoId=Q9HBG7-3; Sequence=VSP_002524, VSP_002525, VSP_002526;
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF244129; AAG14995.1; -
DR EMBL; L42621; AAA92623.1; -
DR EMBL; AL121985; CAC00580.1; -
DR EMBL; AY007142; AAG02002.1; -
DR Genew; HGNC:6730; LY9.
DR MIM; 600684; -
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS08335; IG LIKE, 2.
DR Alternative splicing; Antigen; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Repeat; Signal; Transmembrane.
KW SIGNAL 1 47 Potential.
FT CHAIN 48 655 T-lymphocyte surface antigen Ly-9.
FT DOMAIN 48 454 Extracellular (Potential).
FT TRANSMEM 455 476 Potential.
FT DOMAIN 477 655 Cytoplasmic (Potential).
FT DOMAIN 48 158 Ig-like V-type 1.
FT DOMAIN 159 235 Ig-like C2-type 1.
FT DOMAIN 251 363 Ig-like V-type 2.
FT DOMAIN 364 452 Ig-like C2-type 2.
FT DISULFID 172 242 Potential.
FT DISULFID 178 222 Potential.
FT DISULFID 377 446 Potential.
FT DISULFID 383 427 Potential.
FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 413 413 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 424 424 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 359 448 Missing (in isoform 3).
FT VARSPLIC 500 513 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 524 554 /FTID=VSP_002525.
FT PARQPTPTSDSSDNLTTTEEDSDRPEVHK -> Q (in
FT isoform 3).
FT /FTID=VSP_002526.
FT Missing (in Ref. 1).
FT CONFLICT 171 171 Missing (in Ref. 4).
FT CONFLICT 602 602 V -> M (in Ref. 4).
FT SEQUENCE 655 AA; 72107 MW; 9FB0A3056D79F80A CRC64;
SQ

```
Query Match      22.6%; Score 382.5; DB 1; Length 655;
Best Local Similarity 33.9%; Pred. No. 1.7e-21;
Matches 101; Conservative 60; Mismatches 100; Indels 37; Gaps 11;

QY 3 QHHLWILLCLQTPWPAAGKSEIFVNGILGESVTFPVNIQBPQVKIIAITS-KTSTA 61
DB 33 QTSLLFLMLGLR-----ASGKDSAPTAVSGILGVSFTPLNLSVDEIENVIWIGPKNALA 88

QY 62 YVTPGDSFETAPVTVTHRNYYRIHALGPNYINLVISDLRMEADAGYKADINTQADPYTTT 121
DB 89 FARPEN-----VTIMVKSYLGRDLITKWSYLSLNSLTLNDAGSYKAGINORNFVETTE 143

QY 122 KRYNLQIYRRLGPKIT-OSLMASVNSTCNVLTCSVEKEEKVNTVNMPL-----GEE 174
DB 144 EBFLLFVYEQLOEPQVTMSKVSENFSCNITLMCSVGAESVLSWTPREPHASESNG 203

QY 175 GNVLIQIFQPEQELTYTCTAQNPNNSD-SISARQLCAD--IANGFTHHTGLLSVLA 231
DB 204 GSILTVSRTPCPDPLFYICTAQNPNVSQRSLSLPHVVGQFCTDPCASRGGTTGET-VVGVLG 262

QY 232 MFLVLVLISL-----VFLFR---LFKRODASKKTIYTYIMASRNTQPAESRIY 279
DB 263 EPTUPLALPACRDTEKVVLMFNTSLISKREBEAATADPLI-----KSRDPYKRVW 314

RESULT 11
Q8BFV0 PRELIMINARY; PRT; 140 AA.
AC Q8BFV0;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:AL30013D22 product:CD84 antigen, full insert sequence
DE (Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:A530016A13 product:CD84 antigen, full insert
DE sequence).
GN Name=Cd84;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RIKEN FANTOM Consortium;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RIKEN FANTOM Consortium;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RIKEN FANTOM Consortium;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[4]
```

```

[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
RX MEDLINE=25030913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK037385; BAC29799.1; -
DR EMBL; AK040694; BAC30670.1; -
DR MGD; MGI:1336885; CD84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 140 AA; 16141 MW; EB437F013EF3869D CRC64;

Query Match      22.3%; Score 378.5; DB 2; Length 140;
Best Local Similarity 58.3%; Pred. No. 5.4e-22;
Matches 77; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MAQHHLWILLCLQTPWPAAGKSEIFVNGILGESVTFPVNIQBPQVKIIAITSKTSV 60
DB 1 MAQHHLWILLCLQTPWPAAGKSEIFVNGILGESVTFPVNIQBPQVKIIAITSKTSV 60

QY 61 AYVTPGDSFETAPVTVTHRNYYRIHALGPNYINLVISDLRMEADAGYKADINTQADPYTT 120
DB 61 AFIPKGVNKAEE-VTITQGTGKRIEIDQYDLVIRDLRMEADAGYKADINEE-TI 117

QY 121 TKRYNLQIYRRL 132
DB 118 TKIYVLIHYRKL 129

RESULT 12
Q8VE93 PRELIMINARY; PRT; 285 AA.
AC Q8VE93;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SLAM family member 9.
GN Name=Slamf9;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RIKEN FANTOM Consortium;
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schuler G.D.,
```


ID Q8BT00 PRELIMINARY; PRT; 285 AA.
AC Q8BT00; TISSUE=B lymphocyte;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Mus musculus B lymphocyte B cells CRL-1702 WEHI 231 cDNA, RIKEN full-length enriched library, clone:G430073H03 product:weakly similar to CD84-H1 (CD2 FAMILY 10).
DE CD84-H1 (CD2 FAMILY 10).
GN Name=Slamf9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Haseizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]

DR EMBL; AK090041; BAC41061.1; -.
DR MGD; MGI:1923692; Slamf9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 285 AA; 31759 MW; 48675E0611027B3B CRC64;

Query Match 21.7%; Score 368; DB 2; Length 285;
Best Local Similarity 36.5%; Pred. No. 8.7e-21;
Matches 93; Conservative 39; Mismatches 111; Indels 12; Gaps 5;

QY 6 LWILLCLQTPPEAAGKDSBFTVNGILGESVTFPPVQIEPRQVKIIIAWTSKTSVAYVTP 65
DB 5 LWSLLLLQEAAGFGSGDDEEVEVIGVQESINLSLEPSNEEIKHIDWLQNNIAIYKP 64
QY 66 GDEETAPVTVTHRYNRYERIHAGFNPNVNLVSDLEMEDAGDYKADINTQADPYTTTKRYN 125
DB 65 GKKGQPAVIMAVDPYRGVRSISSESYSLHISNLTWEDSGLYNAQVNLKTSSESHITKSYH 124
QY 126 LQIVRRLCKPKITQSLMASVNSTCVTLTSCVKEKKNVTYNW-----SPLGEGNVLIQ 179
DB 125 LRVYRLSKPHITVNSNISSEGVNCSITCSIERAGMDVTYIWLSSQDSTNTSHSGSVLS 184
QY 180 IFQPEDQELTYCTTAQNPVSN-NSDSISARQLCADIAMGFRTHHTGL-LSVLAMFFLLV 237
DB 185 TSWRPGRKAPSYTCRVSNPVSNISSHRISVGSFCAD--PGYPERKSMCLLVKSLFLLLL 242
QY 238 LILSSV--FLFRLFK 250
DB 243 LAILTVGLCLFRAQK 257

RESULT 15
Q9D780 PRELIMINARY; PRT; 285 AA.
AC Q9D780;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310026104 product:weakly similar to CD84-H1 (CD2 FAMILY 10).
DE Name=Slamf9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]

Job time : 147.561 secs

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK009505; BA26328.1; -.
DR MGD; MGI:1923692; Slamf9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 285 AA; 31764 MW; 33BDB4AC33A5C1B3 CRC64;

Query Match 21.6%; Score 367; DB 2; Length 285;
Best Local Similarity 35.2%; Pred. No. 1e-20;
Matches 93; Conservative 42; Mismatches 117; Indels 12; Gaps 5;

Qy 6 LWILLCLIQWPEAAGKDSIEFTVNGILGESVTFPVNIQBPQVKIIAMTSKTSVAVYTP 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5 LWSLLLLLQEAQKSGDDEPDEVGVQLQESINLSLEIPSNIEIKHIDWLFQNNIAIVKP 64
Qy 66 GDSSTAPVVTTHRYNRYERHALGNPNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 GKQGPVIMAVDPYRGRVSISSSYSLHSINLTWEDSGLYNAQVNLKTSSEHITKSYH 124
Qy 126 LQIYRLGKPKITQSLMASVNSTCNVLTCSVEKEKNVTYNW-----SPLGEGNVLQ 179
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 LRVYRLSKPHITVNSNISIEGVNCSILTCSIERAGMDVTYIWLSSQDSTNTSHEGSVLS 184
Qy 180 IFQTPEDQELTYTCTAQNPSVN-NSDSISARQLCADIAMGPRHTHTGL-LSVLAMFFLV 237
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 TSWPFGDKAPSYTCEVSNPISNISRISVGSFCAD--PGYLEKPSMLCLIVKSLFLLL 242
Qy 238 LILSSV--FLPRLFKRQDAASKX 259
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
243 LAITVGLCLFRAQKSYETPRVK 266
```

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2005, 03:24:06 ; Search time 5771.83 seconds
(without alignments)
2761.994 Million cell updates/sec

Title: US-09-882-171-483

Perfect score: 1696
Sequence: 1 MAQHLLWLLCLQTPENA.....KASTQSKPGTSSVEIVIX 329

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114004_26025/app.query.fasta_1.910
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09882171 @CGN_1_1_4930 @runat_04022005_114004_26025 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.ey.*
13: gb.un.*
14: gb.vi.*

RESULT 1

AX474268

LOCUS

DEFINITION

AX474268

ACCESSION

VERSION

AX474268.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

1

AUTHORS

Fraser, C.C.

TITLE

Cd2000 and cd2001 molecules and uses thereof

JOURNAL

Patent: EP 1223218-A 29 17-JUL-2002;

Millennium Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

1..1040

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 6.8e-158

Score: 1695.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Length: 1040

Matches: 328

Conservative: 0

Mismatches: 0

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	99.9	1040	6	AX474268 Sequence
2	1695	99.9	1040	9	HSU82988 Human leuko
3	1695	99.9	1067	9	AF054815 Homo sapi
4	1695	99.9	3173	6	BD191209 186 human

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	1695	99.9	3173	6	AX924719	Sequence
6	1695	99.9	3278	9	BC020063	Homo sapi
7	1695	99.9	3296	6	C0718714	Sequence
8	1695	99.9	3299	9	HSJA3324	Homo sapi
9	1695	99.5	984	9	CR541847	Homo sapi
10	1672.5	98.6	1100	9	HSLDACD84	H. sapiens m
11	1488.5	98.4	1118	9	AF054816	Homo sapi
12	1488.5	87.8	967	9	AF054817	Homo sapi
13	1320	77.8	1299	9	HSU96627	Homo sapien
14	1125	66.3	858	9	AF054818	Homo sapi
15	944.5	55.7	1132	10	AF043445	Mus muscu
16	607	35.8	1088	9	HSLDAL	Homo sapi
17	607	35.8	175386	9	AL138930	Human DNA
18	607	35.8	176698	2	AL355996	Homo sapi
19	607	35.8	179614	2	AC012471	Homo sapi
20	607	35.8	189057	2	AC027082	Homo sapi
21	543	32.0	179614	2	AC012471	Homo sapi
22	450	26.5	748	6	CQ431481	Sequence
23	440	25.9	70557	2	AC090143	Homo sapi
24	439	25.9	584	9	HSLDA2	Homo sapi
25	439	25.9	70557	2	AC090143	Homo sapi
26	411	24.2	296	6	BD247970	5' ESTs f
27	411	24.2	296	6	CQ771933	Sequence
28	382.5	22.6	2286	6	AX357541	Sequence
29	382.5	22.6	2286	9	HUMLY9	Homo sapien
30	376	22.2	1104	10	BC019477	Mus muscu
31	374	22.1	2448	9	AF244129	Homo sapi
32	373	22.0	870	6	AX474314	Sequence
33	373	22.0	941	9	BC074754	Homo sapi
34	373	22.0	1139	6	AX474313	Sequence
35	373	22.0	1139	9	AF275725	Homo sapi
36	373	22.0	1170	9	AY034613	Homo sapi
37	373	22.0	1423	6	AX357479	Sequence
38	370.5	21.8	1042	9	HSJA306388	Homo sapi
39	370.5	21.8	1868	6	AX574548	Sequence
40	370.5	21.8	1868	9	AY358159	Homo sapi
41	370.5	21.8	2718	9	HSMB04165	Homo sapi
42	370	21.8	870	6	AX474331	Sequence
43	370	21.8	870	6	AX474332	Sequence
44	370	21.8	870	6	AX474333	Sequence
45	370	21.8	993	6	AX474241	Sequence

ALIGNMENTS

AX474268 1040 bp DNA linear PAT 12-AUG-2002
Sequence 29 from Patent EP1223218.
AX474268
AX474268.1 GI:22213881

Qy	1	MetAlaGlnHisIeuTrpIleLeuLeuLeuCysIleuGlnThrTrpProGluAlaAla	20
Db	43	ATGGCTCAGCACCACTATGGATCTTGCTCTTTGCCCTGCAAACTCGCCGGAAGCAGCT	102
Qy	21	GlyValAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro	40
Db	103	GGAAAAGACTCAGAAATCTTCAAGTGAATGGGATTTCTGGAGAGACTCAGTCATCTTCCT	162
Qy	41	ValAsnIleGlnGluProArgGlnValLysIleIleAlaIleThrSerLysIleThrSerVal	60
Db	163	GTAATATCAAGAACCCAGCAAGTAAATCATTTGCTTGGACTTCTTAAACATCTGT	222
Qy	61	AlaTyrrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn	80
Db	223	GCTTATGTAAACACAGAGACTCAGAAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT	282
Qy	81	TyrTyrrGluArgIleHisAlaLeuGlyProAsnTyrrAsnLeuValIleSerAspLeuArg	100
Db	283	TATTATGAACGGATACATGCCCTTAGGTCGAACTACATCAATCTGGTCATTTAGGATCTGAGG	342
Qy	101	MetGluAspAlaGlyAspTyrrLysAlaAspIleAsnThrGlnAlaAspProTyrrThrThr	120
Db	343	ATGGAGACGACGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACC	402
Qy	121	ThrLysArgTyrrAsnLeuGlnIleTyrrArgArgLeuGlyLysProLysIleThrGlnSer	140
Db	403	ACCAAGCGCTACAACTCGAAATCTATCTCGGCTTGGGAAACCAAAATTTACACAGAT	462
Qy	141	LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu	160
Db	463	TTAATGGCATCTGTGAACAGCACCTGTAATGTTCACACTGACATGCTCTGTAGAGAAAGAA	522
Qy	161	GluLysAsnValThrTyrrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle	180
Db	523	GAAGAAGATCTGACATACAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAAATC	582
Qy	181	PheGlnThrProGluAspGlnGluLeuThrTyrrThrCysThrAlaGlnAsnProValSer	200
Db	583	TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCCAAGACCTCTGTCAGC	642
Qy	201	AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg	220
Db	643	AACAAATTTCTGACTCCATCTCTGCCCCGGAGCTCTGTGCAGACATCCCAATGGGCTTCGT	702
Qy	221	ThrHisIleThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu	240
Db	703	ACTCACACACCGGTGTCTGACGGTGCTGGCTATGTTCTTCTTCGTTGTTCTCATCTG	762
Qy	241	SerSerValPheLeuPheArgLeuPheLysArgGlnAspAlaAlaSerLysIleThr	260
Db	763	TCCTTCAGTGTATTTGTTGCTTTGTTCAAGAGAAGACAAGATGCTGCTCTCAAGAAACCC	822


```
CDS
1..>984
/genes="CD84"
/codon_start=1
/protein_id="CAG46645.1"
/db_xref="GI:49456649"
/translation="MAQHLLWLLCLQWPEAAGKDSIFVTNGILGESVTFPVNIO
BPROVKIIAWTSKTSVAVYTPGDSETPVTVTHRYNRYERIHAGPNYNLVISDLRME
DAGDYKADINTQADPYTTTKRNLQIYRLGPKITQSLMASVNSCTNLTCSVEKE
EKNTVNWSPGLEGNVLOI FOTPEDELTCTCAQNPVNSNDSISAROLCADIAMG
FRTHHTGLLSVLAMFLLVLLSSVFLFRKRDQDAASKTLYTYIMASRNTQPAES
RYDEILQSKVLPSKEESVNTVYSEVQFADKMGKASTQDSKPPGSSYEIV"
ORIGIN
Alignment Scores:
Pred. No.: 3 92e-157 Length: 984
Score: 1687.00 Matches: 327
Percent Similarity: 99.70% Conservativeness: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 9 Gaps: 0
US-09-882-171-483 (1-329) x CR541847 (1-984)
QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20
DB 1 ATGGCTCAGCACCACTATGATCTTCTCTTCTGCTGCAACCTGGCGGAAGCAGCT 60
QY 21 GlyIysAspSerGluLeuPheThrValAsnGlyIleLeuGlyLeuSerValThrPhePro 40
DB 61 GGAAAGACCTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACTTCCCT 120
QY 41 ValAsnIleGlnGluProArgGlnValIleValIleLeuValIleLeuValIleLeuVal 60
DB 121 GTAAATATCCAGAACACCGGCAAGTTAAATCATCTGCTGGACTCTTAAACATCTGTT 180
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 181 GCATTATGTAACACCGAGAGACTCAGAACACGACCGGTAGTTACTGTGACCCACAGAAAT 240
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
DB 241 TATTATGAACGGATACATGCTTAGGTCCGAACCTACAACTCTGTCATTAGCATCTGAGG 300
QY 101 MetGluAspAlaGlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
DB 301 ATGGAAGACGAGAGACTCAAGCAGACATAAATACAGGCTGATCCCTACACCACC 360
QY 121 ThrIysArgTyrAsnLeuGlnIleTyrArgGluLeuGlyLysProIysIleThrGlnSer 140
DB 361 ACCAAGCGCTACAACTGCAAACTATCTGCTGGCTGGGAACCAAAATACACAGAGT 420
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluIleLeu 160
DB 421 TTAATGCGCATCTGTGAACAGACACCTGTAATGTTCACACTGACATGCTCTGTAGAGAAGAA 480
QY 161 GluIysAsnValThrTyrAsnTyrSerProLeuGlyGluGlyAsnValLeuGlnIle 180
DB 481 GAAAGAAGATGTGACATCAATTTGAGTGCCCTGGGAGAGAGGTAATGTCCTTCAATC 540
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
DB 541 TTCAGACTCTGTAGGACCAAGAGCTGACTTACAGGTGTACAGCCAGAACCCCTGTGAGC 600
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 601 AACAAATCTGACTCTCACTCTGCTGCGGCGAGCTCTGTGAGACATCGCAATGGGCTCCGT 660
QY 221 ThrHisThrGlyLeuLeuSerValIleAlaMetPhePheLeuValLeuIleLeu 240
DB 661 ACTCACACACCGGGTGTGAGGCTGTGGCTATGTTCTTCTGCTGTTGTTCTCATCTG 720
QY 241 SerSerValPheLeuPheArgLeuPheIysArgGlnAspAlaAlaSerIysIleThr 260
DB 721 TCTTCAGTGTCTTCTGCTGCTTCTCAAGAGAACACAGATGCTGCTCTCAAGAAACC 780
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
DB 781 ATATACACATATATCATGCTTCAAGGAACACCCAGCAGCAGAGTCCAGAAATCTATGAT 840
QY 281 GluIleLeuGlnSerIysValLeuProSerIysGluGluProValAsnThrValTyrSer 300
DB 841 GAAATCTGTCAGTCCCAAGGTGCTTCCCTCAAGGAAGAGTCAAGTGAACACAGTTTATTC 900
QY 301 GluValGlnPheAlaAspIleMetGlyIleAlaSerThrGlnAspSerIysProProGly 320
DB 901 GAAGTGCAGTTTCTGCTGATAGATGGGAAAGCAGCAGCAGCAGTAAACCTCTCTGGG 960
QY 321 ThrSerSerTyrGluIleValIle 328
DB 961 ACTTCAAGCTATGAAATTTGTGATC 984
RESULT 10
HSLDACD84 1100 bp mRNA linear PRI 04-JAN-2002
LOCUS H.sapiens mRNA for leukocyte differentiation antigen CD84.
DEFINITION Y12632
ACCESSION Y12632.1 GI:18073112
VERSION 1
KEYWORDS leukocyte differentiation antigen.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Gaya, A.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1100)
AUTHORS Gaya, A.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Vallarreal 170, Barcelona 08036, SPAIN
FEATURES
Location/Qualifiers
1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="leukocyte"
/clone_lib="lambda gt10"
70..1089
/codon_start=1
/product="leukocyte differentiation antigen CD84"
/protein_id="CAA73181.1"
/db_xref="GI:18073113"
/db_xref="UniProt/TREMBL:Q8WMI8"
/translation="MAQHLLWLLCLQWPEAAGKDSIFVTNGILGESVTFPVNIO
BPROVKIIAWTSKTSVAVYTPGDSETPVTVTHRYNRYERIHAGPNYNLVISDLRME
DAGDYKADINTQADPYTTTKRNLQIYRLGPKITQSLMASVNSCTNLTCSVEKE
EKNTVNWSPGLEGNVLOI FOTPEDELTCTCAQNPVNSNDSISAROLCADIAMG
FRTHHTGLLSVLAMFLLVLLSSVFLFRKRDQDAASKTLYTYIMASRNTQPAES
RYDEILQSKVLPSKEESVNTVYSEVQFADKMGKASTQDSKPPGSSYEIV"
CDS
sig_peptide 70..132
mat_peptide 133..1086
/product="leukocyte differentiation antigen CD84"
ORIGIN
Alignment Scores:
Pred. No.: 1 23e-155 Length: 1100
Score: 1672.50 Matches: 327
Percent Similarity: 96.46% Conservativeness: 0
Best Local Similarity: 96.46% Mismatches: 1
Query Match: 98.61% Indels: 11
DB: 9 Gaps: 1
US-09-882-171-483 (1-329) x HSLDACD84 (1-1100)
QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20
```

Db 70 ATGGCTCAGCACCACTATGATCTTCTCTCTTCTGCTGCAACCTGCGGAGACAGCT 129
 Qy 21 GlyLysAspSerGluPheThrValAsnGlyLeuGlyGluSerValThrPhePro 40
 Db 130 GGAAAGAGCTCAGAAATCTTACAGTGAATGGATCTTGGAGAGTCACTTCTCCCT 189
 Qy 41 ValAsnIleGlnGluProArgGlnValIleAlaThrThrSerIysThrSerVal 60
 Db 190 GTAAATATCCAAAGAACCGGCAAGTTAAATCATTTGCTTGACCTTCAAACATCTGTT 249
 Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
 Db 250 GCTTATGTAAACACGAGGAGACTCAGAACAGACACCGCTAGTACTGTGACCCACAGAAAT 309
 Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
 Db 310 TATTATGAACGATACATGCTTAGCTCGGAATCAATCTGGTCAATTAGGATCTGAGG 369
 Qy 101 MetGluAspAlaGlyAspTyrIlysalaspIleAsnThrGlnAlaAspProTyrThrThr 120
 Db 370 ATGGAGAGCGGAGGAGACTACAAAGCAGACATAAATACAGAGCTGTATCCCTTACACACC 429
 Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
 Db 430 ACCAAGCGCTACAACTGCAATCTATCGTGGCTTGGAAACCAAAATTTACACAGAGT 489
 Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
 Db 490 TTAATGGCATCTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAGAAGAA 549
 Qy 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
 Db 550 GAAAGAAATGTACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATC 609
 Qy 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
 Db 610 TTCCAGACTCTTGGAGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTCTGCAGC 669
 Qy 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
 Db 670 AACAAATCTTGACTCCATCTCTCCCGGCGACTCTGTGCAGACATCGCAATGGGCTTCCGT 729
 Qy 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuValLeuIleLeu 240
 Db 730 ACTCACCACACCGGGTGTGAGCGTGTGGCTATGTTCTTCTGCTGTCTCATCTCTG 789
 Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAsp----- 254
 Db 790 TCTTCAGTGTGTTTGTTCGGTTGTTCAAGAGACACAAAGGTTCTGCTTGAACACCTTC 849
 Qy 255 -----AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg 269
 Db 850 ACTAAGAACCTTATGCTGCTTCAAGAAACCATATACATATATCATGCTTCAAGG 909
 Qy 270 AsnThrGlnProAlaGluSerArgIleTyrAspGluIleLeuGlnSerLysValLeuPro 289
 Db 910 AACACCCAGCAGAGTCCAGATCTATGATGAATCTCTGAGTCCAGTCCAGGTGTTCCC 969
 Qy 290 SerLysGluGluProValAsnThrValTyrSerGluValGlnPheAlaAspLysMetGly 309
 Db 970 TCCAGGAAGAGCCAGTGAACACAGTTTATCCGAAGTGCAGTCTGCTGATAAGATGGG 1029
 Qy 310 LysAlaSerThrGlnAspSerLysProProGlyThrSerSerTyrGluIleValIle 328
 Db 1030 AAGCCAGACACAGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTATC 1086

RESULT 11
 AF054816 1118 bp mRNA linear PRI 01-JAN-2000
 LOCUS Homo sapiens leukocyte differentiation antigen CD84 isoform CD84a
 DEFINITION (CD84) mRNA, complete cds.
 ACCESSION AF054816

AF054816.1 GI:6650107
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1118)
 AUTHORS Palou,E., Sole,J., Pirotto,F. and Gaya,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
 FEATURES
 source
 1. .1118
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 gene
 1. .1118
 /gene="CD84"
 70. .1107
 /gene="CD84"
 /codon_start=1
 /product="leukocyte differentiation antigen CD84 isoform CD84a"
 /protein_id="AAF21722.1"
 /db_xref="GI:6650108"
 /translation="MAQHLLWLLCLQTPWPEAGKDSKSEIFTVNGILGESVTFPVNIQ
 EPROVKIIAMTSKTSVAVTPGDSATPVTVTHRVYRTHALGNVNLVLSLRKE
 DAGYKADINTQADPYTTKRYNLQIYERLQKPKITQSLASVNSTCNVLTJCSVEKE
 EKNYVNSPLGSEGNVLIQIFQTPEDQELYYTCTAQNPNVNSDSISARQLAIAMG
 FRHTHTGLLSVLAMFLLVILSSVFLRFRRQGRIFPEGSCLNTFTKPNPYAASKK
 TIITYIMASRNTQPAESRIYDEILQSKVLFSEKPVNTVYSEVQFADKMGKASTQDSK
 PPGTSYSVEIVI"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.48e-155 Length: 1118
 Score: 1669.50 Matches: 327
 Percent Similarity: 94.78% Conservative: 0
 Best Local Similarity: 94.78% Mismatches: 1
 Query Match: 98.44% Indels: 17
 DB: 9 Gaps: 1
 US-09-882-171-483 (1-329) x AF054816 (1-1118)
 Qy 1 MetAlaGlnHisHisLeuTyrIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
 Db 70 ATGGCTCAGCACCACTATGATCTTCTCTCTTCTGCTGCAACCTGCGGAGACAGCT 129
 Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
 Db 130 GGAAAGAGCTCAGAAATCTTACAGTGAATGGATCTTGGAGAGTCACTTCTCCCT 189
 Qy 41 ValAsnIleGlnGluProArgGlnValIleAlaThrThrSerIysThrSerVal 60
 Db 190 GTAAATATCCAAAGAACCGGCAAGTTAAATCATTTGCTTGACCTTCAAACATCTGTT 249
 Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
 Db 250 GCTTATGTAAACACGAGGAGACTCAGAACAGACACCGCTAGTACTGTGACCCACAGAAAT 309
 Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
 Db 310 TATTATGAACGATACATGCTTAGCTCGGAATCAATCTGGTCAATTAGGATCTGAGG 369
 Qy 101 MetGluAspAlaGlyAspTyrIlysalaspIleAsnThrGlnAlaAspProTyrThrThr 120
 Db 370 ATGGAGAGCGGAGGAGACTACAAAGCAGACATAAATACAGAGCTGTATCCCTTACACACC 429
 Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
 Db 430 ACCAAGCGCTACAACTGCAATCTATCGTGGCTTGGAAACCAAAATTTACACAGAGT 489
 Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160

Qy	281	GluileLeuGlnSerLys-ValleuProSerLysGluGluProValAsnThrValTyrSe	300
Db	826	-----CAAGGTGCTTCCCTCCCAAGGAAGCCAGTGAACACAGATTATTC	870
Qy	300	rGluValGlnPheAlaAspLysMetClyLysAlaSerThrGlnAspSerLysProGln	320
Db	871	CGAAGTGCAGTTTGGCTGAATAAGTGGGAAGCCAGACACAGGACAGTAACCTCTGG	930
Qy	320	yThrSerSerTyrGluileValile	328
Db	931	GACTTCAGGTATGAATTTGTGATC	955
RESULT 13			
LOCUS	HSU96627	1299 bp mRNA linear	PRI 13-JAN-1999
DEFINITION		Homo sapiens CD84 mRNA, alternatively spliced, complete cds.	
ACCESSION	U96627	U96627.1 GI:4100318	
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 1299)	
JOURNAL		Palou,E., Freed,J.H., Sole,J., Pi.A., Villella,A., Vives,J. and	
FEATURES		Gaya,A.	
source		Direct Submission	
		Submitted (07-APR-1997) Servei Immunologia, Hospital Clinic,	
		Villarreal 170, Barcelona 08036, Spain	
		Location/Qualifiers	
		1..1299	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		70..912	
		/notes="alternatively spliced"	
		/codon_start=1	
		/product="CD84"	
		/protein_id="AA004232.1"	
		/db_xref="GI:4100319"	
		/translations="MAQHLLWILLCLQTWPAAKDKSEIFTVNGLIGESVTFPNVIQ	
		EPQVKDIANTSVAIVTPGDSETAPVVTVTHRYNIEHALGPNNLVISDLRME	
		DAGDYKADINTQDPYTKRNLYRLRGPKKITQSILMASVNSCNVLTSVEKE	
		EKNVTYNWSFLGEENVLQFPPEQEQLTYTCTAQNPVSNNSDSIASBOLCADIAMG	
		FRTHTGLLSVLAMFLLVLLSVLFRLFRRQRRIIPFGKMWLIFSPPGTEALY	
		PRFS"	
ORIGIN			
Alignment Scores:			
Pred. No.:	1.08e-120	Length:	1299
Score:	1320.00	Matches:	253
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	77.83%	Indels:	0
D:	9	Gaps:	0
US-09-882-171-483 (1-329) x HSU96627 (1-1299)			
Qy	1	MetaLaGlnHisLeuTriPheLeuLeuLeuCysLeuGlnThrTrpProGluAlaAala	20
Db	70	ATGGCTCAGCACCACTATGATCTCTCTCTTGGCTGCAACCTCGCCGGAAGCAGCT	129
Qy	21	GlyLysAspSerGluilePheThrValAsnGlylleLeuGlyGluSerValThrPhePro	40
Db	130	CGAAAGAACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCATCTTCCCT	189
Qy	41	ValAsnleGlnGluProArgGlnVallyslelleleatrpThrSerLysThrSerVal	60
Db	190	GFAAATATCCAAGAACCAACGACAGTTAAATCATCTGCTGGACTTCTTAAACATCTGTT	249
Qy	61	AlatyrvValThrProGlyVasppSerGluThrAlaProValValThrValThrHisArgAsn	80

Mon Feb 7 10:55:04 2005

us-09-882-171-483.rge

```

QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
406 ACCAAGATCTACTACCTTTCATATCTACCGTCGACTTAAACACCAAAATTTACACAGAT 465
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 TTGATATCATCTTTGAACAATACCTGTAATATCACACTGACATGCTCTGTGGAAGAA 525
QY 161 GluLysAsnValThrTyrAsnThrSerProLeuGlyGluGlyAsnValLeuGlnIle 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
526 GAAAGAGATGTCATATAGCTGGAGTCCCTTTGGAGAGAAAAGCAATGCTCTTCAAATC 585
QY 181 PheGlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
586 GTCCACTCCCCCATGACCAAACTGACCTACACATGTACAGCCCAAGACCCCTGTACG 645
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
646 AACAGTTCGACTCTGTCTACTGTCCAGCAGCCATGTACAGAC---ACTCCAAGCTTCCAT 702
QY 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
703 CCTGGCCTGCTGTGTTGCCAGGAGATTGGCCGTCTCTTCTGCTTATTCTCATCCG 762
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAla----- 255
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
763 ATGTTGGCATTTCTGTTCCGTTTGTATAGAGAGCGGAGCAGGATTGCTCTGGAAGCA 822
QY 256 -----AlaSerLysLysThrIleTyrThrIleMetAlaSerArgAsnThrGlnPro 273
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
823 GATGATGCTCAAGAGAAACAGTATATGCTGTAGTT-----TCAAGAAATGCTCAACCC 876
QY 274 AlaGluSerArgIleTyrAspGluIleLeuGlnSerLysValLeuProSerLysGluGlu 293
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
877 ACAGAGTCCAGATCTATGATGAATCCCTCAGTCCAGATGCTGCTCTGTAAGAAAGAT 936
QY 294 ProValAsnThrValTyrSerGluValGlnPheAlaAspLysMetGlyLysAlaSerThr 313
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
937 CCGGTGACCAACCATTTATTCCTCAGTGCAGCTTCTGAGAGATGAGAGAAACCAACATG 996
QY 314 GlnAspSerLysProGlyThrSerSerTyrGluIleValIle 328
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
997 AAGGACAGAGTCTGCCTAAGGCTTTGGGTATGTAATGAAATTTGTGTC 1041

```

Search completed: February 5, 2005, 09:29:27
Job time : 5781.83 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 11:54:40 ; Search time 89.3239 Seconds
(without alignments)
861.643 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220

Perfect score: 1039
Sequence: 1 KDSIFTVNGILGESVTFPV.....NNSDSISARQLCADIAMGPR 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039	100.0	328	5	AAB47878 SCZ/CD84.
2	1039	100.0	328	5	AAB47878 Human CD8
3	1039	100.0	328	8	ADL82907 Human PRO
4	1039	100.0	328	8	ADL82907 Human PRO
5	1039	100.0	328	8	ADL82907 Human PRO
6	1039	100.0	328	8	ADL82907 Human PRO
7	1039	100.0	328	2	ADP23943 PRO polyp
8	1039	100.0	329	2	ADP23943 PRO polyp
9	1039	100.0	329	2	ADP23943 PRO polyp
10	1039	100.0	329	6	ADP23943 PRO polyp
11	1039	100.0	329	7	ADP23943 PRO polyp
12	352	33.9	526	8	ADL57243 Human NOV
13	352	33.9	526	8	ADL57243 Human NOV
14	352	33.9	551	5	ADL57105 Human NOV
15	352	33.9	565	8	ADL57105 Human NOV
16	352	33.9	610	5	ADL57103 Human NOV
17	352	33.9	615	8	ADL57103 Human NOV
18	343.5	33.1	654	8	ADL57103 Human NOV
19	343.5	33.1	654	8	ADL57103 Human NOV
20	332	32.0	217	5	ADL57103 Human NOV
21	332	32.0	217	7	ADL57103 Human NOV
22	332	32.0	236	5	ADL57103 Human NOV
23	332	32.0	236	7	ADL57103 Human NOV
24	332	32.0	270	5	ADL57103 Human NOV
25	332	32.0	270	7	ADL57103 Human NOV

26	332	32.0	289	4	AAB47878	Aae12078 Dendritic
27	332	32.0	289	5	AAB47878	Aae26243 Human CD2
28	332	32.0	289	5	AAB47878	Aae26251 Human CD2
29	332	32.0	289	5	AAB47878	Aae26253 Human CD2
30	332	32.0	289	5	AAB47878	Abp65110 Hypoxia-i
31	332	32.0	289	7	ABW01823	Abw01823 Human CD2
32	332	32.0	289	7	ABW01833	Abw01833 Human CD2
33	332	32.0	289	7	ABW01831	Abw01831 Human CD2
34	331	31.9	289	5	AAB47878	Aae26250 Human CD2
35	331	31.9	289	7	ABW01830	Abw01830 Human CD2
36	329	31.7	289	5	AAB47878	Aae26252 Human CD2
37	329	31.7	289	7	ABW01832	Abw01832 Human CD2
38	316.5	30.5	203	5	AAB47878	Aae26232 Human CD2
39	316.5	30.5	203	7	ABW01811	Abw01811 Human CD2
40	316.5	30.5	309	5	AAB47878	Aae26222 Human CD2
41	316.5	30.5	309	7	ABW01801	Abw01801 Human CD2
42	316.5	30.5	331	5	ABW0183	Abw0183 Human pol
43	316.5	30.5	331	5	AAB47878	Aae26220 Human CD2
44	316.5	30.5	331	6	ABR39107	AbR39107 Human NTB
45	316.5	30.5	331	6	ABU03145	Abu03145 Human imm

ALIGNMENTS

RESULT 1

AAB47878
ID AAB47878 standard; protein; 328 AA.

AC AAB47878;

DT 02-MAY-2002 (first entry)

DE SCZ/CD84.

XX SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele;
XX polymorphic marker; chromosome 1q22.

OS Homo sapiens.

XX WO200202054-A2.

XX 10-JAN-2002.

XX 23-APR-2001; 2001WO-US013040.

XX 21-APR-2000; 2000US-0198873P.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Brzustowicz LM, Bassett AS;

XX WPI; 2002-171605/22.

XX N-PSDB; AAI72383.

XX Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by
XX determining presence or absence of an allele of a linked polymorphic
XX marker present on chromosome 1q22, were the marker is linked to a variant
XX form of the SCZ gene.

XX Example 6; Page 70; 82pp; English.

XX This sequence is encoded by the SCZ gene which was isolated using the
XX method of the invention. The SCZ gene has been previously identified as
XX CD84, GenBank Accession No: NM_003874. CD84 is a 73 kDa antigen present
XX on platelets, monocytes and circulating B cells. This protein may be
XX involved in the processes by which the brain responds to biological
XX stimuli. Therefore they may provide targets for therapeutic intervention
XX in the treatment of schizophrenia. The SCZ sequence may be used in a new
XX method of diagnosing susceptibility to schizophrenia in a patient. The
XX method comprises determining the presence or absence of an allele of a
XX linked polymorphic marker in the DNA of the patient. The polymorphic
XX marker is present in chromosome 1q22 and is linked to a gene (SCZ) having

```
CC a variant form associated with a phenotype of schizophrenia
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 1039; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAVYTPGDSAPVVTTHRNY 60
Db |||||
QY 22 KDSIFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAVYTPGDSAPVVTTHRNY 81
Db |||||
QY 61 YERIHALGPNYLVISDLRMEADGDKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
Db |||||
QY 82 YERIHALGPNYLVISDLRMEADGDKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141
Db |||||
QY 121 MASVNSTCNVTITCSVEKEKNVTYNSPLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
Db |||||
QY 142 MASVNSTCNVTITCSVEKEKNVTYNSPLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 201
Db |||||
QY 181 NSDSISARQLCADIAMGFR 199
Db |||||
QY 202 NSDSISARQLCADIAMGFR 220
Db |||||

RESULT 2
AAE26238
ID AAE26238 standard; protein; 328 AA.
AC AAE26238;
XX
XX 14-NOV-2002 (first entry)
DT
DE Human CD84 protein.
XX
KW Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein;
KW immune proliferative disorder; immune disorder; rheumatoid arthritis;
KW carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease;
KW Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic;
KW osteoarthritis; allergic inflammatory disorder; viral infection; asthma;
KW psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis;
KW diabetes mellitus; septic shock; chronic obstructive pulmonary disease;
KW emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis;
KW acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic;
KW immunosuppressive; neuroprotective; antiinflammatory; Crohn's disease;
KW osteopathic; antibacterial; immunomodulator; inflammatory bowel disease;
KW jaundice; dermatological; ulcerative colitis; AIDS; CD84.
XX
OS Homo sapiens.
XX
XX EP1223218-A1.
XX
XX 17-JUL-2002.
XX
XX 02-NOV-2001; 2001EP-00309339.
XX
XX 03-NOV-2000; 2000US-00706167.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Fraser CC;
XX
XX WPI; 2002-520680/67.
XX
XX N-PSDB; AAD43563.
XX
XX Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
XX like domains and SLAM associated protein, termed CD2000 or CD2001, useful
XX for treating immune, inflammatory, or hepatic circulatory disorders.
XX
XX Disclosure; Page 76-77; 138pp; English.
XX
XX The invention relates to nucleic acid molecule, designated CD2000 which
XX encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains
CC
```

```
CC and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is
CC useful for treating disorder such as immune proliferative disorders,
CC immune disorders (e.g. carcinoma), viral infection, autoimmune disorders
CC (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's
CC disease), T cell disorder (e.g. acquired immune deficiency syndrome
CC (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative
CC colitis), inflammatory disorders (e.g. rheumatoid arthritis and
CC osteoarthritis), allergic inflammatory disorders (e.g. asthma and
CC psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and
CC insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock,
CC chronic obstructive pulmonary disease (e.g. emphysema), bronchitis,
CC cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis,
CC acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in
CC gene therapy. CD2000 DNA is useful in screening assays, detection assays
CC (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomics), and in methods of treatment (e.g.
CC therapeutic and prophylactic). The present sequence is human CD84 protein
CC used in the invention
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 1039; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAVYTPGDSAPVVTTHRNY 60
Db |||||
QY 22 KDSIFTVNGILGESVTFPPVNIQBPQVKIIAWTSKTSVAVYTPGDSAPVVTTHRNY 81
Db |||||
QY 61 YERIHALGPNYLVISDLRMEADGDKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
Db |||||
QY 82 YERIHALGPNYLVISDLRMEADGDKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141
Db |||||
QY 121 MASVNSTCNVTITCSVEKEKNVTYNSPLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
Db |||||
QY 142 MASVNSTCNVTITCSVEKEKNVTYNSPLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 201
Db |||||
QY 181 NSDSISARQLCADIAMGFR 199
Db |||||
QY 202 NSDSISARQLCADIAMGFR 220
Db |||||

RESULT 3
ADL82907
ID ADL82907 standard; protein; 328 AA.
XX
XX ADL82907;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human PRO24934, SEQ ID 109.
XX
XX
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.
XX
XX Homo sapiens.
XX
XX WO2004024097-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029097.
XX
XX 16-SEP-2002; 2002US-0411392P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX Wu TD;
XX
```

DR WPI: 2004-329389/30.
DR N-PSDB; AD182906.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX
PS Claim 10; Fig 109; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IGA deficiency, selective Igm
CC deficiency, selective deficiency of IGC subclasses, immunodeficiency with
CC hyper Igm, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, hypoadrenocorticism, glomerulonephritis, or
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 328 AA;

Query Match 100.0%; Score 1039; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAIVTPGDSAPVTVTHRNY 60
DB 22 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAIVTPGDSAPVTVTHRNY 81
QY 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPVTYTKRYNLQIYRLGPKITQSL 120
DB 82 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPVTYTKRYNLQIYRLGPKITQSL 141
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLQIFQTPEDQELTYTCTAQNPSN 180
DB 142 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLQIFQTPEDQELTYTCTAQNPSN 201
QY 181 NSDSISARQLCADIAMGFR 199
DB 202 NSDSISARQLCADIAMGFR 220

RESULT 4
ADO05708
ID ADO05708 standard; protein; 328 AA.

AC ADO05708;
XX
XX
DT 15-JUL-2004 (first entry)
XX

Human leukocyte differentiation antigen CD84.

DE T cell; antiallergic; immunosuppressive; virucide; antibacterial;
KW antiparasitic; cytostatic; gene therapy; human; CD83;
KW leukocyte differentiation antigen.

XX Homo sapiens.

XX WO2004032867-A2.

XX 22-APR-2004.

XX 09-OCT-2003; 2003WO-US032065.

XX 09-OCT-2002; 2002US-0417102P.

PR 09-OCT-2002; 2002US-0417103P.

PR 09-OCT-2002; 2002US-0417243P.
PR 18-OCT-2002; 2002US-0419575P.
PR 08-NOV-2002; 2002US-0424777P.
PR 08-NOV-2002; 2002US-0424881P.
XX (TOLE-) TOLERRX INC.
XX
XX Rao P, Szymanska G;
XX
XX WPI: 2004-340801/31.
DR N-PSDB; ADO05707.
DR GENBANK; 6650105.
XX

Treating a condition that benefits from modulating regulatory or effector
T cell function comprises administering an agent that modulates the
expression or activity of a gene or polypeptide (e.g. PTGER2, TGPbeta1,
Jagged-1 or GPR-32).

Example; SEQ ID NO 8; 161pp; English.

PS The invention relates to treating a subject having a condition that
XX benefits from modulating the balance of regulatory T cell function
XX relative to effector T cell function, or vice versa, in a subject. The
CC method involves administering an agent that modulates the expression or
CC activity of a molecule selected from PTGER2 and TGPbeta1, or Jagged-1,
CC GPR-32, CD83, CD84, CD89, serotonin R, BY555, serotonin R2C, GPR63,
CC histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-
CC 3-related kinase to the subject, such that treatment occurs. The methods
CC are useful for diagnosing, preventing or treating conditions
CC characterized by a too-vigorous or weak effector T cell or regulatory T
CC cell response to antigens associated with the condition, such as in an
CC allergic response, an autoimmune disorder, a viral infection, a microbial
CC infection, a parasitic infection or a tumour. The present sequence
CC represents a human leukocyte differentiation CD84 antigen, preferentially
CC expressed in regulatory T cells.

XX Sequence 328 AA;

Query Match 100.0%; Score 1039; DB 8; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAIVTPGDSAPVTVTHRNY 60
DB 22 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAIVTPGDSAPVTVTHRNY 81

QY 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPVTYTKRYNLQIYRLGPKITQSL 120
DB 82 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPVTYTKRYNLQIYRLGPKITQSL 141

QY 121 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLQIFQTPEDQELTYTCTAQNPSN 180
DB 142 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLQIFQTPEDQELTYTCTAQNPSN 201

QY 181 NSDSISARQLCADIAMGFR 199

DB 202 NSDSISARQLCADIAMGFR 220

RESULT 5

ADQ19067

ID ADQ19067 standard; protein; 328 AA.

XX ADQ19067;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX Homo sapiens.

XX

PN WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038193.
 XX
 PR 26-NOV-2002; 2002US-0429739P.
 XX
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX
 PI Aziz N, Ginsburg WM, Ziolknik A;
 XX WPI; 2004-441208/41.
 DR
 XX
 XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 XX Example 2; SEQ ID NO 1886; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 1039; DB 8; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7e-88;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
 Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 81
 QY 61 YERIHAGPNVNLVLSDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
 Db 82 YERIHAGPNVNLVLSDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141
 QY 121 MASVNSTCNVTLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 180
 Db 142 MASVNSTCNVTLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
 QY 181 NSDSISARQLCADIAMGFR 199
 Db 202 NSDSISARQLCADIAMGFR 220

RESULT 6
 ADP23943
 ID ADP23943 standard; protein; 328 AA.
 XX
 AC ADP23943;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO:1121.
 XX
 KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.

XX WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX
 DR WPI; 2004-419628/39.
 DR N-PSDB; ADP23942.
 XX
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 XX Claim 7; SEQ ID NO 1121; 2940pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 1039; DB 8; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7e-88;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
 Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 81
 QY 61 YERIHAGPNVNLVLSDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
 Db 82 YERIHAGPNVNLVLSDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141
 QY 121 MASVNSTCNVTLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 180
 Db 142 MASVNSTCNVTLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
 QY 181 NSDSISARQLCADIAMGFR 199
 Db 202 NSDSISARQLCADIAMGFR 220

```

RESULT 7
AAW74891
ID AAW74891 standard; protein; 329 AA.
XX
AC AAW74891;
XX
DT 25-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 164 clone HSAWF26.
XX
KW Human; secreted protein; testis; tumour; foetal brain tissue;
KW fusion protein; cancer; central nervous system; seizure; diagnosis;
KW neurodegenerative disease.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Misc-difference 329
FT /label= unknown
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98WO-US004493.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 07-MAR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.

```

```

PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0048974P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
XX Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
XX Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
XX Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 1998-506364/43.
XX N-PSDB; AAV59674.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 641-642; 721pp; English.
XX
XX This sequence represents a secreted human protein encoded by the nucleic
XX
XX

```

CC acid molecule designated Gene 164 from the human cDNA clone HSAW26
CC (deposited as clone ATCC 97903 and ATCC 209049). The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)

XX Sequence 329 AA;

Query Match 100.0%; Score 1039; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDSIFTVNGILGESVTFPVNIOEPQKVIKIAWTSKTSVAVYTPGDSAPVVTTHRNY 60
DB 22 KDSIFTVNGILGESVTFPVNIOEPQKVIKIAWTSKTSVAVYTPGDSAPVVTTHRNY 81
QY 61 YRIIHALGPNYLNIVSDLRMEDAGDYKADINTQADPYTTTKRYNLIQYRRLGKPKITQSL 120
DB 82 YRIIHALGPNYLNIVSDLRMEDAGDYKADINTQADPYTTTKRYNLIQYRRLGKPKITQSL 141
QY 121 MASVNSTCNVTITCSVEKEKNVTYNWSPGLBEGNVLIQIFQTPDEQLTYTCTAQNPSVN 180
DB 142 MASVNSTCNVTITCSVEKEKNVTYNWSPGLBEGNVLIQIFQTPDEQLTYTCTAQNPSVN 201
QY 181 NSDSISARQLCADIAMGFR 199
DB 202 NSDSISARQLCADIAMGFR 220

RESULT 8

ABG95343
ID ABG95343 standard; protein; 329 AA.

XX AC ABG95343;

XX DT 15-JAN-2003 (first entry)

XX DE Human novel secreted protein #164.

XX KW Human; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.

XX OS Homo sapiens.

XX PN US6420526-B1.

XX PD 16-JUL-2002.

XX PF 08-SEP-1998; 98US-00149476.

XX PR 07-MAR-1997; 97US-0038621P.

PR 07-MAR-1997; 97US-0040161P.

PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040163P.

PR 07-MAR-1997; 97US-0040333P.

PR 07-MAR-1997; 97US-0040334P.

PR 07-MAR-1997; 97US-0040336P.

PR 07-MAR-1997; 97US-0040626P.

PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043368P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043588P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 13-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.

PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057659P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 12-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Emer R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI: 2002-634796/68.
DR N-PSDB; ABS73661.
XX
XX New isolated human secreted protein for diagnosing, preventing, treating
PT or ameliorating medical conditions and used as a food additive or
PT preservative.
XX
XX Example 1; SEQ ID NO 483; 129pp; English.
XX
XX The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of 309 cDNA
CC sequences also given in the specification. The protein is used in a
CC pharmaceutical composition used to prevent, treat or ameliorate a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents one of the novel human
CC secreted proteins of the invention. Note: This sequence did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=6420526B1
XX
SQ Sequence 329 AA;
Query Match 100.0%; Score 1039; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KDSIFVTNGILGSEVTFPPNVIQBPQVKIIAWTSKTSVAVYTFGDSSTAPVVTTHRNY 60
Db 22 KDSIFVTNGILGSEVTFPPNVIQBPQVKIIAWTSKTSVAVYTFGDSSTAPVVTTHRNY 81
Qy 61 YERTHALGPNYNLVISLRLMEDAGDYKADINTQADPYTTTKRYNLQYRRLGKPKITQSL 120
Db 82 YERTHALGPNYNLVISLRLMEDAGDYKADINTQADPYTTTKRYNLQYRRLGKPKITQSL 141

Qy 121 MASVNSTCNVTLTCSVEKEKNVTYNNWSPLEEGNVLQIFQTPEDQELTYTCTAQNPSVN 180
Db 142 MASVNSTCNVTLTCSVEKEKNVTYNNWSPLEEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
Qy 181 NSDSISARQLCADIAMGPR 199
Db 202 NSDSISARQLCADIAMGPR 220
RESULT 9
ABO34537
ID ABO34537 standard; protein; 329 AA.
XX ABO34537;
XX
XX 22-SEP-2003 (first entry)
XX Region of human secreted protein encoded by cDNA sequence #164.
KW Human; secreted protein; hyperproliferative disorder; leukaemia;
KW breast cancer; wound; reproductive disorder; blood-related disorder;
KW haemophilia; thrombocytopaenia; autoimmune disorder; multiple sclerosis;
KW Wiskott-Aldrich syndrome; autoimmune disorder; thymic hypoplasia;
KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;
KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;
KW angina pectoris; cerebral ischaemia; congenital heart defect;
KW respiratory disorder; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;
KW immunosuppressive; antibacterial; haemostatic; thrombolytic;
KW anticoagulant; neuroprotective; thyromimetic; antiallergic;
KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antiangiinal;
KW cerebroprotective; cardiant; nootropic; antiparkinsonian;
KW antiinflammatory.
XX
XX Homo sapiens.
XX OS
XX US2003049618-A1.
XX
XX 13-MAR-2003.
XX
XX 16-MAR-2001; 2001US-00809391.
XX
XX 07-MAR-1997; 97US-0038621P.
XX 07-MAR-1997; 97US-0040162P.
XX 07-MAR-1997; 97US-0040163P.
XX 07-MAR-1997; 97US-0040333P.
XX 07-MAR-1997; 97US-0040334P.
XX 07-MAR-1997; 97US-0040626P.
XX 11-APR-1997; 97US-0043311P.
XX 11-APR-1997; 97US-0043312P.
XX 11-APR-1997; 97US-0043313P.
XX 11-APR-1997; 97US-0043314P.
XX 11-APR-1997; 97US-0043315P.
XX 11-APR-1997; 97US-0043568P.
XX 11-APR-1997; 97US-0043569P.
XX 11-APR-1997; 97US-0043576P.
XX 11-APR-1997; 97US-0043578P.
XX 11-APR-1997; 97US-0043580P.
XX 11-APR-1997; 97US-0043669P.
XX 11-APR-1997; 97US-0043670P.
XX 11-APR-1997; 97US-0043671P.
XX 11-APR-1997; 97US-0043672P.
XX 11-APR-1997; 97US-0043674P.
XX 23-MAY-1997; 97US-0047492P.
XX 23-MAY-1997; 97US-0047500P.
XX 23-MAY-1997; 97US-0047501P.
XX 23-MAY-1997; 97US-0047502P.
XX 23-MAY-1997; 97US-0047503P.
XX 23-MAY-1997; 97US-0047581P.
XX 23-MAY-1997; 97US-0047582P.

```
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.

XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R. A.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFI/) LAFLEUR D W.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
WPI; 2003-521800/49.
DR N-PSDB; ACD82804.
XX
New genes and its encoded prostate cancer antigen proteins, useful for
preventing, treating, ameliorating or diagnosing e.g. prostate cancers,
thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
ischemia.
Claim 3; SEQ ID NO 483; 260pp; English.
XX
The present invention relates to the isolation of novel human secreted
proteins and the polynucleotide sequences encoding them. The invention
also discloses vectors, host cells, antibodies, and recombinant methods
for producing human secreted proteins. The polypeptide and polynucleotide
sequences for the secreted proteins are useful for preventing, treating,
ameliorating or diagnosing medical conditions such as hyperproliferative
disorders (e.g. leukaemia or breast cancers), wounds, reproductive
disorders, blood-related disorders (e.g. haemophilia or
thrombocytopenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or
thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,
multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),
viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
pectoris, cerebral ischaemia or congenital heart defects), respiratory
disorders, neurological disorders (e.g. Alzheimer's disease or
Parkinson's disease), and inflammations (e.g. Crohn's disease). The
polynucleotide or polypeptide may also be used as vaccine adjuvants.
AB034374-AB034815 represent human secreted proteins or their fragments.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from the
USPTO web site at seqdata.uspto.gov/psipdsIDentry.html
XX
Sequence 329 AA;
Query Match 100.0%; Score 1039; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDSIFTVNGILGESVTFPVNIQBPQVKIIAWTSKTSVAYVTPGDSSTAPVVTTHRNY 60
DB 22 KDSIFTVNGILGESVTFPVNIQBPQVKIIAWTSKTSVAYVTPGDSSTAPVVTTHRNY 81
```


QY 61 YRIHALGPNYNLVISDLRWDAGDYKADINTQADPYTTTKRYNLIQYVRLGKPKITQSL 120
Db |||||||
QY 121 MASVNSTCNVLTCSVEKEKNVTYNWSPLGEGNVLIQIFQTPEDQELTYTCTAQNPSVN 180
Db |||||||
QY 181 NSDSISARQLCADIANGFR 199
Db |||||||
QY 202 NSDSISARQLCADIANGFR 220

RESULT 10
AD123198
ID AD123198 standard; protein; 329 AA.

XX AD123198;

XX 22-APR-2004 (first entry)

XX Novel human secreted protein seq id 483.

XX cytostatic; gene therapy; cancer; human; secreted protein.

XX Homo sapiens.

XX US2003175858-A1.

XX 18-SEP-2003.

XX 18-JUN-2001; 2001US-00882171.

XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043586P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047452P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.

PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.

XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.

PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GEE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLO/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KIYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greené JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2003-898535/82.
DR N-PSDB; ADI22889.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
XX Claim 11; SEQ ID NO 483; 256pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a
CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The is the amino acid sequence of a novel human
CC secreted protein of the invention.
XX
SQ Sequence 329 AA;
Query Match 100.0%; Score 1039; DB 7; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDS E I F T V N G I L G E S V T F P V N I Q E P R Q V K I I A W T S K T S V A Y V T P G D S E T A P V V T V T H R N Y 60
Db 22 KDS E I F T V N G I L G E S V T F P V N I Q E P R Q V K I I A W T S K T S V A Y V T P G D S E T A P V V T V T H R N Y 81
QY 61 Y E R I H A L G P N Y N L V I S D L R M E D A G D Y K A D I N T Q A D P Y T T K R Y N L Q I Y R L G K P K I T O S L 120
Db 82 Y E R I H A L G P N Y N L V I S D L R M E D A G D Y K A D I N T Q A D P Y T T K R Y N L Q I Y R L G K P K I T O S L 141
QY 121 M A S V N S T C N V T I T C S V E K E K N V T N W S P L G E G N V L Q I F Q P E D Q E L Y T T C T A Q N P V S N 180
Db 142 M A S V N S T C N V T I T C S V E K E K N V T N W S P L G E G N V L Q I F Q P E D Q E L Y T T C T A Q N P V S N 201
QY 181 N S D S I S A R Q L C A D I A M G F R 199
Db 202 N S D S I S A R Q L C A D I A M G F R 220
RESULT 11
ADH74200
ID ADH74200 standard; protein; 329 AA.
XX
AC ADH74200;
XX
DT 25-MAR-2004 (first entry)

XX Human secreted protein #164.
DE human; secreted protein; cancer; haematopoietic disorder;
XX endocrine disorder; immune system disease; inflammatory disorder.
KW Homo sapiens.
OS US2003225248-A1.
PN 04-DEC-2003.
PD 10-JUN-2002; 2002US-00164861.
PF 07-MAR-1997; 97US-0038621P.
PF 07-MAR-1997; 97US-0040161P.
PF 07-MAR-1997; 97US-0040162P.
PF 07-MAR-1997; 97US-0040163P.
PF 07-MAR-1997; 97US-0040333P.
PF 07-MAR-1997; 97US-0040334P.
PF 07-MAR-1997; 97US-0040336P.
PF 07-MAR-1997; 97US-0040628P.
PF 11-APR-1997; 97US-0043311P.
PF 11-APR-1997; 97US-0043312P.
PF 11-APR-1997; 97US-0043313P.
PF 11-APR-1997; 97US-0043315P.
PF 11-APR-1997; 97US-00433568P.
PF 11-APR-1997; 97US-0043569P.
PF 11-APR-1997; 97US-0043576P.
PF 11-APR-1997; 97US-0043578P.
PF 11-APR-1997; 97US-0043580P.
PF 11-APR-1997; 97US-0043669P.
PF 11-APR-1997; 97US-0043670P.
PF 11-APR-1997; 97US-0043671P.
PF 11-APR-1997; 97US-0043672P.
PF 11-APR-1997; 97US-0043674P.
PF 23-MAY-1997; 97US-0047492P.
PF 23-MAY-1997; 97US-0047500P.
PF 23-MAY-1997; 97US-0047501P.
PF 23-MAY-1997; 97US-0047502P.
PF 23-MAY-1997; 97US-0047503P.
PF 23-MAY-1997; 97US-0047581P.
PF 23-MAY-1997; 97US-0047582P.
PF 23-MAY-1997; 97US-0047583P.
PF 23-MAY-1997; 97US-0047584P.
PF 23-MAY-1997; 97US-0047585P.
PF 23-MAY-1997; 97US-0047586P.
PF 23-MAY-1997; 97US-0047587P.
PF 23-MAY-1997; 97US-0047588P.
PF 23-MAY-1997; 97US-0047589P.
PF 23-MAY-1997; 97US-0047590P.
PF 23-MAY-1997; 97US-0047592P.
PF 23-MAY-1997; 97US-0047593P.
PF 23-MAY-1997; 97US-0047594P.
PF 23-MAY-1997; 97US-0047595P.
PF 23-MAY-1997; 97US-0047596P.
PF 23-MAY-1997; 97US-0047597P.
PF 23-MAY-1997; 97US-0047598P.
PF 23-MAY-1997; 97US-0047599P.
PF 23-MAY-1997; 97US-0047600P.
PF 23-MAY-1997; 97US-0047601P.
PF 23-MAY-1997; 97US-0047612P.
PF 23-MAY-1997; 97US-0047613P.
PF 23-MAY-1997; 97US-0047614P.
PF 23-MAY-1997; 97US-0047615P.
PF 23-MAY-1997; 97US-0047617P.
PF 23-MAY-1997; 97US-0047618P.
PF 23-MAY-1997; 97US-0047632P.
PF 23-MAY-1997; 97US-0047633P.
PF 06-JUN-1997; 97US-0048964P.
PF 13-JUN-1997; 97US-0048974P.
PF 13-JUN-1997; 97US-0049610P.

PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 2004-131264/13.
DR N-PSDB; ADH73891.
XX
PT Isolated nucleic acid molecules encoding human secreted proteins, useful
PT for preventing, diagnosing and treating disorders associated with
PT aberrant expression and activity.
XX
PS Claim 11; SEQ ID NO 483; 142bp; English.
XX
CC The invention relates to isolated nucleic acid molecules and the human
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,
CC endocrine disorders, diseases of the immune system, inflammatory
CC disorders and many others. Full details of disorders that may be
CC prevented, diagnosed and/or treated by the above methods are given in the
CC specification. The nucleic acid molecules may be used to produce their
CC proteins. The nucleic acid and it's complementary sequences may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The SPs may also be used
CC as antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of SP expression and activity. The anti-SP
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-SP antibodies may also be used as diagnostic
CC agents for detecting the presence of the proteins in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents the amino acid sequence of a human secreted protein.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1039; DB 8; Length 329;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIFFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSVAVYTPGDSPTAPVTVTHRNY 60
DB 22 KDSIFFTVNGILGESVTFPVNIQEPQVKIIAWTSKTSVAVYTPGDSPTAPVTVTHRNY 81

QY 61 YERIHALGNPNLVISDLRMEDAGYKADINTQADPPYTTTKRYNLQIYRRLGKPKITQSL 120
DB 82 YERIHALGNPNLVISDLRMEDAGYKADINTQADPPYTTTKRYNLQIYRRLGKPKITQSL 141

QY 121 MASVNSTCNVTLTCSVEKEKNVTYNWSPGLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
DB 142 MASVNSTCNVTLTCSVEKEKNVTYNWSPGLGEGNVLOIFQTPEDQELTYTCTAQNPSVN 201

QY 181 NSDSISARQLCADIAMGFR 199
DB 202 NSDSISARQLCADIAMGFR 220

RESULT 12
ADL57243
ID ADL57243 standard; protein; 526 AA.
XX
AC ADL57243;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOV5c protein SEQ ID NO:188.
XX
KW human; antidiabetic; anorectic; cardiac; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; gene therapy;
KW fibroblast growth factor receptor 4; FGF4;
KW complement factor I precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LfV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 319
FT /label= RLKPKITWSLRHSDGICRLTCSVEDGNGTVMYVTTPLQKEAVWSQ
FT /note= "Optionally absent"
FT
FT Misc-difference 406
FT /label= Ser, Gly
FT Misc-difference 489
FT /label= Glu, Lys
FT Misc-difference 506
FT /note= "Optionally absent"
XX
PN WO2004022723-A2.
XX
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-US028141.
XX

CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antipneumic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies
CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinnase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence represents a NOVX polypeptide
CC of the invention.
XX
SQ Sequence 526 AA;

Query Match 33.9%; Score 352; DB 8; Length 526;
Best Local Similarity 38.1%; Pred. No. 8.4e-24;
Matches 77; Conservative 41; Mismatches 70; Indels 14; Gaps 5;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPROVKIIAHTS-KTSVAYVTPGSDTAPVVTVTHRN 59
DB 8 KDSAPTIVSGILGSGVTPLNLSVDTEIENVIGPKNALAFARPEN-----VTINVK 62
QY 60 YYERIHAGPNYNLVSLDLMEDAGDYKADINTQADPYTTTKRYNLIQYRLGKPKIT-Q 118
DB 63 YLGRDLITKWSYSLCISNLTLNDAGSYKAIQNRNFVTTTEEBFTLVYVQLQEPQVTMK 122
QY 119 SLMASVNSTCNVTLTCSVEKEKNTVNWSP-----GEGNVLIQFQPEDEQLTYTC 172
DB 123 SVKVSFNSCNITLMCSVKAESVLSWTPREPHASESNGGSLTIVSRTPCPDLPYIC 182
QY 173 TAQNPVSNNSD-SISARQLCAD 193
DB 183 TAQNPVSQRSPLPHVHQVQCTD 204

RESULT 14

ID ABG96270 standard; protein; 551 AA.

XX ABG96270;

AC ABG96270;

DT 11-DEC-2002 (first entry)

DE Human immunoglobulin superfamily protein IGSFP-8.

XX Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder;
KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;
KW paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;
KW primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma;
KW autoimmune disorder; inflammatory disorder;

KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; asthma;
KW autoimmune thyroiditis; contact dermatitis; Crohn's disease;
KW diabetes mellitus; glomerulonephritis; Goodpasture's syndrome; gout;
KW Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;
KW multiple sclerosis; osteoarthritis; osteoporosis; pancreatitis;
KW Reiter's syndrome; rheumatoid arthritis; Sjogren's syndrome; uveitis;
KW trauma; viral infection; bacterial infection; fungal infection;
KW parasitic infection; protozoal infection; helminthic infection;
KW gene therapy; human.
XX
OS Homo sapiens.
XX WO200272794-A2.
PN 19-SEP-2002.
XX 12-MAR-2002; 2002WO-US009052.
XX 12-MAR-2001; 2001US-0275249P.
PR 31-AUG-2001; 2001US-0316810P.
PR 21-SEP-2001; 2001US-0323977P.
PR 26-OCT-2001; 2001US-0348447P.
PR 02-NOV-2001; 2001US-0343880P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Xu Y, Thangavelu K, Warren BA, Tang YT, Duggan BM,
PI Tran UK, Baughn MR, Honcheil CD, Burford N, Forsythe LJ, Yang J;
PI Mason PW;
XX WPI: 2002-723340/78.
XX N-PSDB; ABS76363.
XX New human immunoglobulin superfamily proteins and polynucleotides, useful
PT for diagnosing, treating or preventing disorders with aberrant IGSFP
PT expression, such as autoimmune, inflammatory or cell proliferative
PT diseases.
XX
XX Claim 1; Page 129-130; 145pp; English.
PS
XX The present invention relates to new immunoglobulin superfamily proteins
CC (IGSFP). The polypeptides, polynucleotides, agonists and antagonists are
CC useful for diagnosing, treating or preventing disorders associated with
CC aberrant expression of IGSFP, particularly cell proliferative, e.g.
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC thrombocytopenia or cancers including leukaemia, lymphoma, sarcoma or
CC myeloma, and autoimmune or inflammatory disorders, e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies, anaemia, asthma, autoimmune
CC thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus,
CC glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,
CC Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis,
CC osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid
CC arthritis, Sjogren's syndrome, uveitis, trauma, or viral, bacterial,
CC fungal, parasitic, protozoal or helminthic infections. They are also
CC useful in the assessment of the effects of exogenous compounds on the
CC expression of nucleic acid and amino acid sequences of IGSFP. The present
CC amino acid sequence represents a human IGSFP protein of the invention
XX
SQ Sequence 551 AA;

Query Match 33.9%; Score 352; DB 5; Length 551;
Best Local Similarity 38.1%; Pred. No. 9e-24;
Matches 77; Conservative 41; Mismatches 70; Indels 14; Gaps 5;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPROVKIIAHTS-KTSVAYVTPGSDTAPVVTVTHRN 59
DB 48 KDSAPTIVSGILGSGVTPLNLSVDTEIENVIGPKNALAFARPEN-----VTINVK 102
QY 60 YYERIHAGPNYNLVSLDLMEDAGDYKADINTQADPYTTTKRYNLIQYRLGKPKIT-Q 118
DB 103 YLGRDLITKWSYSLCISNLTLNDAGSYKAIQNRNFVTTTEEBFTLVYVQLQEPQVTMK 162

QY 119 SLMASVNSTCNVLTCSVEKEKNVTYNWSPL-----GEGNVLQIFQTPEDQLTYTC 172
Db 163 SVKVSFNSCNITLMCSVKGAESVLYSWTPREPHASESNGSILTVSRTPCDPLPYIC 222
QY 173 TAQNPVSNNSD-SISARQLCAD 193
Db 223 TAQNPVSQRSLSLPVHVGOFCITD 244

RESULT 15
ADK98560
ID ADK98560 standard; protein; 565 AA.
XX
AC ADK98560;
XX
DT 03-JUN-2004 (first entry)
DE Human immune response associated protein IRAP-23 protein.
XX
KW immune response associated protein; IRAP; antiarteriosclerotic;
KW cytostatic; neuroprotective; antiparkinsonian; hepatotropic;
KW cerebroprotective; antiinflammatory; neurotropic; vasotropic;
KW arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease;
KW Parkinson's; Crohn's; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004020593-A2.
XX
PD 11-MAR-2004.
XX
PF 26-AUG-2003; 2003WO-US026988.
XX
PR 30-AUG-2002; 2002US-0407561P.
PR 11-SEP-2002; 2002US-0410178P.
PR 13-SEP-2002; 2002US-0410571P.
PR 18-OCT-2002; 2002US-0419906P.
PR 25-OCT-2002; 2002US-0421445P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;
PI Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;
XX
DR WPI; 2004-239178/22.
DR N-PSDB; ADK98595.
XX
PT New isolated immune response associated proteins (IRAP) polypeptide and
PT polynucleotide, useful for diagnosing and/or treating disorders with
PT aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
PT and stroke.
XX
PS Claim 1; SEQ ID NO 23; 207pp; English.
XX
CC The invention relates to a novel isolated immune response associated
CC protein (IRAP) comprising any of 35 fully defined sequences given in the
CC specification. The polypeptide of the invention demonstrates
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, cerebroprotective, antiinflammatory, neurotropic and
CC vasotropic activities and may be useful for treating a disease or
CC condition associated with decreased expression or overexpression of
CC functional immune response associated proteins, while the antibody is
CC useful for diagnosing a condition or disease associated with the
CC expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke,
CC Alzheimer's disease, Parkinson's disease and Crohn's disease.
CC Furthermore, the molecules of the invention may be utilised during gene
CC therapy procedures. The current sequence is that of a human IRAP protein
CC of the invention.
XX
SQ Sequence 565 AA;

Query Match 33.9%; Score 352; DB 8; Length 565;
Best Local Similarity 38.1%; Pred. NO. 9.3e-24;

Matches 77; Conservative 41; Mismatches 70; Indels 14; Gaps 5;
Qy 1 KDSEIFTVNGILGESVTFPNQIEPRQVKIIAWTS-KTSVAYVTPGDSEAPVVTVTHRN 59
Db 48 KDSAPTUVSGILGGSVTLPLNISVDTEIENVIGPKNALAFAPKEN-----VTIMVKS 102
Qy 60 YYERIHALGPNYNLIVISDLRMEADAGYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118
Db 103 YLGRLDITKWSYSLCISNLTINDAGSYKAQINQNFVETTEEEFTLFVYBQLQEPQVTMK 162
Qy 119 SLMASVNSTCNVLTCSVEKEKNVTYNWSPL-----GEGNVLQIFQTPEDQLTYTC 172
Db 163 SVKVSFNSCNITLMCSVKGAESVLYSWTPREPHASESNGSILTVSRTPCDPLPYIC 222
Qy 173 TAQNPVSNNSD-SISARQLCAD 193
Db 223 TAQNPVSQRSLSLPVHVGOFCITD 244

Search completed: February 4, 2005, 12:11:03
Job time : 90.3239 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 12:04:15 ; Search time 22.9505 Seconds
(without alignments)
646.143 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220
Perfect score: 1039
Sequence: 1 K0SEIFTVNGILGESVTFPV.....NNSDSISARQLCADIAMGFR 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1039	100.0	328	4	US-09-949-016-6428 Sequence 6428, Ap
2	1039	100.0	329	4	US-09-149-476-483 Sequence 483, App
3	1039	100.0	332	4	US-09-949-016-7327 Sequence 7327, Ap
4	182	17.5	143	3	US-09-227-357-192 Sequence 192, App
5	160	15.4	298	1	US-08-348-792-4 Sequence 4, Appli
6	160	15.4	298	2	US-08-462-738-4 Sequence 4, Appli
7	160	15.4	298	3	US-09-199-955-4 Sequence 4, Appli
8	160	15.4	298	3	US-08-880-875-4 Sequence 4, Appli
9	160	15.4	305	1	US-08-348-792-6 Sequence 6, Appli
10	160	15.4	305	2	US-08-462-738-6 Sequence 6, Appli
11	160	15.4	305	3	US-09-199-955-6 Sequence 6, Appli
12	160	15.4	305	3	US-08-880-875-6 Sequence 6, Appli
13	160	15.4	307	1	US-08-348-792-8 Sequence 8, Appli
14	160	15.4	307	2	US-08-462-738-8 Sequence 8, Appli
15	160	15.4	307	3	US-09-199-955-8 Sequence 8, Appli
16	160	15.4	307	3	US-08-880-875-8 Sequence 8, Appli
17	160	15.4	335	1	US-08-348-792-2 Sequence 2, Appli
18	160	15.4	335	2	US-08-462-738-2 Sequence 2, Appli
19	160	15.4	335	3	US-09-199-955-2 Sequence 2, Appli
20	160	15.4	335	3	US-08-880-875-2 Sequence 2, Appli
21	160	15.4	335	4	US-09-369-248A-3 Sequence 3, Appli
22	153	14.7	329	1	US-08-348-792-12 Sequence 12, Appl
23	153	14.7	329	2	US-08-462-738-12 Sequence 12, Appl
24	153	14.7	329	3	US-09-199-955-12 Sequence 12, Appl
25	153	14.7	329	3	US-08-880-875-12 Sequence 12, Appl
26	153	14.7	343	1	US-08-348-792-10 Sequence 10, Appl
27	153	14.7	343	2	US-08-462-738-10 Sequence 10, Appl

28	153	14.7	343	3	US-09-199-955-10 Sequence 10, Appl
29	153	14.7	343	3	US-08-880-875-10 Sequence 10, Appl
30	146	14.1	144	4	US-09-513-999C-4353 Sequence 4353, Ap
31	139.5	13.4	285	4	US-09-369-248A-2 Sequence 2, Appli
32	138	13.3	450	4	US-09-907-794A-320 Sequence 320, App
33	138	13.3	450	4	US-09-905-125A-320 Sequence 320, App
34	138	13.3	450	4	US-09-902-775A-320 Sequence 320, App
35	138	13.3	450	4	US-09-906-700-320 Sequence 320, App
36	138	13.3	450	4	US-09-903-603A-320 Sequence 320, App
37	138	13.3	450	4	US-09-904-920A-320 Sequence 320, App
38	138	13.3	450	4	US-09-909-064-320 Sequence 320, App
39	138	13.3	450	4	US-09-905-381A-320 Sequence 320, App
40	138	13.3	450	4	US-09-906-618-320 Sequence 320, App
41	136	13.1	365	4	US-09-949-016-6907 Sequence 6907, Ap
42	136	13.1	391	4	US-09-949-016-7325 Sequence 7325, Ap
43	135.5	13.0	642	1	US-08-217-299-1 Sequence 1, Appli
44	135.5	13.0	698	2	US-08-602-725-36 Sequence 36, Appl
45	135.5	13.0	702	4	US-08-949-016-6484 Sequence 6484, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-6428
; Sequence 6428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6428

Query Match	100.0%;	Score 1039;	DB 4;	Length 328;
Best Local Similarity	100.0%;	Pred. No. 1.2e-101;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	K0SEIFTVNGILGESVTFPVNIOEPQVKIIAWTSKTSVAYVTPGSETAPVVTTHRNY	60	
Db	22	K0SEIFTVNGILGESVTFPVNIOEPQVKIIAWTSKTSVAYVTPGSETAPVVTTHRNY	81	
QY	61	YERIHAGNPNVIVISDLRMDAGDYKADINTQADPVTTKRYNQLQYRRLGPKITQSL	120	
Db	82	YERIHAGNPNVIVISDLRMDAGDYKADINTQADPVTTKRYNQLQYRRLGPKITQSL	141	
QY	121	MASVNSTCNVTLTCSVEKEKNVYNWSPGLGEGNVLIQIFQTPEDQELTYTCTAQNPSN	180	
Db	142	MASVNSTCNVTLTCSVEKEKNVYNWSPGLGEGNVLIQIFQTPEDQELTYTCTAQNPSN	201	
QY	181	NDSISARQLCADIAMGFR	199	
Db	202	NDSISARQLCADIAMGFR	220	

RESULT 2
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,569
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 1039; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDSIFTVNGILGESVTFPPVNIQEPROVKIIAMTSKTSVAYVTPGDSAPVVTVTHRNY 60
DB 22 KDSIFTVNGILGESVTFPPVNIQEPROVKIIAMTSKTSVAYVTPGDSAPVVTVTHRNY 81
QY 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGPKKITQSL 120
DB 82 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGPKKITQSL 141
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLIQIFQTPDQELTYTCTAQNPSN 180
DB 142 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLIQIFQTPDQELTYTCTAQNPSN 201
QY 181 NSDSISARQLCADIAMGFR 199
DB 202 NSDSISARQLCADIAMGFR 220

RESULT 3
US-09-949-016-7327
Sequence 7327, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7327
LENGTH: 332
TYPE: PRT
ORGANISM: Human
US-09-949-016-7327

Query Match 100.0%; Score 1039; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KDSIFTVNGILGESVTFPPVNIQEPROVKIIAMTSKTSVAYVTPGDSAPVVTVTHRNY 60
DB 26 KDSIFTVNGILGESVTFPPVNIQEPROVKIIAMTSKTSVAYVTPGDSAPVVTVTHRNY 85
QY 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGPKKITQSL 120
DB 86 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGPKKITQSL 145
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLIQIFQTPDQELTYTCTAQNPSN 180
DB 146 MASVNSTCNVTLTCSVEKEKNVTYNNWSPGLGEGNVLIQIFQTPDQELTYTCTAQNPSN 205
QY 181 NSDSISARQLCADIAMGFR 199
DB 206 NSDSISARQLCADIAMGFR 224

RESULT 4
US-09-227-357-192
Sequence 192, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 192
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (92)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (143)
OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-192

Query Match 17.5%; Score 182; DB 3; Length 143;
Best Local Similarity 35.8%; Pred. No. 2.1e-11;
Matches 38; Conservative 24; Mismatches 44; Indels 0; Gaps 0;
QY 8 VNGILGESVTPPVNIQEPROVKIIAWTSKTSVAVVTPGDSPTAPVVTVTHRYVERIAL 67
DB 30 VVAVLQESISLPLIPDPEEVENIWSHKS LATVPQKEGHPATIMVTNPHYQQQVSFL 89
QY 68 GPNTNVLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGK 113
DB 90 DPXYSLHSINLSWEDSGLYQAQVNLRTSQISTMQOYNLCVYRWLSE 135
RESULT 5
US-08-348-792-4
Sequence 4, Application US/08348792
Patent No. 5576423
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-792-4

Query Match 15.4%; Score 160; DB 1; Length 298;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;
QY 12 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAVVTPGDSPTAPVVTVTHRN 59
DB 39 LGSKVLLPFTYERINKSNKSIHIVVTWAKSLNSVENKIVSLDPSEAGPPRYLGRKXF 98
QY 60 YYERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 99 YLE-----NLTGIRSRKDEGWYMLT-----EKNVSVQRFCLQLRLYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVLTCTCSVEKEKNVTYNWS-----PL--GEEGNVLQIFQTPDQELT 169
DB 148 VLNKQTENGCTCTLIIGCTVVERKGD-HVAYSWEKAGTHPLNPANSHLLSLTLGPOHADNI 206

QY 170 YTCTAQNPNVNSDSIS 186
Db 207 YICTVSNPISNNSQTS 223

RESULT 6

US-08-462-738-4
; Sequence 4, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-462-738-4

Query Match

Best Local Similarity 25.4%; Score 160; DB 2; Length 298;

Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSTK-----SVAYVTPGDSETPVVTTHRN 59

Db 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDRYKF 98

QY 60 YVERIHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKIT 117

Db 99 YLE-----NLTGIRESKKEDEGWYMTL-----EKNVSVQRFCLQLRIYEQVSTPEIK 147

QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 169

Db 148 VLNKTQENGCTTLIGCTVEKGD-HVAYSWSERKAGTHPLNPANSSHLLSLTLGPHQADNI 206

QY 170 YTCTAQNPNVNSDSIS 186

Db 207 YICTVSNPISNNSQTS 223

RESULT 7

US-08-462-738-4

Query Match

Best Local Similarity 25.4%; Score 160; DB 2; Length 298;

Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSTK-----SVAYVTPGDSETPVVTTHRN 59

Db 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDRYKF 98

QY 60 YVERIHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKIT 117

Db 99 YLE-----NLTGIRESKKEDEGWYMTL-----EKNVSVQRFCLQLRIYEQVSTPEIK 147

QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 169

Db 148 VLNKTQENGCTTLIGCTVEKGD-HVAYSWSERKAGTHPLNPANSSHLLSLTLGPHQADNI 206

QY 170 YTCTAQNPNVNSDSIS 186

Db 207 YICTVSNPISNNSQTS 223

US-09-199-955-4

Query Match

Best Local Similarity 25.4%; Score 160; DB 3; Length 298;

Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSTK-----SVAYVTPGDSETPVVTTHRN 59

Db 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDRYKF 98

QY 60 YVERIHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKIT 117

Db 99 YLE-----NLTGIRESKKEDEGWYMTL-----EKNVSVQRFCLQLRIYEQVSTPEIK 147

QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 169

Db 148 VLNKTQENGCTTLIGCTVEKGD-HVAYSWSERKAGTHPLNPANSSHLLSLTLGPHQADNI 206

QY 170 YTCTAQNPNVNSDSIS 186

Db 207 YICTVSNPISNNSQTS 223

US-09-199-955-4

Query Match

Best Local Similarity 25.4%; Score 160; DB 3; Length 298;

Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSTK-----SVAYVTPGDSETPVVTTHRN 59

Db 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDRYKF 98

QY 60 YVERIHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKIT 117

Db 99 YLE-----NLTGIRESKKEDEGWYMTL-----EKNVSVQRFCLQLRIYEQVSTPEIK 147

QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 169

Db 148 VLNKTQENGCTTLIGCTVEKGD-HVAYSWSERKAGTHPLNPANSSHLLSLTLGPHQADNI 206

QY 170 YTCTAQNPNVNSDSIS 186

Db 207 YICTVSNPISNNSQTS 223

US-09-199-955-4

Query Match

Best Local Similarity 25.4%; Score 160; DB 3; Length 298;

Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSTK-----SVAYVTPGDSETPVVTTHRN 59

Db 39 LGSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPRYLGDRYKF 98

QY 60 YVERIHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGPKIT 117

Db 99 YLE-----NLTGIRESKKEDEGWYMTL-----EKNVSVQRFCLQLRIYEQVSTPEIK 147

QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLIQFQTPEDQELT 169

Db 148 VLNKTQENGCTTLIGCTVEKGD-HVAYSWSERKAGTHPLNPANSSHLLSLTLGPHQADNI 206

QY 170 YTCTAQNPNVNSDSIS 186

Db 207 YICTVSNPISNNSQTS 223

US-09-199-955-4

Query Match

```

; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,777
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-880-875-4

Query Match 15.4%; Score 160; DB 3; Length 298;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGSVTPP-----VNIQEPQVKIIAWTSKT-----SVAYVPPGDSGETAPVVTVTHRN 59
DB 39 LGSKVLLPLAYERINKSKMNSIHHVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDYKF 98
QY 60 YVERIHALGPNYNLIVSLDMEDAGDYKADINTQADPYTTTKRYNQ--LYRRLGKPKIT 117
DB 99 YLE-----NLTGIBRESKDEGWYLMTL-----EKNVSVQRFCLQRLRYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVTLTCSVKEEKNVTYNWS-----PL--GEGSNVLQIFQTPEDQELT 169
DB 148 VLNKTOENGCTLLIGCTVEKGD-HVAYSNSKAGTHPLNPANSHLLSLTLGPQHADNI 206
QY 170 YTCTAQNPNVNSDSIS 186
DB 207 YICTVSNPISNNSQTS 223

```

RESULT 9
 US-08-348-792-6
 ; Sequence 6, Application US/08348792
 ; Patent No. 5576423
 ; GENERAL INFORMATION:
 ; APPLICANT: Aversa, Gregorio
 ; APPLICANT: Chang, Chia-Chun J.
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: de Vries, Jan E.
 ;
 ; APPLICANT: de Vries, Jan E.
 ; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
 ; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA

```

;
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-738-6

Query Match 15.4%; Score 160; DB 2; Length 305;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGSVTFP-----VNIOEPQVKIIAWTST-----SVAYVTPGDSAPVVTVTHN 59
DB 39 LGSKVLPLTYERINKSMNKSIHVVTMAKSLNSVENKIVSLDPSEAGPPRYLGDYRKF 98
QY 60 YVERIHALGPNYLVISLDMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 99 YLE-----NLTGIRESKDEGWYMTL-----EKNVSVQVFCQLRLYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLOIFOTPEDELT 169
DB 148 VLNKTQENGCTLLIGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 170 YTCTAQNPNVNSDSIS 186
DB 207 YICTVSNPISNNSQTFS 223

RESULT 11
US-09-199-955-6
; Sequence 6, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,955
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,473
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-199-955-6

Query Match 15.4%; Score 160; DB 3; Length 305;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGSVTFP-----VNIOEPQVKIIAWTST-----SVAYVTPGDSAPVVTVTHN 59
DB 39 LGSKVLPLTYERINKSMNKSIHVVTMAKSLNSVENKIVSLDPSEAGPPRYLGDYRKF 98
QY 60 YVERIHALGPNYLVISLDMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 99 YLE-----NLTGIRESKDEGWYMTL-----EKNVSVQVFCQLRLYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVLTCSVEKEKNVTYNS-----PL--GEGNVLOIFOTPEDELT 169
DB 148 VLNKTQENGCTLLIGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 170 YTCTAQNPNVNSDSIS 186
DB 207 YICTVSNPISNNSQTFS 223

RESULT 12
US-08-880-875-6
; Sequence 6, Application US/08880875
; Patent No. 6399065
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435

```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/481,777
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/348,792
;; FILING DATE: 02-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ching, Edwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: DX0436K
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-852-9196
;; TELEFAX: 415-496-1200
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acids
;; LENGTH: 305 amino acids
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-880-875-6

Query Match 15.4%; Score 160; DB 3; Length 305;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFP-----VNIQEPQVKIIAWTSKT-----SVAVTPGDSCTAPVVTVTHRN 59
DB LSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSEAGPPRYLGDRYKF 98
QY 60 YIERHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 99 YLE-----NLTGIGRESKEDGWLMTL-----EKNVSVQRFCLQLRLYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVTLTCSVEKEKNVTYNWS-----PL--GEGNVLIQIFQTPEDQBLT 169
DB 148 VLNKQTGCTCTLLIGCTVEKGD-HVAYSWEKAGTHPLNPANSSHLLSLTLGPOHADNI 206
QY 170 YTCTAQNPNVNSDSIS 186
DB 207 YICTVSNPISNNSQTFSS 223

RESULT 13
US-08-348-792-8
; Sequence 8, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-852-9196
;; TELEFAX: 415-496-1200
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 307 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-348-792-8

Query Match 15.4%; Score 160; DB 1; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFP-----VNIQEPQVKIIAWTSKT-----SVAVTPGDSCTAPVVTVTHRN 59
DB LSKVLLPLTYERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSEAGPPRYLGDRYKF 70
QY 60 YIERHALGPNVNLVSDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 71 YLE-----NLTGIGRESKEDGWLMTL-----EKNVSVQRFCLQLRLYEQVSTPEIK 119
QY 118 QSLMASVNSTCNVTLTCSVEKEKNVTYNWS-----PL--GEGNVLIQIFQTPEDQBLT 169
DB 120 VLNKQTGCTCTLLIGCTVEKGD-HVAYSWEKAGTHPLNPANSSHLLSLTLGPOHADNI 178
QY 170 YTCTAQNPNVNSDSIS 186
DB 179 YICTVSNPISNNSQTFSS 195

RESULT 14
US-08-462-738-8
; Sequence 8, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids

```

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-738-8

Query Match 15.4%; Score 160; DB 2; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSKT-----SVAVYTPGDSAPVVTVTHRN 59
Db 11 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDYK 70
QY 60 YIERIHALGPNNVNLISDLRMDAGDYKADINTQADPYTTTKRYNLQ--LYRRLGPKKIT 117
Db 71 YLE-----NLTGIGRESRKEDEGWYMTL-----EKNVSVORFCLQLRLYEQVSTPEIK 119
QY 118 QSLMASVNSTCNVTLTCSVEKEEKVNTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
Db 120 VLNKTOENGCTCLILGCTVEKGD--HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 178
QY 170 YTCTAQNPNVSNNSDSIS 186
Db 179 YICTVSNPISNNSQTF 195

Search completed: February 4, 2005, 12:17:04
Job time : 23.9905 secs

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-738-8

Query Match 15.4%; Score 160; DB 2; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFF-----VNIQEPQVKIIAWTSKT-----SVAVYTPGDSAPVVTVTHRN 59
Db 11 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDYK 70
QY 60 YIERIHALGPNNVNLISDLRMDAGDYKADINTQADPYTTTKRYNLQ--LYRRLGPKKIT 117
Db 71 YLE-----NLTGIGRESRKEDEGWYMTL-----EKNVSVORFCLQLRLYEQVSTPEIK 119
QY 118 QSLMASVNSTCNVTLTCSVEKEEKVNTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
Db 120 VLNKTOENGCTCLILGCTVEKGD--HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 178
QY 170 YTCTAQNPNVSNNSDSIS 186
Db 179 YICTVSNPISNNSQTF 195

RESULT 15
US-09-199-955-8
; Sequence 8, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,955
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,473
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-199-955-8
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 12:15:12 ; Search time 65.5796 Seconds
(without alignments)
988.338 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220
Perfect score: 1039
Sequence: 1 KDSIEFTVNGILGESVTPPV.....NNSDSISARQLCADIAMGFR 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues
Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1039	100.0	328	14	US-10-104-943-4
2	1039	100.0	328	14	US-10-436-523-30
3	1039	100.0	329	10	US-09-809-391-483
4	1039	100.0	329	10	US-09-882-171-483
5	1039	100.0	329	15	US-10-164-861-483
6	352	33.9	551	15	US-10-471-449-8
7	352	33.9	610	10	US-09-860-836B-11
8	343.5	33.1	654	14	US-10-104-943-7
9	343.5	33.1	654	16	US-10-310-612-2
10	343.5	33.1	654	16	US-10-328-538-2
11	332	32.0	217	14	US-10-436-523-79
12	332	32.0	236	14	US-10-436-523-82
13	332	32.0	270	14	US-10-436-523-77

14	332	32.0	289	14	US-10-220-946-18
15	332	32.0	289	14	US-10-436-523-76
16	332	32.0	289	14	US-10-436-523-89
17	332	32.0	289	14	US-10-436-523-91
18	332	32.0	289	15	US-10-170-385-131
19	332	32.0	289	14	US-10-436-523-88
20	329	31.7	289	14	US-10-436-523-90
21	321.5	30.9	285	14	US-10-436-523-100
22	316.5	30.5	203	14	US-10-436-523-16
23	316.5	30.5	309	14	US-10-436-523-5
24	316.5	30.5	331	14	US-10-104-943-2
25	316.5	30.5	331	14	US-10-436-523-3
26	316.5	30.5	331	15	US-10-264-237-2559
27	316.5	30.5	331	16	US-10-614-853-22
28	316.5	30.5	332	14	US-10-245-752-76
29	316.5	30.5	332	14	US-10-245-859-76
30	316.5	30.5	332	14	US-10-245-103-76
31	316.5	30.5	332	14	US-10-245-107-76
32	316.5	30.5	332	14	US-10-245-143-76
33	316.5	30.5	332	14	US-10-245-771-76
34	316.5	30.5	332	14	US-10-245-851-76
35	316.5	30.5	332	14	US-10-245-883-76
36	316.5	30.5	332	14	US-10-237-535-76
37	316.5	30.5	332	14	US-10-238-183-76
38	316.5	30.5	332	14	US-10-238-283-76
39	316.5	30.5	332	14	US-10-238-370-76
40	316.5	30.5	332	14	US-10-245-055-76
41	316.5	30.5	332	14	US-10-245-147-76
42	316.5	30.5	332	14	US-10-245-710-76
43	316.5	30.5	332	14	US-10-245-739-76
44	316.5	30.5	332	14	US-10-246-210-76
45	316.5	30.5	332	14	US-10-239-196-76

ALIGNMENTS

RESULT 1
US-10-104-943-4
; Sequence 4, Application US/10104943
; Publication No. US20030092017A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL IMMUNOGLOBULIN SUPERFAMILY MEMBE
; TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0135 NP
; CURRENT APPLICATION NUMBER: US/10/104,943
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,037
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/281,223
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-943-4

Query Match 100.0%; Score 1039; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KDSIEFTVNGILGESVTPPVNIQEPQVKIIANTSKTSVAYVTPGDSAPVVTVTHRNY 60
Db 22 KDSIEFTVNGILGESVTPPVNIQEPQVKIIANTSKTSVAYVTPGDSAPVVTVTHRNY 81
Qy 61 YERIHAGPNYLVISDLRMDAGDYKADINTQADPVTTTKRYNLQIYRRLGPKPKITQSL 120
Db 82 YERIHAGPNYLVISDLRMDAGDYKADINTQADPVTTTKRYNLQIYRRLGPKPKITQSL 141
Qy 121 MASVNSTCNVTLTCSVEKEKNVTYNWSPGLGEGNVLIQIFQTPEDQELTYTCTAQNPSVN 180

Db 142 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
Qy 181 NSDSISARQLCADIAMGFR 199
Db 202 NSDSISARQLCADIAMGFR 220

RESULT 2

US-10-436-523-30
; Sequence 30, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 30
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-30

Query Match 100.0%; Score 1039; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KDSIEFTVNGILGESVTFPNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTVTHRYN 60
Db 22 KDSIEFTVNGILGESVTFPNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTVTHRYN 81
Qy 61 YERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
Db 82 YERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
Qy 121 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 180
Db 142 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
Qy 181 NSDSISARQLCADIAMGFR 199
Db 202 NSDSISARQLCADIAMGFR 220

RESULT 3

US-09-809-391-483
; Sequence 483, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 483
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals stop translation
US-09-809-391-483

Query Match 100.0%; Score 1039; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KDSIEFTVNGILGESVTFPNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTVTHRYN 60
Db 22 KDSIEFTVNGILGESVTFPNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTVTHRYN 81
Qy 61 YERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
Db 82 YERIHALGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
Qy 121 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 180
Db 142 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN 201
Qy 181 NSDSISARQLCADIAMGFR 199
Db 202 NSDSISARQLCADIAMGFR 220

RESULT 4

US-09-882-171-483
; Sequence 483, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581

PRIOR APPLICATION NUMBER:	60/056,879
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,880
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,894
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,911
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,636
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,874
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,910
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,864
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,631
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,845
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,892
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/057,761
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/047,595
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,599
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,588
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,585
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,586
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,590
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,594
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,589
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,593
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,614
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/043,578
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,576
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/047,501
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/043,670
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/056,632
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,664
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,875
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,881
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,909
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,875
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,862
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,887
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,908
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/048,964
PRIOR FILING DATE:	1997-06-06
PRIOR APPLICATION NUMBER:	60/057,650

```
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match      100.0%; Score 1039; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAVYTPGDSAPVVTVTHRN 60
Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAVYTPGDSAPVVTVTHRN 81

Qy 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLIQYRRLGPKKITQSL 120
Db 82 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLIQYRRLGPKKITQSL 141

Qy 121 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQIFOTPEQELTYTCTAQNPSN 180
Db 142 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQIFOTPEQELTYTCTAQNPSN 201

Qy 181 NSDSISARQLCADIAMGFR 199
Db 202 NSDSISARQLCADIAMGFR 220

RESULT 5
US-10-164-861-483
; Sequence 483, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002PI
; CURRENT APPLICATION NUMBER: US/10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 483
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals stop translation
US-10-164-861-483

Query Match      100.0%; Score 1039; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAVYTPGDSAPVVTVTHRN 60
Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAVYTPGDSAPVVTVTHRN 81

Qy 61 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLIQYRRLGPKKITQSL 120
Db 82 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLIQYRRLGPKKITQSL 141

Qy 121 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQIFOTPEQELTYTCTAQNPSN 180
Db 142 MASVNSTCNVLTCSVEKEKNVTYNSPLGEGNVLIQIFOTPEQELTYTCTAQNPSN 201

Qy 181 NSDSISARQLCADIAMGFR 199
Db 202 NSDSISARQLCADIAMGFR 220
```

```
RESULT 6
US-10-471-449-8
; Sequence 8, Application US/10471449
; Publication No. US2004009771A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry; XU, Yuming;
; APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
; APPLICANT: TANG, Y. Tom; DUGGAN, Brendan M.;
; APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
; APPLICANT: HONCHELL, Cynthia D.; BURFORD, Neil;
; APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
; APPLICANT: MASON, Patricia M.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0925 USN
; CURRENT APPLICATION NUMBER: US/10/471,449
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US02/09052
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/275,249
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/316,810
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/323,977
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/348,447
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/343,880
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7500099CDI
US-10-471-449-8

Query Match      33.9%; Score 352; DB 15; Length 551;
Best Local Similarity 38.1%; Pred. No. 2.6e-24;
Matches 77; Conservative 41; Mismatches 70; Indels 14; Gaps 5;

Qy 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAWTS-KTSVAVYTPGDSAPVVTVTHRN 59
Db 48 KDSAPTVVSGILGGSVTLPLNISVDTEIENVIGPKNALAFARPKN-----VTIMVKS 102

Qy 60 YERIHAGPNYNLVISDLRMDAGDYKADINTQADPYTTTKRYNLIQYRRLGPKKIT-Q 118
Db 103 YLGRLDITKWSYSLICISNLTLNDAGSKAQINORNFVITEEFTLFVYEQLOEPQVTMK 162

Qy 119 SLMASVNSTCNVLTCSVEKEKNVTYNSPL-----GSEGNVLQIFOTPEQELTYTC 172
Db 163 SVKVSFNFSNITLMCSVKGAESVLYSWTPREPHASESGSGSILTVSRTPCPDPLPYIC 222

Qy 173 TAQNPVSNNSD-SISARQLCAD 193
Db 223 TAQNPVSQRSLPVPVHGQFCTD 244

RESULT 7
US-09-860-836B-11
; Sequence 11, Application US/09860836B
; Publication No. US20030054002A1
; GENERAL INFORMATION:
; APPLICANT: WAKELAND, WARD
; APPLICANT: WANDSTRADT, AMY
; APPLICANT: MOREL, LAURENCE
; TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
; FILE REFERENCE: UTSD:722US
; CURRENT APPLICATION NUMBER: US/09/860,836B
```

		Query Match	33.1%;	Score	343.5;	DB	16;	Length	654;	
		Best-Local Similarity	36.8%;	Pred.	No.-2,1e-23;					
		Matches	74;	Conservative	40;	Mismatches	74;	Indels	13; Gaps	4;
QY	1	KDSIFTVNGILGESVTFPPNIOEQPVKIATWS-KTSVAIVTQDSDSETAPVVTIHRN	59							
				:	:	:	:	:	:	:
DB	48	KDSAPTVMVGILGGSVTLPLNTVDTEINVIWGPKNALAFARPKN-----VTIMKKS	102							
				:	:	:	:	:	:	:
QY	60	YYERIHAGFNPNLVISDLRMDAGDYKDADINTQADPYTTTKRYNLQIVRRIGCKPKITOS	119							

```
Db 103 YLGLDITKWSYSLCTNLNLDAGSKAQINORNFVITTEFTLFLVFEQLOEPQVTWK 162
Qy 120 LMASVNSTCVITLTCSEVEKEKNVTYNWSP-----GEGNVLOIFQTPEDQELTYTCT 173
Db 163 SVKVSFNFCNITLCSVKGAESVLYSWTPREPHASENGSGSLTYSRTPCDPDLPICT 222
Qy 174 AQPVSNNSD-SISARQLCAD 193
Db 223 AQPVSORSRLPVHVGQFCTD 243
```

```
RESULT 11
US-10-436-523-79
; Sequence 79, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-79
```

```
Query Match 32.0%; Score 332; DB 14; Length 217;
Best Local Similarity 38.1%; Pred. No. 5.7e-23;
Matches 69; Conservative 37; Mismatches 69; Indels 6; Gaps 1;

Qy 8 VNGILGESVTFPVNIQEPQVKIIAWTSKTSVAVVTPGDSCTAPVVTVTHRYVERIHAL 67
Db 11 VVAVLOESISLPLEIPDPDEVENIWSHKSLSLATVVPKGEHPATIMVTHNYQGVQVSL 70
Qy 68 GPNVNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSILMASVNST 127
Db 71 DPSYSLHISNLWSDSGLYQAQVNLRTSQISTMQQVNLVYRWLSEPOITVNFESSGEGA 130
Qy 128 CNVTLTCSVEKEKNVTYNWSPLE-----EGNVLOIFQTPEDQELTYTCTAQNPSVNN 181
Db 131 CSMSLVCSVEKAGMDMTYSWLSRGDSTYTFHEGVLSTSWRPGDSALSCTCRANNPISNV 190
Qy 182 S 182
Db 191 S 191
```

```
RESULT 12
US-10-436-523-82
; Sequence 82, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 236
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-82

Query Match 32.0%; Score 332; DB 14; Length 236;
Best Local Similarity 38.1%; Pred. No. 6.4e-23;
Matches 69; Conservative 37; Mismatches 69; Indels 6; Gaps 1;

Qy 8 VNGILGESVTFPVNIQEPQVKIIAWTSKTSVAVVTPGDSCTAPVVTVTHRYVERIHAL 67
Db 30 VVAVLOESISLPLEIPDPDEVENIWSHKSLSLATVVPKGEHPATIMVTHNYQGVQVSL 89
Qy 68 GPNVNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSILMASVNST 127
Db 90 DPSYSLHISNLWSDSGLYQAQVNLRTSQISTMQQVNLVYRWLSEPOITVNFESSGEGA 149
Qy 128 CNVTLTCSVEKEKNVTYNWSPLE-----EGNVLOIFQTPEDQELTYTCTAQNPSVNN 181
Db 150 CSMSLVCSVEKAGMDMTYSWLSRGDSTYTFHEGVLSTSWRPGDSALSCTCRANNPISNV 209
Qy 182 S 182
Db 210 S 210
```

```
RESULT 13
US-10-436-523-77
; Sequence 77, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-523-77
```

```
Query Match 32.0%; Score 332; DB 14; Length 270;
Best Local Similarity 38.1%; Pred. No. 7.7e-23;
Matches 69; Conservative 37; Mismatches 69; Indels 6; Gaps 1;

Qy 8 VNGILGESVTFPVNIQEPQVKIIAWTSKTSVAVVTPGDSCTAPVVTVTHRYVERIHAL 67
Db 11 VVAVLOESISLPLEIPDPDEVENIWSHKSLSLATVVPKGEHPATIMVTHNYQGVQVSL 70
Qy 68 GPNVNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSILMASVNST 127
Db 71 DPSYSLHISNLWSDSGLYQAQVNLRTSQISTMQQVNLVYRWLSEPOITVNFESSGEGA 130
Qy 128 CNVTLTCSVEKEKNVTYNWSPLE-----EGNVLOIFQTPEDQELTYTCTAQNPSVNN 181
Db 131 CSMSLVCSVEKAGMDMTYSWLSRGDSTYTFHEGVLSTSWRPGDSALSCTCRANNPISNV 190
Qy 182 S 182
Db 191 S 191
```

```
RESULT 14
US-10-220-946-18
; Sequence 18, Application US/10220946
; Publication No. US20030124575A1
; GENERAL INFORMATION:
```

APPLICANT: No. US20030124575Alartis AG
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Weiner, Gudrun
APPLICANT: Jaritz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Kalthoff, Frank Stephan
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31347 PCT
CURRENT APPLICATION NUMBER: US/10/220,946
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/192,934
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/205,026 (US 60/279,243)
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/205,020
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/205,769
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/205,767
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 289
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-220-946-18

Query Match 32.0%; Score 332; DB 14; Length 289;
Best Local Similarity 38.1%; Pred. No. 8.4e-23;
Matches 69; Conservative 37; Mismatches 69; Indels 6; Gaps 1;
QY 8 VNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSETAPVVTVTHRNYYERIHAL 67
DB 30 VVAVLQESISLPLEIPDEEVENIWSHKSLSATVVPKGEHPATIMVNTNPHYQGVQVSL 89
QY 68 GPNYLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
DB 90 DPSYLSLHISNLWSDSGLYQAQVNLRTSQISTMQQYNLCVYRWLSBPQITVNFESSGE 149
QY 128 CNVTLTCSVEKEEKVNTYNSPLGE-----EGNVLIQIFQTPEDQELTYTCTAQNPSNN 181
DB 150 CSMNLVCSVEKAGMDMTYSLWLSRGDSTYTFHEGVLSTSWRPGDSALSCTCRANNPISNV 209
QY 182 S 182
DB 210 S 210

RESULT 15
US-10-436-523-76
Sequence 76, Application US/10436523
Publication No. US20030180888A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFERENCE: 7853-244-999
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens
US-10-436-523-76

Query Match 32.0%; Score 332; DB 14; Length 289;

Best Local Similarity 38.1%; Pred. No. 8.4e-23;
Matches 69; Conservative 37; Mismatches 69; Indels 6; Gaps 1;
QY 8 VNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSETAPVVTVTHRNYYERIHAL 67
DB 30 VVAVLQESISLPLEIPDEEVENIWSHKSLSATVVPKGEHPATIMVNTNPHYQGVQVSL 89
QY 68 GPNYLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
DB 90 DPSYLSLHISNLWSDSGLYQAQVNLRTSQISTMQQYNLCVYRWLSBPQITVNFESSGE 149
QY 128 CNVTLTCSVEKEEKVNTYNSPLGE-----EGNVLIQIFQTPEDQELTYTCTAQNPSNN 181
DB 150 CSMNLVCSVEKAGMDMTYSLWLSRGDSTYTFHEGVLSTSWRPGDSALSCTCRANNPISNV 209
QY 182 S 182
DB 210 S 210

Search completed: February 4, 2005, 12:32:18
Job time : 66.5796 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: February 4, 2005, 12:03:57 ; Search time 19,2216 Seconds
(without alignments)
996.126 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220
Perfect score: 1039
Sequence: 1 KDSEIFTVNGILGESVTPV.....NNSDSISARQLCADIAMGFR 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295	28.4	629	2 A46500	Ly-9.2 antigen - m
2	174	16.7	240	2 S01299	OX-45 membrane gly
3	165.5	15.9	240	2 JL0143	antigen BCM1 precu
4	160	15.4	335	2 S58892	signaling lymphocy
5	139	13.4	458	1 WWMGR1	biliary glycoprote
6	139	13.4	521	2 JC1508	biliary glycoprote
7	136	13.1	521	2 S34338	biliary glycoprote
8	135.5	13.0	702	2 A36319	carcinoembryonic a
9	132	12.7	458	2 JC1509	biliary glycoprote
10	131.5	12.7	344	2 A27681	non-specific cross-
11	125	12.0	338	2 JC4776	limbic-system-asso
12	122.5	11.8	321	2 JH0395	biliary glycoprote
13	122.5	11.8	351	2 JH0396	biliary glycoprote
14	122.5	11.8	417	2 JH0394	transmembrane carc
15	122.5	11.8	464	2 C30127	biliary glycoprote
16	122.5	11.8	526	1 A32164	opioid-binding pro
17	121.5	11.7	338	2 JC1238	opioid-binding pro
18	121.5	11.7	345	2 S03199	opioid-binding pro
19	121.5	11.7	345	2 JC1239	opioid-binding cel
20	120.5	11.6	345	2 JC4025	50K glycoprotein p
21	119.5	11.5	338	2 JC5519	neurotrophin - rat
22	119	11.5	344	2 I56551	carcinoembryonic a
23	118	11.4	265	2 A55811	T-cell surface gly
24	118	11.4	347	2 S41638	cell-adhesion mole
25	115.5	11.1	458	2 S23989	T-cell surface gly
26	113.5	10.9	351	1 RWHUC2	pregnancy-specific
27	113.5	10.9	419	2 JC4123	carcinoembryonic a
28	110.5	10.6	349	2 A34815	gene 2B4 protein -
29	110	10.6	398	2 I49443	

30	110	10.6	518	2 JC4024	poliovirus recepto
31	108	10.4	272	2 I48268	biliary glycoprote
32	107.5	10.3	286	2 A28333	carcinoembryonic a
33	107	10.3	243	2 A53244	leukocyte antigen
34	106.5	10.3	458	2 S68177	C-CAM2a protein is
35	106.5	10.3	519	2 A44783	ecto-ATPase precu
36	106.5	10.3	1232	2 T43027	neural cell adhesi
37	104.5	10.1	417	2 A28277	pregnancy-specific
38	104.5	10.1	419	2 A33258	pregnancy-specific
39	104.5	10.1	426	2 B33258	pregnancy-specific
40	104.5	10.1	7962	2 I38346	elastic titin - hu
41	102.5	9.9	1323	2 PNO568	connectin JB - chi
42	102.5	9.9	4162	2 T42633	connectin/titin -
43	102	9.8	324	2 G43354	pregnancy-specific
44	102	9.8	326	2 F43354	pregnancy-specific
45	102	9.8	333	2 A43354	pregnancy-specific

ALIGNMENTS

RESULT 1

A46500

Ly-9.2 antigen - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A46500

R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.

J. Immunol. 149, 1636-1641, 1992

A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.

A:Reference number: A46500; MUID:92373005; PMID:1506686

A:Accession: A46500

A>Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-629 <SAN>

A:Cross-references: GB:M84412; NID:G198931; PIDN:AAA39468.1; PID:G198932

A:Experimental source: C57BL/6

A>Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)

C:Keywords: transmembrane protein

Query Match 28.4%; Score 295; DB 2; Length 629;
Best Local Similarity 34.9%; Pred. No. 6.1e-17;
Matches 67; Conservative 31; Mismatches 88; Indels 6; Gaps 1;

QY	7	TVNGILGESVTPPNVNIQEPQVKIIA	WTSTKTSVAVVTPGDSETPAVVTVTHRNYIERIHA	66
DB	234	TVVGILGEPVTLPLEFRATATKQNVV	VLNTSVISQERRCAATADSRKPKGSEERRV	293
QY	67	LGPNYNLVISDLRMDAGDYKADINTQ	ADPYTTTKRYNLIQIYRLKPKKITQSLMASVNS	126
DB	294	SDQDQSLKISQLKXMEDAGPYHAYVC	SEASRDPVSRHFTLLVYKRLKPSVTKSPVHMMG	353
QY	127	TCNVLTCTCSEKKEKNVTYNWSP	LGEEG-----NVLQIFQTPEDQELTYTCTAQN	180
DB	354	ICEVLTCTSDGCGNNVTYTMPLQNK	AVNSQKSHLVNSWSEGEHLNFTCTAHNPVSN	413
QY	181	NSDSISAROLCA	192	
DB	414	SSSQFSFGTICS	425	

RESULT 2

S01299

OX-45 membrane glycoprotein precursor - rat

N:Alternate names: MRC OX-45 antigen

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C:Accession: S01299

R:Killeen, N.; Moesner, R.; Arvieux, J.; Willis, A.; Williams, A.F.

EMBO J. 7, 3087-3091, 1988

A:Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the

A:Reference number: S01299; MUID:89030603; PMID:3181129

A:Accession: S01299

A:Molecule type: mRNA
A:Residues: 1-240 <KIL>
A/Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805
C/Superfamily: B-cell surface glycoprotein blast-1
C/Keywords: glycoprotein; membrane protein; surface antigen
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F:38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 16.7%; Score 174; DB 2; Length 240;
Best Local Similarity 26.2%; Pred. No. 2.6e-07;
Matches 51; Conservative 36; Mismatches 86; Indels 22; Gaps 6;
QY 1 KDSIEFTVNGILGESVTFPPNIOEPQVKLIW---TSKTSVAVYVTPGDSAPVVTHT 57
DB 24 QDSVPNNVAITGNSVTLTLIKHPLASVQRLTWLHTNQKILEYFNGKK-----TVFE 77
QY 58 RNYERIHALGPNYNIIVISDLRMEDAGD-YKADINTQADPYTTTKRYNLQIYRRLGKPKI 116
DB 78 SVFKDRVLDKTNGLRIYNSKEDRGDYMRMLHETEDQWKIT-----MEVDLVSKPAI 133
QY 117 TQSLMASVNSTCNVTLTCSVEKEKNVTNW-----SPLGEGNVLIQIFQPEQDELTY 170
DB 134 KIEKTNLTDSCHLRLSKV--EDQGVDTWYEDSGPPQRPNGVYLEITITPHNKSTFY 191
QY 171 TCTAQNPNVNSDSI 185
DB 192 TCOVSNPVSSENDTL 206

RESULT 3
JL0143
antigen BCM1 precursor - mouse
N/Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004
C/Accession: JL0143; S21319; A47469; B47469
R/Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seldin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A/Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.
A/Reference number: JL0143; MUID:90278362; PMID:1693656
A/Accession: JL0143
A:Molecule type: mRNA
A:Residues: 1-240 <WON>
A/Cross-references: UNIPROT:P18181; EMBL:X17501; NID:950134; PIDN:CAA35542.1; PID:950135
R/Wong, Y.W.; Williams, A.F.; Kingmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
A/Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.
A/Reference number: S21319
A/Accession: S21319
A/Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-240 <WON2>
A/Cross-references: EMBL:X53262; NID:950138; PIDN:CAA37604.1; PID:950139
R/Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A/Title: Identification, by protein sequencing and gene transfection, of sgp-60 as the m
A/Reference number: A47469; MUID:93234508; PMID:8475091
A/Accession: A47469
A:Molecule type: protein
A:Residues: 74-80 <CAB>
A/Experimental source: EL-4 lymphoma cells
A/Note: sequence extracted from NCBI backbone (NCBIP:129658)
A/Accession: B47469
A:Molecule type: protein
A:Residues: 84-98 <CA2>
A/Experimental source: EL-4 lymphoma cells
A/Note: sequence extracted from NCBI backbone (NCBIP:129660)
C/Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t
C/Superfamily: B-cell surface glycoprotein blast-1
C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linked

F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-217/Product: antigen BCM1 #status predicted <MAT>
F:218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F:32,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 15.9%; Score 165.5; DB 2; Length 240;
Best Local Similarity 24.2%; Pred. No. 1.4e-06;
Matches 47; Conservative 40; Mismatches 92; Indels 15; Gaps 5;

QY 8 VNGILGESVTFPPNIOEPQVKIITAWTSKTSVAVYVTPGDSAPVVTHTNRYERIHAL 67
DB 31 INATGSNVTLIKHDPGLGPKYKRIITWLTHTNQKILEYNNSTK---TIFSEFKGRVYLE 87
QY 68 GPNVNLIVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
DB 88 ENNGALHISNVKEDKGYTVMRLRETE--NELKITLEVDPVPPKPSIEINKTEASTDS 144
QY 128 CNVTLTCSVEKEKNVTNW-----SPLGEGNVLIQIFQPEQDELTYTCTAQNPNVNN 181
DB 145 CHLRLSCV--KDQHDVYTWYESSGPPFKKSPGYVLDTIVTPQNKSTFYTCQVSNPVSSK 202
QY 182 SDSISARQLCADIA 195
DB 203 NDTVYFTLPC-DLA 215

RESULT 4

S58892
signaling lymphocytic activation molecule - human
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text change 09-Jul-2004
C/Accession: S58892
R/Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.
Nature 376, 260-263, 1995
A/Title: A novel receptor involved in T-cell activation.
A/Reference number: S58892; MUID:95342241; PMID:7617038
A/Accession: S58892
A/Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-335 <COC>
A/Cross-references: UNIPROT:Q13291; EMBL:U33017; NID:984968; PIDN:AAA75380.1; PID:984949

Query Match 15.4%; Score 160; DB 2; Length 335;
Best Local Similarity 25.4%; Pred. No. 6e-06;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

QY 12 LGESVTFP-----VNIQEPQVKIIIAWTSKT-----SVAYVTPGDSAPVVTVTHRN 59
DB 39 LGSKVLLPLTVTERINKSMNKSIIHVVTMAKSLNSVENKIVSLDPSAGPPVILGDRYKF 98
QY 60 YVERIHALGPNYNIIVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
DB 99 YLE-----NLTLGIRSKKDEGWYLMTL-----EKNVSQVRFCLQLRLYEQVSTPEIK 147
QY 118 QSLMASVNSTCNVTLTCSVEKEKNVTNWS-----PL--GEGNVLIQIFQPEQDEL 169
DB 148 VLNKTQENGCTLLIGCTVEKGD-HVAYSSEKAGTHPLNPANSHLLSLTLGQPHADNI 206
QY 170 YTCTAQNPNVNSDSIS 186
DB 207 YICTVSNPISNNSQTFS 223

RESULT 5

WMSR1
biliary glycoprotein A precursor - mouse
N/Alternate names: carcinoembryonic antigen mmCGM1a; murine hepatitis virus receptor
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C/Accession: JCI1505; A45006; A41563; S11626; S11625
R/McCuaig, K.; Rosenberg, M.; Nedeliec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993

A>Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1505
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-458 <MCC>
A/Cross-references: UNIPROT:P31809
R:McCuaig, K.; Turbide, C.; Beauchemin, N.
Cell Growth Differ. 3, 163-174, 1992
A>Title: mmCGM1a: a mouse carcinoembryonic antigen gene family member, generated by alternative splicing
A:Reference number: A49006; MUID:92338096; PMID:1633107
A:Accession: A49006
A:Molecule type: mRNA
A:Residues: 1-458 <MC2>
A/Cross-references: GB:X1531; NID:953020; PIDN:CAA3409.1; PID:G53021
A>Note: sequence extracted from NCBI backbone (NCBIN:109445, NCBI:109446)
R:Veksel, G.S.; Pensiero, M.N.; Cardellicchio, C.B.; Williams, R.K.; Jiang, G.S.; Holme J. Vitol. 65, 6881-6891, 1991
A>Title: Cloning of the mouse hepatitis virus (MHV) receptor: expression in human and hamster cells
A:Reference number: A41563; MUID:92046352; PMID:1719235
A:Accession: A41563
A:Molecule type: mRNA
A:Residues: 1-458 <DVE>
A/Cross-references: GB:M77196; NID:G194002; PIDN:AAA37858.1; PID:G194003
R:Beauchemin, N.
submitted to the EMBL Data Library, May 1990
A:Reference number: S11626
A:Accession: S11626
A:Molecule type: mRNA
A:Residues: 'PQ', 82-458 <BEA>
A/Cross-references: EMBL:X1531
R:Beauchemin, N.; Turbide, C.; Afar, D.; Bell, J.; Raymond, M.; Stanners, C.P.; Fuks, A. Cancer Res. 49, 2017-2021, 1989
A>Title: A mouse analogue of the human carcinoembryonic antigen.
A:Reference number: S11625; MUID:89195121; PMID:2702644
A:Accession: S11625
A:Molecule type: mRNA
A:Residues: 'PQ', 82-321 <BE2>
A/Cross-references: EMBL:X1531
C:Comment: This protein is expressed at the cell surface and plays a determinant role in cell-cell interactions.
C:Genetics:
A:Gene: Bgpb; Bgpl
A:Map position: 7
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-458/Product: biliary glycoprotein A #status predicted <MHR>
F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:429-447/Domain: transmembrane #status predicted <TMN>
F:449-458/Domain: intracellular #status predicted <CYT>
F:71,89,104,148,152,199,206,210,226,258,290,294,304,317,333,375/Binding site: carbohydrate binding site
F:167-217,261-301,346-394/Disulfide bonds: #status predicted

Query Match 13.4%; Score 139; DB 1; Length 458;
Best Local Similarity 27.4%; Pred. No. 0.00052;
Matches 49; Conservative 22; Mismatches 86; Indels 22; Gaps 6;

Qy 25 PROVKTIAWTSKTSVAVYTPGDSAPVVTVTHRNY----YERIHALGPNYLNIVISDLRM 80
Db 59 PLALGAFAYKGNNTAI----DKEIARFVPNSNMFTGQAYSGREIYNSGSLLFQMITM 114
Qy 81 EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCWTLTCSVEKEE 140
Db 115 KDMGVVTLDM-TDENYRRTQATVRFHVHPILLKPNITSNNSNPVEGDDSVSLTCDSTYDP 173
Qy 141 KNVTYNSPLGE-----EGN-VLIQFQTPEDQELTYTCTAQNPNVS--NNSDSIS 186
Db 174 DNIYLSNRNGESLSEGRDLKLSGRTLLNVRNDTGPVVCETRNPNVSNRSDPFS 232

RESULT 6

JC1508
biliary glycoprotein D - mouse
N:Alternate names: biliary glycoprotein 1
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: JC1508; S65940; S36852
R:McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A>Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A:Reference number: JC1505; MUID:93273228; PMID:8500759
A:Accession: JC1508
A:Molecule type: mRNA
A:Residues: 1-521 <MCC>
A/Cross-references: UNIPROT:P31809; EMBL:X67279; NID:G50170; PIDN:CAA47696.1; PID:G50171
A:Experimental source: strain CD1; tissue colon
R:Nedellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Biochem. 231, 104-114, 1995
A>Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A:Reference number: S65939; MUID:95354678; PMID:7628460
A:Accession: S65940
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-21 <NED>
A/Cross-references: EMBL:X84054; NID:G1039337
A:Experimental source: strain BALB/c
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A:Comment: This protein is expressed at the cell surface and plays a determinant role in cell-cell interactions.
C:Genetics:
A:Gene: Bgpb; Bgpl
A:Map position: 7
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology <CEAN>
C:Keywords: glycoprotein; receptor; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <IMM1>
F:160-219/Domain: immunoglobulin homology <IMM1>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:71,89,104,148,199,206,210,226,258,290,294,304,317,333,375/Binding site: carbohydrate binding site

Query Match 13.4%; Score 139; DB 2; Length 521;
Best Local Similarity 27.4%; Pred. No. 0.00061;
Matches 49; Conservative 22; Mismatches 86; Indels 22; Gaps 6;

Qy 25 PROVKTIAWTSKTSVAVYTPGDSAPVVTVTHRNY----YERIHALGPNYLNIVISDLRM 80
Db 59 PLALGAFAYKGNNTAI----DKEIARFVPNSNMFTGQAYSGREIYNSGSLLFQMITM 114
Qy 81 EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCWTLTCSVEKEE 140
Db 115 KDMGVVTLDM-TDENYRRTQATVRFHVHPILLKPNITSNNSNPVEGDDSVSLTCDSTYDP 173
Qy 141 KNVTYNSPLGE-----EGN-VLIQFQTPEDQELTYTCTAQNPNVS--NNSDSIS 186
Db 174 DNIYLSNRNGESLSEGRDLKLSGRTLLNVRNDTGPVVCETRNPNVSNRSDPFS 232

RESULT 7

S34338
biliary glycoprotein F - mouse
N:Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S34338; JC1510; A41093
R:Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A:Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A:Reference number: S34338
A:Accession: S34338
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <HUA>
R:McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein
A;Reference number: JCI1505; MUID:93273228; PMID:8500759
A;Accession: JCI1510
A;Molecule type: mRNA
A;Residues: 1-81, 'Q', 83-141, 'P', 143-521 <MCC>
A;Cross-references: GB:X67281
R;Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A;Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A;Reference number: A41093; MUID:91288498; PMID:1648219
A;Accession: A41093
A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-59 <WIL>
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: Bgpf
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (C

Query Match 13.1%; Score 136; DB 2; Length 521;
Best Local Similarity 26.8%; Pred. No. 0.0011;
Matches 48; Conservative 27; Mismatches 82; Indels 22; Gaps 6;
QY 25 PROVKIIAMTSKTSVAIVTPGDSAPVVTTHRNYYRIHA---LGNYNLAVISDLRM 80
Db 59 PLALGAPAWYKGNPVS---TNAEIVHFTGINKITTPGAHSGRETVYNSGSLLRQTVV 114
QY 81 EDAGDYKADINTQADPYTTKRYNLOIYRRLKPKITQSLMASVNSTCNVTLTCSVEKEE 140
Db 115 KDTGVVTIEM--TDENFRTEATVQFHVHQLLKPNTNNSNPVSGDVSLSLTCDSYTD 173
QY 141 KNTVYNWSPLGE-----EGN-VLQIFQTPEDQELTYTCTAQNPNV--NNSDSIS 186
Db 174 DNITLYWSRNGESLSGDRLLKUSEGNRTLLNVRNDTGPVCETRNPVSVNRSDPFS 232

RESULT 8
A36319
carcinoembryonic antigen precursor - human
N;Alternate names: CEA; meconium antigen 100
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: A36319; A27773; A25845; S08106; S31737; A44476; I54224; I59098; A26
R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruyama, A.; Hassauer, M.; Shively,
Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
A;Reference number: A36319; MUID:90258861; PMID:2342461
A;Accession: A36319
A;Molecule type: DNA
A;Residues: 1-702 <SCH>
A;Cross-references: UNIPROT:P06731; GB:M17303; NID:9178676; PIDN:AA859513.1; PID:9178677
A;Note: the authors show the codons TTA for residue '641-Phe and CAG for residue 646-Thr
R;Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A;Title: Isolation and characterization of full-length functional cDNA clones for human
A;Reference number: A27773; MUID:88038876; PMID:3670312
A;Accession: A27773
A;Molecule type: mRNA
A;Residues: 1-702 <BEA>
A;Cross-references: GB:M29540; NID:9180222; PIDN:AAA51967.1; PID:9180223
R;Barnett, T.; Goebel, S.J.; Northduft, M.A.; Elving, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: A31037
A;Molecule type: mRNA

A;Residues: 1-702 <BAR>
A;Cross-references: GB:M29540; NID:9180222; PIDN:AAA51967.1; PID:9180223
A;Note: the authors translated the codon GTG for residue 130 as Leu
R;Oikawa, S.; Nakazato, H.; Kosaki, G.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
A;Reference number: A25845; MUID:87128144; PMID:3814146
A;Accession: A25845
A;Molecule type: mRNA
A;Residues: 5-702 <OIK>
A;Cross-references: GB:M15042; NID:9180198; PIDN:AAA51963.1; PID:9180199
R;Oikawa, S.
submitted to the EMBL Data Library, September 1989
A;Reference number: S08106
A;Accession: S08106
A;Molecule type: mRNA
A;Residues: 5-319, 321-702 <O12>
A;Cross-references: EMBL:X16455; NID:929854; PIDN:CAA34474.1; PID:9825638
R;Barnett, T.
submitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcinoemb
A;Reference number: S31737
A;Accession: S31737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BA2>
A;Cross-references: EMBL:X62151
R;Khan, W.N.; Fraengemyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoemb
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: A44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
R;Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
A;Reference number: I54224; MUID:91139118; PMID:2286372
A;Accession: I54224
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: GB:M60964; NID:9180215; PIDN:AAA51964.1; PID:9180217
R;Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A;Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon
A;Reference number: I59098; MUID:87204247; PMID:3033671
A;Accession: I59098
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 331-702 <RE2>
A;Cross-references: GB:M16234; NID:9180240; PIDN:AAA51972.1; PID:9180241
R;Stiepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105
A;Reference number: A26831; MUID:87326349; PMID:3632664
A;Accession: A26831
A;Molecule type: protein
A;Residues: 35-64 <SIE>
R;Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A;Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at t
A;Reference number: A35490; MUID:90321257; PMID:2372297
A;Accession: A35490
A;Molecule type: protein
A;Residues: 'X', 140-151, 'X', 153, 'X', 155-156 <THO>
A;Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer
C;Comment: This heavily glycosylated membrane protein of unknown function is a widely use
C;Comment: This protein may be processed at its C-terminus. It is anchored to the membra
C;Genetics:
A;Gene: GDB:CEA
A;Cross-references: GDB:119054; OMIM:114890

A:Molecule type: protein		A:Residues: 35-69 <PAX>		A:Khan, W.N.; Fraengmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.	
A:Title: Identification of three new genes and estimation of the size of the carinoembryonic antigen precursor amino-terminal homology <CEAN>		A:Reference number: A4476; MUID:93052339; PMID:1427854		A:Accession: E4476	
A:Status: preliminary; not compared with conceptual translation		A:Molecule type: DNA		A:Residues: 35-141 <KHA>	
A:Accession: F4476		A:Status: preliminary; not compared with conceptual translation		A:Residues: 35-137, 'L', 139-141 <KH2>	
A:Comment: This protein appears to be processed at the carboxyl terminus and anchored th		A:Genetics:		A:Gene: GDB:NCA	
A:Cross-references: GDB:120221; OMIM:163980		A:Map position: 19q13.2-19q13.2		A:Introns: 22/1	
A:Notes: the list of introns may be incomplete		C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal homology <CEAN>		C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatidylserine	
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>		F:1-34/Domain: signal sequence #status predicted <SIG>		F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>	
F:160-217/Domain: immunoglobulin homology <IMM2>		F:252-301/Domain: immunoglobulin homology <IMM2>		F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>	
F:404,111,115,152,173,197,224,256,274,288,292/Binding site: carboxylate (Asn) (covalent)		F:309/Binding site: carboxylate (Asn) (covalent) #status predicted		F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form	
Query Match		12.7%; Score 131.5; DB 2; Length 344;		Best Local Similarity	
Matches		54; Conservative		29; Mismatches	
67; Indels		65; Gaps		12;	
QY		19 PVNIQPRQVKIIA-----W-----TSKTSVAYV-----TPGDSAPVVT		54	
Db		42 PFNVAEGKEVLLLAHNLQNRIQYSWYKGERVDGNSLIVGYVIGTQATPGPA-----		94	
QY		55 VTHRVNYYERHAGPNVNLVISDLRMEDAGDY-----KAD-INTQADPVTYTKRYNLQY		108	
Db		95 -----YSGRETIYPNASTLIQNVTONDTGFTYTLQVIKSDLVNEEA-----TQGFH--VY		141	
QY		109 RLRLGPKITQSLMASVNSTCNVTLTCSVEKEKNVTYNNSPLGE-----EGNV--		156	
Db		142 PELPKPSISSNNSNPVEDKDAVATC--EPEVQNTYTLWWNGOSLPVSPRLQSLNGNWT		199	
QY		157 LQIFQTPEQELTYTCTAQNPSV--NNSDSISARQL		190	
Db		200 LTLSSVKRNDAGSYECEIQNPASANRSDPVTNLVL		234	
RESULT 11		JC4776		limbic-system-associated memb	
JC4776		limbic-system-associated membrane protein precursor - human		C:Species: Homo sapiens (man)	
C:Date: 10-May-1996		#sequence_revision 16-Aug-1996		#text_change 09-Jul-2004	
C:Accession: JC4776		R:Pimenta, A.F.; Fischer, I.; Levitt, P.		Gene 170, 189-195, 1996	
A:Title: cDNA cloning and structural analysis of the human		limbic-system-associated memb		A:Reference number: JC4776; MUID:96235133; PMID:8666243	
A:Accession: JC4776		A:Molecule type: mRNA		A:Residues: 1-338 <PIM>	
A:Cross-references: UNIPROT:Q13449; GB:U41901; NID:gi276898; PIDN:AAC50569.1; PID:gi2768		A:Experimental source: brain		C:Comment: This is a neuronal surface glycoprotein distributed in cortical and subcortic	
C:Genetics:		A:Gene: lamp		C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi	

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: JH0396
R/Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A/Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A/Reference number: JH0394; MUID:91222218; PMID:2025273
A/Accession: JH0396
A/Molecule type: mRNA
A/Residues: 1-351 <KUR>
A/Cross-references: UNIPROT:P13688; GB:M72238; NID:g179436; PID:AAAS8393.1; PID:g179436
A/Experimental source: leukocyte
C/Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C/Keywords: glycoprotein; transmembrane protein
F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-351/Product: biliary glycoprotein i #status predicted <MAT>
F/160-217/Domain: immunoglobulin homology <IMM1>
F/252-301/Domain: immunoglobulin homology <IMM2>
Query Match 11.8%; Score 122.5; DB 2; Length 351;
Best Local Similarity 24.4%; Pred. No. 0.009; Mismatches 65; Indels 65; Gaps 13;
Matches 52; Conservative 31; Mismatches 65; Indels 65; Gaps 13;
QY 17 TFPVNIQEPQVKII-----AW-----TSKTSVAY-----VTPGDSAPV 52
DB 40 SMPFVNAEGKVELLVHNLPPQLFGYSWYKGERVGNRQIVGVAIGTQQTGPGNSG-- 97
QY 53 VVTVHRYNRYERHALGPNVNLVSDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQ 106
DB 98 -----RETIY-----PNASLLIQNTQDGTGYTLQVKSGLVNEEA-----TGQPH-- 139
QY 107 IYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNNW-----SP---LGEEG 154
DB 140 VYPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWNNQSLPVSRLQLSNGN 197
QY 155 NVLQIFQTPEDQELTYTCTAQNPPVS--NNSDSIS 186
DB 198 RTLTLLSVTRNDTGPYECEIQNPVSANRSDPVT 230
Query Match 11.8%; Score 122.5; DB 2; Length 351;
Best Local Similarity 24.4%; Pred. No. 0.009; Mismatches 65; Indels 65; Gaps 13;
Matches 52; Conservative 31; Mismatches 65; Indels 65; Gaps 13;
QY 17 TFPVNIQEPQVKII-----AW-----TSKTSVAY-----VTPGDSAPV 52
DB 40 SMPFVNAEGKVELLVHNLPPQLFGYSWYKGERVGNRQIVGVAIGTQQTGPGNSG-- 97
QY 53 VVTVHRYNRYERHALGPNVNLVSDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQ 106
DB 98 -----RETIY-----PNASLLIQNTQDGTGYTLQVKSGLVNEEA-----TGQPH-- 139
QY 107 IYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNNW-----SP---LGEEG 154
DB 140 VYPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWNNQSLPVSRLQLSNGN 197
QY 155 NVLQIFQTPEDQELTYTCTAQNPPVS--NNSDSIS 186
DB 198 RTLTLLSVTRNDTGPYECEIQNPVSANRSDPVT 230
Query Match 11.8%; Score 122.5; DB 2; Length 417;
Best Local Similarity 24.4%; Pred. No. 0.011; Mismatches 65; Indels 65; Gaps 13;
Matches 52; Conservative 31; Mismatches 65; Indels 65; Gaps 13;
QY 17 TFPVNIQEPQVKII-----AW-----TSKTSVAY-----VTPGDSAPV 52
DB 40 SMPFVNAEGKVELLVHNLPPQLFGYSWYKGERVGNRQIVGVAIGTQQTGPGNSG-- 97

QY 53 VVTVHRYNRYERHALGPNVNLVSDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQ 106
DB 98 -----RETIY-----PNASLLIQNTQDGTGYTLQVKSGLVNEEA-----TGQPH-- 139
QY 107 IYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNNW-----SP---LGEEG 154
DB 140 VYPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWNNQSLPVSRLQLSNGN 197
QY 155 NVLQIFQTPEDQELTYTCTAQNPPVS--NNSDSIS 186
DB 198 RTLTLLSVTRNDTGPYECEIQNPVSANRSDPVT 230
RESULT 15
C30127
Transmembrane carcinoembryonic antigen 3 precursor - human
N/Alternate names: CD66 splice form BGPC
C/Species: Homo sapiens (man)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: C30127; I52597
R/Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.;
J. Cell Biol. 108, 267-276, 1989
A/Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNA
A/Reference number: A92752; MUID:89139550; PMID:2537311
A/Accession: C30127
A/Molecule type: mRNA
A/Residues: 1-464 <BAR>
A/Cross-references: UNIPROT:Q16170; EMBL:X16356; EMBL:X14784
R/Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeisner, S.E.; Hajibaghe
Blood 84, 200-210, 1994
A/Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, exp
A/Reference number: I52597; MUID:94289702; PMID:8018919
A/Accession: I52597
A/Status: preliminary; translated from GB/EMBL/DBDJB
A/Molecule type: mRNA
A/Residues: 1-464 <RES>
A/Cross-references: GB:S71326; NID:g550030; PID:AAAB31183.1; PID:g550031
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C/Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>
F/160-217/Domain: immunoglobulin homology <IMM1>
F/252-301/Domain: immunoglobulin homology <IMM2>
F/341-398/Domain: immunoglobulin homology <IMM3>
F/424-455/Domain: transmembrane #status predicted <TMW>
F/104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/Bindi
Query Match 11.8%; Score 122.5; DB 2; Length 464;
Best Local Similarity 24.4%; Pred. No. 0.013; Mismatches 65; Indels 65; Gaps 13;
Matches 52; Conservative 31; Mismatches 65; Indels 65; Gaps 13;
QY 17 TFPVNIQEPQVKII-----AW-----TSKTSVAY-----VTPGDSAPV 52
DB 40 SMPFVNAEGKVELLVHNLPPQLFGYSWYKGERVGNRQIVGVAIGTQQTGPGNSG-- 97
QY 53 VVTVHRYNRYERHALGPNVNLVSDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQ 106
DB 98 -----RETIY-----PNASLLIQNTQDGTGYTLQVKSGLVNEEA-----TGQPH-- 139
QY 107 IYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNNW-----SP---LGEEG 154
DB 140 VYPELPKPSISSNNSNPVEDKDAVFTC--EPETQDTTYLWNNQSLPVSRLQLSNGN 197
QY 155 NVLQIFQTPEDQELTYTCTAQNPPVS--NNSDSIS 186
DB 198 RTLTLLSVTRNDTGPYECEIQNPVSANRSDPVT 230
Search completed: February 4, 2005, 12:15:57
Job time : 20.2216 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 11:55:35 ; Search time 87.4394 Seconds
(without alignments)
1165.422 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220

Perfect score: 1039

Sequence: 1 KDSIPTVNGILGESVTFPV.....NNSDSISARQLCADIAMGFR 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1039	100.0	272	Q9UB7	Q9ub7 homo sapien
2	1039	100.0	280	Q95660	Q95660 homo sapien
3	1039	100.0	328	Q6FHA8	Q6fha8 homo sapien
4	1039	100.0	328	O15430	O15430 homo sapien
5	1039	100.0	339	Q8WMI8	Q8wmi8 homo sapien
6	1039	100.0	345	Q9UIB8	Q9uib8 homo sapien
7	1003	96.5	197	Q9UIT7	Q9uit7 homo sapien
8	1003	96.5	241	Q9UIB6	Q9uib6 homo sapien
9	610.5	58.8	329	Q9Z178	Q9z178 mus musculus
10	352	33.9	655	LY9_HUMAN	LY9_HUMAN
11	332	32.0	289	Q96A28	Q96a28 homo sapien
12	328.5	31.6	285	Q8VE93	Q8ve93 mus musculus
13	323.5	31.1	285	Q8BT00	Q8bt00 mus musculus
14	321.5	30.9	285	Q9D780	Q9d780 mus musculus
15	316.5	30.5	332	SLF6_MOUSE	SLF6_MOUSE
16	295	28.4	538	Q8C9E4	Q8c9e4 mus musculus
17	295	28.4	645	Q6NZB6	Q6nzb6 mus musculus
18	295	28.4	649	Q7TMP7	Q7tmp7 mus musculus
19	295	28.4	654	LY9_MOUSE	LY9_MOUSE
20	294	28.3	544	Q8C2D4	Q8c2d4 mus musculus
21	283.5	27.3	140	Q8BFV0	Q8bfv0 m mus muscu
22	280.5	27.0	296	Q8N6Y8	Q8n6y8 homo sapien
23	280.5	27.0	328	Q9NY23	Q9ny23 homo sapien
24	280.5	27.0	335	Q9NQ25	Q9nq25 homo sapien
25	278.5	26.8	335	Q9NY08	Q9ny08 homo sapien
26	269	25.9	335	Q8CJ65	Q8cj65 mus musculus
27	268	25.8	294	Q91XAO	Q91xao mus musculus
28	268	25.8	300	Q8CJ63	Q8cj63 mus musculus
29	268	25.8	333	Q8BHK6	Q8bhk6 m mus muscu
30	268	25.8	335	Q8BTL2	Q8btl2 mus musculus
31	268	25.8	335	Q8CJ64	Q8cj64 mus musculus

32	239	23.0	351	1	SLF6_MOUSE	Q9et39 mus musculus
33	180	17.3	228	2	Q8ND32	Q8nd32 homo sapien
34	177.5	17.1	198	2	Q6UWG1	Q6uwg1 homo sapien
35	174	16.7	240	1	CD48_RAT	P10252 rattus norv
36	172.5	16.6	211	2	Q8ZRI7	Q6zr17 homo sapien
37	170	16.4	193	2	Q6P2J4	Q6p2j4 homo sapien
38	165.5	15.9	240	1	CD48_MOUSE	P18181 mus musculus
39	165.5	15.9	240	2	Q6P905	Q6p905 mus musculus
40	160	15.4	207	2	Q9HBE9	Q9hbe9 homo sapien
41	160	15.4	288	2	Q9NQ26	Q9nq26 homo sapien
42	160	15.4	335	1	SLAM_HUMAN	Q13291 homo sapien
43	160	15.4	335	2	Q96QR3	Q96qr3 homo sapien
44	156	15.0	413	2	Q64OR3	Q64or3 mus musculus
45	154.5	14.9	338	2	Q95MM6	Q95mm6 bos taurus

ALIGNMENTS

RESULT 1

ID	Q9UB7	PRELIMINARY;	PRT;	272 AA.
AC	Q9UB7;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Leukocyte differentiation antigen CD84 isoform CD84d.			
GN	Name=CD84;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Palou E., Sole J., Piroto F., Gaya A.;			
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF054817; AAF21723.1; -.			
DR	InterPro: IPR003599; IG.			
DR	InterPro: IPR007110; IG-like.			
DR	SMART; SM00409; IG; 1; IG-like.			
DR	PROSITE; P550835; IG_LIKE; 1.			
SQ	SEQUENCE 272 AA; 30514 MW; 6A2E13AA4E22E13E CRC64;			

Query Match 100.0%; Score 1039; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KDSIPTVNGILGESVTFPVNIQEPQVKIIAWTSTSVAYVTPGDSAPVVTTHRNY	60
DB	22	KDSIPTVNGILGESVTFPVNIQEPQVKIIAWTSTSVAYVTPGDSAPVVTTHRNY	81
QY	61	YERIHAGNYNLVSLRMDAGDYKADINTOADPYTTTKRNLQIYRRLGPKKITQSL	120
DB	82	YERIHAGNYNLVSLRMDAGDYKADINTOADPYTTTKRNLQIYRRLGPKKITQSL	141
QY	121	MASVNSTCNVTLTCSVEKEKNVTYNWSPLGEGGNVLQIFQTPEDQELTYTCTAQNPSN	180
DB	142	MASVNSTCNVTLTCSVEKEKNVTYNWSPLGEGGNVLQIFQTPEDQELTYTCTAQNPSN	201
QY	181	NDSISARQLCADIAMGFR	199
DB	202	NDSISARQLCADIAMGFR	220

RESULT 2

Q95660	PRELIMINARY;	PRT;	280 AA.
AC	Q95660;		
DT	01-MAY-1999 (Tremblrel. 10, Created)		
DT	01-MAY-1999 (Tremblrel. 10, Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	CD84.		
OS	Homo sapiens (Human).		

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Palou E., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U96627; AAD04232.1; -;
 DR InterPro; IPR003599; IG.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 SQ SEQUENCE 280 AA; 31651 MW; A043E048E762A718 CRC64;
 Query Match 100.0%; Score 1039; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e-82;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSAPVVTTHRNY 60
 Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSAPVVTTHRNY 81
 Qy 61 YERIHAGPNYNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
 Db 82 YERIHAGPNYNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141
 Qy 121 MASVNSTCNVLTCSVEKEKNVTYNWSPGLGEGNVLIQFQTPDEQLTYTCTAQNPSVN 180
 Db 142 MASVNSTCNVLTCSVEKEKNVTYNWSPGLGEGNVLIQFQTPDEQLTYTCTAQNPSVN 201
 Qy 181 NSDSISARQLCADIAMGFR 199
 Db 202 NSDSISARQLCADIAMGFR 220
 RESULT 3
 Q6FHAS PRELIMINARY; PRT; 328 AA.
 ID Q6FHAS
 AC Q6FHAS;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DE CD84 protein (Fragment).
 GN Names=CD84;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., Labaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CE541847; CAG46645.1; -;
 DR InterPro; IPR003599; IG.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PS00835; IG LIKE; 1.
 FT NON_TER 328 328
 SQ SEQUENCE 328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;
 Query Match 100.0%; Score 1039; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.9e-82;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSAPVVTTHRNY 60
 Db 22 KDSIFTVNGILGESVTFPPVNIQEPQVKIIAMTSKTSVAVYTPGDSAPVVTTHRNY 81
 Qy 61 YERIHAGPNYNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 120
 Db 82 YERIHAGPNYNLVISLDMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL 141

QY 121 MASVNSTCNVLTCSVEKEKNVTYNWSPGLGEGNVLIQFQTPDEQLTYTCTAQNPSVN 180
 Db 142 MASVNSTCNVLTCSVEKEKNVTYNWSPGLGEGNVLIQFQTPDEQLTYTCTAQNPSVN 201
 QY 181 NSDSISARQLCADIAMGFR 199
 Db 202 NSDSISARQLCADIAMGFR 220
 RESULT 4
 O15430 PRELIMINARY; PRT; 328 AA.
 ID O15430
 AC O15430; Q8WLPI;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Leukocyte antigen CD84 (leukocyte differentiation antigen CD84 isoform CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
 GN Name=CD84;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97454416; PubMed=9310491;
 RA de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
 RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";
 RL Blood 90:2398-2405(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Palou E., Sole J., Piroto F., Gaya A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86188202; PubMed=3008886;
 RA Andreesen R., Bross K.J., Osterholz J., Emrich F.;
 RT "Human macrophage maturation and heterogeneity: analysis with a newly
 generated set of monoclonal antibodies to differentiation antigens.";
 RL Blood 67:1257-1264(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729;
 RA Krause S.W., Reihl M., Heinz S., Ebner R., Andreesen R.;
 RT "Characterization of MAX.3 antigen, a glycoprotein expressed on mature
 macrophages, dendritic cells and blood platelets: identity with
 CD84.";
 RL Biochem. J. 346:729-736(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Ffrench J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

61	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	120
82	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	141
121	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	180
142	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	201
181	NSDSISARQLCADIAMGFR	199
202	NSDSISARQLCADIAMGFR	220
<p>RESULT 6</p> <p>Q9UIB8 PRELIMINARY; PRT; 345 AA.</p> <p>ID Q9UIB8; Q9UIB8; PRT; 345 AA.</p> <p>AC Q9UIB8; Q9UIB8; PRT; 345 AA.</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Created)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE Leukocyte differentiation antigen CD84 isoform CD84a.</p> <p>GN Name=CD84;</p> <p>OS Homo sapiens (Human)</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>OX NCBI_TaxID=9606;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Palou E., Sole J., Pirotto F., Gaya A.;</p> <p>RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; AF054816; AAF21722.1; --</p> <p>DR Genew; HGNC:1704; CD84.</p> <p>DR InterPro; IPR003599; IG.</p> <p>DR InterPro; IPR007110; IG-like.</p> <p>DR SMART; SM00409; IG.</p> <p>DR PROSITE; PS50835; IG LIKE; 1.</p> <p>SQ SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62DE CRC64;</p> <p>Query Match 100.0%; Score 1039; DB 2; Length 345;</p> <p>Best Local Similarity 100.0%; Pred. No. 2e-82;</p> <p>Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>		
61	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	120
82	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	141
121	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	180
142	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	201
181	NSDSISARQLCADIAMGFR	199
202	NSDSISARQLCADIAMGFR	220
<p>RESULT 7</p> <p>Q9UIB7 PRELIMINARY; PRT; 197 AA.</p> <p>ID Q9UIB7; Q9UIB7; PRT; 197 AA.</p> <p>AC Q9UIB7; Q9UIB7; PRT; 197 AA.</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Created)</p> <p>DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE Leukocyte antigen CD84 (Fragment).</p> <p>GN Name=CD84;</p> <p>OS Homo sapiens (Human)</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>OX NCBI_TaxID=9606;</p>		
61	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	120
82	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	141
121	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	180
142	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	201
181	NSDSISARQLCADIAMGFR	199
202	NSDSISARQLCADIAMGFR	220
<p>RESULT 8</p> <p>Q9UIB6 PRELIMINARY; PRT; 339 AA.</p> <p>ID Q9UIB6; Q9UIB6; PRT; 339 AA.</p> <p>AC Q9UIB6; Q9UIB6; PRT; 339 AA.</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Created)</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE Leukocyte differentiation antigen CD84 precursor.</p> <p>OS Homo sapiens (Human)</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>OX NCBI_TaxID=9606;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Gaya A.;</p> <p>RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; Y12632; CAA73181.1; --</p> <p>DR SMART; SM00409; IG.</p> <p>DR PROSITE; PS50835; IG LIKE; 1.</p> <p>Signal.</p> <p>FT SIGNAL</p> <p>FT CHAIN</p> <p>SQ SEQUENCE 339 AA; 38082 MW; E78D6D5CAC8D3604 CRC64;</p> <p>Query Match 100.0%; Score 1039; DB 2; Length 339;</p> <p>Best Local Similarity 100.0%; Pred. No. 2e-82;</p> <p>Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>		
61	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	120
82	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	141
121	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	180
142	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	201
181	NSDSISARQLCADIAMGFR	199
202	NSDSISARQLCADIAMGFR	220
<p>RESULT 5</p> <p>Q8WWI8 PRELIMINARY; PRT; 339 AA.</p> <p>ID Q8WWI8; Q8WWI8; PRT; 339 AA.</p> <p>AC Q8WWI8; Q8WWI8; PRT; 339 AA.</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Created)</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE Leukocyte differentiation antigen CD84 precursor.</p> <p>OS Homo sapiens (Human)</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>OX NCBI_TaxID=9606;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Gaya A.;</p> <p>RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; Y12632; CAA73181.1; --</p> <p>DR SMART; SM00409; IG.</p> <p>DR PROSITE; PS50835; IG LIKE; 1.</p> <p>Signal.</p> <p>FT SIGNAL</p> <p>FT CHAIN</p> <p>SQ SEQUENCE 339 AA; 38082 MW; E78D6D5CAC8D3604 CRC64;</p> <p>Query Match 100.0%; Score 1039; DB 2; Length 339;</p> <p>Best Local Similarity 100.0%; Pred. No. 2e-82;</p> <p>Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>		
61	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	120
82	YERIHALGPNYNLVISDLRMEDAGYKADINTQADPYTTTKRYNLQIYRRLGPKKITQSL	141
121	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	180
142	MASVNSTCNVTLTCSVEKEEKNTVNSPLGEGNVLQIFQTPEDQELTYTCTAQNPSVN	201
181	NSDSISARQLCADIAMGFR	199
202	NSDSISARQLCADIAMGFR	220
<p>RESULT 4</p> <p>Q8WWI7 PRELIMINARY; PRT; 339 AA.</p> <p>ID Q8WWI7; Q8WWI7; PRT; 339 AA.</p> <p>AC Q8WWI7; Q8WWI7; PRT; 339 AA.</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Created)</p> <p>DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)</p> <p>DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)</p> <p>DE Leukocyte differentiation antigen CD84 precursor.</p> <p>OS Homo sapiens (Human)</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>OX NCBI_TaxID=9606;</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RA Gaya A.;</p> <p>RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.</p> <p>DR EMBL; Y12632; CAA73181.1; --</p> <p>DR SMART; SM00409; IG.</p> <p>DR PROSITE; PS50835; IG LIKE; 1.</p> <p>Signal.</p> <p>FT SIGNAL</p> <p></p>		

```

RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=20208572; PubMed=10746783;
RA Palou E., Piroto F., Sole J., Freed J.H., Peral B., Vilardell C.,
RA Vilella R., Vives J., Gaya A.;
RT "Genomic characterization of CD84 reveals the existence of five
RT isoforms differing in their cytoplasmic domains.";
RL Tissue Antigens 55:118-127(2000).
DR EMBL; AF101031; AAF06840.1; -.
DR EMBL; AF101030; AAF06840.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1
FT NON_TER 197
FT SEQUENCE 197 AA; 21889 MW; 2E660BF5FA871D88 CRC64;

Query Match 96.5%; Score 1003; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.4e-79;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
DB 6 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 65
GN [1]
QY 61 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 120
DB 66 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 125
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNWSPLEEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
DB 126 MASVNSTCNVTLTCSVEKEKNVTYNWSPLEEGNVLOIFQTPEDQELTYTCTAQNPSVN 185
QY 181 NSDSISARQLCA 192
DB 186 NSDSISARQLCA 197
GN [1]

RESULT 8
QYUIB6 PRELIMINARY; PRT; 241 AA.
AC QYUIB6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Leukocyte differentiation antigen CD84 isoform CD84s.
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Palou E., Sole J., Piroto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF054818; AAF21724.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR SEQUENCE 241 AA; 26902 MW; F0121BC1609B6C52 CRC64;

Query Match 96.5%; Score 1003; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-79;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
DB 22 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 81
QY 61 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 120
DB 66 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 125
GN [1]

RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=20208572; PubMed=10746783;
RA Palou E., Piroto F., Sole J., Freed J.H., Peral B., Vilardell C.,
RA Vilella R., Vives J., Gaya A.;
RT "Genomic characterization of CD84 reveals the existence of five
RT isoforms differing in their cytoplasmic domains.";
RL Tissue Antigens 55:118-127(2000).
DR EMBL; AF101031; AAF06840.1; -.
DR EMBL; AF101030; AAF06840.1; JOINED.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1
FT NON_TER 197
FT SEQUENCE 197 AA; 21889 MW; 2E660BF5FA871D88 CRC64;

Query Match 96.5%; Score 1003; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.4e-79;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
DB 6 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 65
GN [1]
QY 61 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 120
DB 66 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 125
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNWSPLEEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
DB 126 MASVNSTCNVTLTCSVEKEKNVTYNWSPLEEGNVLOIFQTPEDQELTYTCTAQNPSVN 185
QY 181 NSDSISARQLCA 192
DB 186 NSDSISARQLCA 197
GN [1]

RESULT 9
QYUIB6 PRELIMINARY; PRT; 329 AA.
AC QYUIB6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD84 leukocyte antigen.
GN Name=CD84; Synonyms=CD84;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RA Engel P.;
RL "Molecular cloning, characterization, and chromosomal localization of
RL the mouse homologue of CD84, a member of the CD2 family of cell
RL surface molecules.";
RL Immunogenetics 49:249-255(1999).
DR EMBL; AF043445; AAD02273.1; -.
DR MGD; MGI:1336885; CD84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR SEQUENCE 329 AA; 37345 MW; 43BB1A5AF1989E0 CRC64;

Query Match 58.8%; Score 610.5; DB 2; Length 329;
Best Local Similarity 61.7%; Pred. No. 5e-45;
Matches 119; Conservative 32; Mismatches 39; Indels 3; Gaps 2;

QY 1 KDSIEFTVNGILGESVTFPPVNIQEPQVKIIAWTSKTSVAYVTPGDSAPVVTTHRNY 60
DB 22 KDADPVVNGILGESVTFLLNIQEPKKIDNIWTSQSSVAFIKPGVKNKAS--VTIIQGT 79
QY 61 YERIHAGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSL 120
DB 80 KGRIFIDQYDLVIRDLRMEDAGTYKADINEENE--TITKIYLYLHIYRLKTPKITQSL 138
QY 121 MASVNSTCNVTLTCSVEKEKNVTYNWSPLEEGNVLOIFQTPEDQELTYTCTAQNPSVN 180
DB 139 ISSLNNTCNVTLTCSVEKEKDVTSNPPGKSNVLOIVHSPMDQKLTYTCTAQNPSVN 198
QY 181 NSDSISARQLCAD 193
DB 199 SSDSVTVQCPCTD 211
GN [1]

RESULT 10
LY9_HUMAN STANDARD; PRT; 655 AA.
AC Q9HBG7; Q14775; Q9H4N5; Q9NQ24;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9) (CD229 antigen).
GN Name=LY9;
```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL Immunogenetics 51:788-793(2000).
[2]
RN SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).
RX MEDLINE=96128248; PubMed=8537117;
RA Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
RA McKenzie I.F.;
RT "Isolation and characterization of cDNA clones for Humly9: the human
RT homologue of mouse Ly9.";
RL Immunogenetics 43:13-19(1996).
[3]
RN SEQUENCE OF 1-151 FROM N.A.
RP Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
RA Zhou J., Yu W., Tang H., Mei G., Teang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q9HBG7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9HBG7-2; Sequence=VSP_002525;
CC Name=3;
CC IsoId=Q9HBG7-3; Sequence=VSP_002524, VSP_002525, VSP_002526;
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF244129; AAG14995.1; -;
DR EMBL; L42621; AAA92623.1; -;
DR EMBL; AL121985; CAC00580.1; -;
DR EMBL; AY007142; AAG02002.1; -;
DR Genbank; HGNC:6730; Ly9.
DR MIM; 600684; -;
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR KW Alternative splicing; Antigen; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Repeat; Signal; Transmembrane.
FT SIGNAL 1 47 Potential.
FT CHAIN 48 655 T-lymphocyte surface antigen Ly-9.
FT DOMAIN 48 454 Extracellular (Potential).
FT TRANSMEM 455 476 Potential.
FT DOMAIN 477 655 Cytoplasmic (Potential).
FT DOMAIN 48 158 Ig-like V-type 1.
FT DOMAIN 159 235 Ig-like C2-type 1.

FT DOMAIN 251 363 Ig-like V-type 2.
FT DOMAIN 364 452 Ig-like C2-type 2.
FT DISULFID 172 Potential.
FT DISULFID 178 Potential.
FT DISULFID 377 446 Potential.
FT DISULFID 383 427 Potential.
FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 413 413 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 424 424 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 359 448 Missing (in isoform 3).
FT VARSPLIC 500 513 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 524 554 /FTID=VSP_002525.
FT CONFLICT 171 171 /FTID=VSP_002526.
FT CONFLICT 602 602 Missing (in Ref. 1).
FT SEQUENCE 655 AA; 72107 MW; 9F80A3056D79F80A CRC64;
SQ
Query Match 33.9%; Score 352; DB 1; Length 655;
Best Local Similarity 38.1%; Pred. No. 4.4e-22;
Matches 77; Conservative 41; Mismatches 70; Indels 14; Gaps 5;
QY 1 KDEIFTVNGILGESVTPVNIQEQPVQVKIIAWTS-KTSVAVVTPGDSAPVVTTHRN 59
Db KDSAPTWSGILGGSVTLPLNISVDTEIENVIGPKNALAFAPKEN-----VTIMVKS 102
QY 60 YVERHALGPNNYLVISLMEADGDKADINTQADPYTTTKRYNLQIVRRLGKPKIT-Q 118
Db YLGRLDITKWSYSLCISNLTNDAGSYKAQINQRNFVTESEFTLFVTEQLQEPVTTWK 162
QY 119 SUMASVNSTCNVTLTCSVEKEKKNVYTNWSP-----GEEGNVLQIFQTPEDQELTYTC 172
Db SVKVENFSCNITLMCSVKGAESVLYSWTPREPHASENGSGSILVTSRTPCDPDLPLYC 222
QY 173 TAQNPVNSND-SISARQLCAD 193
Db TAQNPVQSRSLPVHVGFCTD 244
RESULT 11
Q96A28 PRELIMINARY; PRT; 289 AA.
ID Q96A28;
AC Q96A28; (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CD84-H1 (CD2 family 10) (SLAM family member 9).
GN Name=SLAMF9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RA Zhang W., Wan T., Li N., He L., Yuan Z., Yu M., Cao X.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21541411; PubMed=11685473; DOI=10.1007/s002510100364;
RA Fennelly J.A., Tiwari B., Davis S.J., Evans E.J.;
RT "CD2F-10; a new member of the CD2 subset of the immunoglobulin
RT superfamily.";
RL Immunogenetics 53:599-602(2001).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Pooled tissue;


```
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=B lymphocyte;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
Sasakawa D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AKO90041; BAC41061.1;
DR MGD; MGI:1923692; Slamf9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; I9.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
SQ SEQUENCE 285 AA; 31759 MW; 48675E0611027B3B CRC64;

Query Match 31.1%; Score 323.5; DB 2; Length 285;
Best Local Similarity 36.2%; Pred. No. 4.8e-20;
Matches 72; Conservative 31; Mismatches 89; Indels 7; Gaps 2;
QY 2 DSEFTYNGILGSGVTFPVNIQEPKVIKTAWTSKTSVAVVTPGDSAPVVTWTRNY 61
```



```
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
[6]
SEQUENCE FROM N.A.
RT STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK009505; BAB26328.1; -.
DR MGD; MGI:1923692; Slamf9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 285 AA; 31764 MW; 33BDB4A633A5C1B3 CRC64;
Query Match 30.9%; Score 321.5; DB 2; Length 285;
Best Local Similarity 35.7%; Pred. No. 7.2e-20;
Matches 71; Conservative 32; Mismatches 89; Indels 7; Gaps 2;
QY 2 DSIFTVNGILGSEVTFPVNIQBPVQKIIAMTSKTSVAVVTPGDSETPAVVTVTRNYY 61
Db 22 DEDEEVGVGLQESINLSIEIPSENEIKHIDWLFQNNIAIVRPGKGQPAVIMAVDPYR 81
QY 62 ERIHALGPNVNLVSLRMDAGDYKADINTQADPYTTTKRYNLQIYRLGPKITQSILM 121
Db 82 GRVSISESSYSLHISNLTWEDSLYNAQVNLKTSSEHTSKSYHLRVYRLSKPHITVNSN 141
QY 122 ASVNSFCNTVLTCSVEKEKNYTNW-----SPIGEENGLVQIFQTPEDQLTCTTAQ 175
Db 142 ISEGVNCLSLTCSIRAGMDVTYIWLSSQDSTNTSHSGSVLTSWRPGDKAPSYTCRVS 201
QY 176 NPVSN-NSDSISARQLCAD 193
Db 202 NPISNISRRISVGSFCAD 220
RESULT 15
SLF6 HUMAN
ID SLF6 HUMAN STANDARD; PRT; 332 AA.
AC Q96DU3; Q96DV0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE SLAM family member 6 precursor (NK-T-B-antigen) (NTB-A) (Activating NK
DE receptor) (UNQ61123/PRO20080).
GN Name=SLAMF6; Synonyms=KALI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., FUNCTION, PHOSPHORYLATION, TISSUE SPECIFICITY, AND
RP INTERACTION WITH SH2D1A/SAP; PTN6 AND PTN11.
RC TISSUE=Lymphoid;
RX MEDLINE=21382389; PubMed=11489943;
RA Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro R.,
RA Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta L.,
RA Moretta A.;
RA "NTB-A, a novel SH2D1A-associated surface molecule contributing to the
RT inability of natural killer cells to kill Epstein-Barr virus-infected
RT B cells in X-linked Lymphoproliferative disease.";
```

```
RL J. Exp. Med. 194:235-246(2001).
RN [2]
RP ERRATUM.
RA Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro R.,
RA Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta L.,
RA Moretta A.;
RA J. Exp. Med. 194:705-705(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yangura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.L.,
RA Godowski P., Gray A.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE OF 22-36.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites."
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Triggers cytolytic activity only in natural killer cells
CC -!- (NK) expressing high surface densities of natural cytotoxicity
CC receptors.
CC -!- SUBUNIT: Interacts with PTN6 and, upon phosphorylation, with PTN11
CC and SH2D1A/SAP.
CC -!- TISSUE SPECIFICITY: Expressed by all (resting and activated)
CC natural killer cells (NK), T and B lymphocytes.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AJ277141; CAC59749.1; -.
CC EMBL; AJ306388; CAC59750.1; -.
CC EMBL; AY358159; AAQ88526.1; -.
CC Genew; HGNC:21392; SLAMF6.
CC H-InvDB; HIX0019182; -.
CC MIM; 606446; -.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; ig; 1.
CC PROSITE; PSS00835; IG_LIKE; 1.
CC Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
CC phosphorylation; Receptor; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 332 SLAM family member 6.
FT DOMAIN 22 226 Extracellular (Potential).
FT TRANSMEM 227 247 Potential.
FT DOMAIN 248 332 Cytoplasmic (Potential).
FT DOMAIN 132 209 Ig-like.
FT DISULFID 147 195 By similarity.
FT CARBOHYD 58 58 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 87 87 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 137 137 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 161 161 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 203 203 N-linked (GlcNAc. .) (Potential).
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 5, 2005, 03:16:45 ; Search time 700.371 Seconds
(without alignments)
2780.804 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQTWPEAA.....KASTQDKPPGSSVEIVIX 329

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DRV=xlh
-Q/cgn2_1/USPTO.spool/US09882171/runat_04022005_114003_26015/app.query.fasta_1.910
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09882171 @CNG 1_1_586 @runat_04022005_114003_26015 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DE TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1695	99.9	1040	6 AAD43563	Aad43563 Human CD8
2	1695	99.9	1067	12 ADO05707	Ado05707 Human leu
3	1695	99.9	1067	12 ADQ19066	Adq19066 Human sof
4	1695	99.9	3173	2 AAV59674	AAV59674 Human sec
5	1695	99.9	3173	6 ABS73661	ABs73661 Human CDN

6	1695	99.9	3173	9 ACD82804	ACd82804 CDNA sequ
7	1695	99.9	3173	10 ADI22889	Adi22889 CDNA enco
8	1695	99.9	3173	12 ADH73891	Adh73891 Human sec
9	1695	99.9	3299	12 ADL82906	Adl82906 Human PRO
10	1695	99.9	3299	13 ADP23942	Adp23942 PRO polyP
11	1695	99.9	3300	6 AAI72383	Aai72383 CD84 codi
12	1695	99.9	3326	12 ADQ23399	Adq23399 Human sof
13	1695	99.9	3687	11 ACN92105	ACn92105 Breast ca
14	450	26.5	748	4 AAL24045	Aal24045 Human bre
15	411	24.2	296	2 AAX41382	Aax41382 Human sec
16	382.5	22.6	1723	12 ADK98595	Adk98595 Human imm
17	382.5	22.6	1849	6 ABS76363	ABs76363 DNA enco
18	382.5	22.6	2286	6 AAS20420	Aas20420 Human DNA
19	378.5	22.3	1581	12 ADL57104	Adl57104 Human NOV
20	378.5	22.3	1848	12 ADL57102	Adl57102 Human NOV
21	374	22.1	2448	12 ADO63781	Ado63781 Human Ly-
22	374	22.1	2448	12 ADO78173	Ado78173 Human Ly-
23	373	22.0	1139	6 AD43596	Ad43596 Human CD2
24	373	22.0	1139	6 ABV77939	ABv77939 Hypoxia-i
25	373	22.0	1139	10 AAD63407	Aad63407 Human CD2
26	373	22.0	1423	5 ADI9728	Adi9728 Dendritic
27	370.5	21.8	1225	10 ABX08617	ABx08617 CDNA enco
28	370.5	21.8	1463	6 ABS76360	ABs76360 DNA enco
29	370.5	21.8	1541	5 AAH42524	Aah42524 Nucleotid
30	370.5	21.8	1541	13 ADS09883	Adso9883 Human the
31	370.5	21.8	1868	6 ABK69998	Abk69998 CDNA enco
32	370.5	21.8	1868	9 ADA37158	Ada37158 Human PRO
33	370.5	21.8	1868	9 ADA01343	Ada01343 Human PRO
34	370.5	21.8	1868	9 ADA43772	Ada43772 Human CDN
35	370.5	21.8	1868	9 ADA43540	Ada43540 Human CDN
36	370.5	21.8	1868	9 ADA01215	Ada01215 Human PRO
37	370.5	21.8	1868	9 ADA01099	Ada01099 Human CDN
38	370.5	21.8	1868	9 ADA43656	Ada43656 Human CDN
39	370.5	21.8	1868	9 ADA06918	Ada06918 Human PRO
40	370.5	21.8	1868	9 ADA08406	Ada08406 Novel hum
41	370.5	21.8	1868	9 AD89699	Ad89699 Human PRO
42	370.5	21.8	1868	9 ADB86982	ADB86982 Human PRO
43	370.5	21.8	1868	9 ADB66137	ADB66137 Human CDN
44	370.5	21.8	1868	10 ADB99815	ADB99815 Human PRO
45	370.5	21.8	1868	10 ADB99470	ADB99470 Novel hum

ALIGNMENTS

RESULT 1
AAD43563
ID AAD43563 standard; DNA; 1040 BP.

XX
AC AAD43563;
DT 14-NOV-2002 (first entry)
XX

DE Human CD84 DNA.

XX Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein;
KW Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein;
KW Immune proliferative disorder; immune disorder; rheumatoid arthritis;
KW Carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease;
KW Hashimoto's disease; acquired immune deficiency syndrome; hepatitis;
KW Osteoarthritis; allergic inflammatory disorder; viral infection; asthma;
KW Psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis;
KW Diabetes mellitus; septic shock; chronic obstructive pulmonary disease;
KW emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis;
KW acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic;
KW immunosuppressive; neuroprotective; antiinflammatory; Crohn's disease;
KW osteopathic; antibacterial; immunomodulator; inflammatory bowel disease;
KW jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
PH CDS 42..1028
FT /tag= a
FT /product= "Human CD84 protein"

XX PN EP1223218-A1.
 XX PD 17-JUL-2002.
 XX PF 02-NOV-2001; 2001EP-00309339.
 XX PR 03-NOV-2000; 2000US-00706167.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Fraser CC;
 XX WPI: 2002-620680/67.
 XX P-PSDB; AAE26238.
 PT Novel isolated polypeptide containing immunoglobulin and immunoglobulin-like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders.
 XX PT Disclosure; Page 76; 138pp; English.
 XX CC The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. asthma and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in gene therapy. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 DNA used in the invention
 XX SQ Sequence 1040 BP; 308 A; 256 C; 231 G; 245 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.9e-164 Length: 1040
 Score: 1695.00 Matches: 328
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.94% Indels: 0
 DB: Gaps: 0

US-09-882-171-483 (1-329) x AAD43563 (1-1040)

QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAla 20
 Db 42 ATGGCTCAGCACACCTATGGATCTTGCCTTGCCTGCAAACTGGCCGGAAGCAGCT 101
 QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
 Db 102 GGAAGAAGCTCAGAAATCTTCACAGTGAATGGATCTTGGGAGAGTCAGTCATTTCCT 161
 QY 41 ValAsnIleGlnLupProGlnValIleIleAlaTrpThrSerIysThrSerVal 60
 Db 162 GTAATATATCCAGAACCCAGCGAAGTAAATCATTCCTGGCTTGAACCTTAAACATCTGT 221
 QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
 Db 222 GCTTATGTAAACACGAGACTCAGAACAGACCCGCTAGTACTGTGACCCACAGAAAT 281
 QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100

Db 282 TATTATGAACGATACATGCCTTAGTCCGAACTACATCTGGTCTATTAGCATCTGAGG 341
 QY 101 MetGluAspAlaGlyAspTyrIlysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
 Db 342 ATGGAAGACGCGAGGAGACTACAAAGCAGACATAAAATACACAGGCTGATCCCTACACCAC 401
 QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgIleuGlyLysProIysIleThrGlnSer 140
 Db 402 ACCAAGCGCTACACCTGCAATCTATCGTGGCTTGGGAAACCAAAATTTACACAGAGT 461
 QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
 Db 462 TTAATGGCATCTGTGAACAGCACCTGTAAATGTCACTGACATGCTCTGTAGAGAAGAA 521
 QY 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
 Db 522 GAAAAGAAATGTACATACAAATTTGGAGTCCCTGGGAGAAGAGGTAATGTCTTCAAAATC 581
 QY 181 PheGlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
 Db 582 TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACAGGTGTACAGCCAGAACCTCTGAGC 641
 QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
 Db 642 AACAAATCTGACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 701
 QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
 Db 702 ACTCACACACCGGGTTGCTGAGCGTGTGGCTATGTTCTTCTGCTTGTCTCATTTCTG 761
 QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerIysLysThr 260
 Db 762 TCTTCAGTGTCTTCTGCTTGTTCAGAGAACAGATGCTGCTCTCAAGAAACC 821
 QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
 Db 822 ATATACATATATCATGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAAATCTATGAT 881
 QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
 Db 882 GAAATCTCTGAGTCCCAAGTGTCTTCCCTCCCAAGGAAGAGCCAGTGAACACAGTTTATTC 941
 QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320
 Db 942 GAAGTGCAGTTTGTCTGATAGATGGGAAAGCCAGCACAGGACAGTAACCTCTCTGGG 1001
 QY 321 ThrSerSerTyrGluIleValIle 328
 Db 1002 ACTTCAAGCTATGAAATTTGTGATC 1025
 RESULT 2
 ADO05707
 ID ADO05707 standard; DNA; 1067 BP.
 XX AC ADO05707;
 XX DT 15-JUL-2004 (first entry)
 XX DE Human leukocyte differentiation antigen CD84 encoding DNA.
 XX KW T cell; antiallergic; immunosuppressive; virucide; antibacterial;
 KW antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds;
 KW leukocyte differentiation antigen.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 70..1056
 XX FT /*tag= a
 XX FT /product= "CD84"
 XX PN WO2004032867-A2.

XX PD 22-APR-2004.
 XX PF 09-OCT-2003; 2003WO-US032065.
 XX PR 09-OCT-2002; 2002US-0417102P.
 PR 09-OCT-2002; 2002US-0417103P.
 PR 09-OCT-2002; 2002US-0417243P.
 PR 18-OCT-2002; 2002US-0419575P.
 PR 08-NOV-2002; 2002US-0424777P.
 PR 08-NOV-2002; 2002US-0424881P.
 XX (TOLE-) TOLERRX INC.
 XX PA Rao P, Szymanska G;
 XX PI WPI; 2004-340801/31.
 XX DR P-PSDB; ADO05708.
 DR GENBANK; 6650105.
 XX
 XX Treating a condition that benefits from modulating regulatory or effector
 PT T cell function comprises administering an agent that modulates the
 PT expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbeta1,
 PT Jagged-1 or GPR-32).
 XX
 XX Example; SEQ ID NO 7; 161pp; English.
 XX
 XX The invention relates to treating a subject having a condition that
 CC benefits from modulating the balance of regulatory T cell function
 CC relative to effector T cell function, or vice versa, in a subject. The
 CC method involves administering an agent that modulates the expression or
 CC activity of a molecule selected from PTGER2 and TGFbeta1, or Jagged-1,
 CC GPR-32, CD83, CD84, CD89, serotonin R, BY55, serotonin R2C, GPR63, and P-
 CC histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and P-
 CC 3-related kinase to the subject, such that treatment occurs. The methods
 CC are useful for diagnosing, preventing or treating conditions
 CC characterized by a too-vigorous or weak effector T cell or regulatory T
 CC cell response to antigens associated with the condition, such as in an
 CC allergic response, an autoimmune disorder, a viral infection, a microbial
 CC infection, a parasitic infection or a tumour. The present sequence
 CC represents a DNA encoding a human leukocyte differentiation CD84 antigen,
 CC preferentially expressed in regulatory T cells.
 XX
 XX Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 5,07e-164 Length: 1067
 Score: 1695.00 Matches: 328
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.94% Indels: 0
 DB: 12 Gaps: 0
 US-09-882-171-483 (1-329) x ADO05707 (1-1067)
 QY 1 MetAlaGlnHisHisLeuTrrleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAa 20
 DB 70 ATGGCTCAGCACCACTTATGGATCTTCTCTTCTGCTGCAAACTTGGCCGGAAGCAGCT 129
 QY 21 GlyLysAspSerGluLeuPheThrValAsnGlyLeuGlyGluSerValThrPhePro 40
 DB 130 GGAAAGACCTCAGNAATCTTCACAGTGAATGGGATCTTGGAGAGTCAGTCACCTTCCCT 189
 QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
 DB 190 GTAAATATCCAAGAACCCAGCAAGTAAATCATCTTGGACTTCTTAAACATCTGTT 249
 QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisAsn 80
 DB 250 GCTTATGTAACACAGAGACTCAGAAACAGCACCCGCTAGTACTGTGACCCACAGAAAT 309
 QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100

DB 310 TATTATGAACGGATACATGCCCTTAGGTCGGAACCTCAATCTGGTCAATTAGCATCTGAGG 369
 QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
 DB 370 ATGGAGAGCGCAGGAGACTACAAAGCAGACATAAATACACAGCTGATCCCTACACCACC 429
 QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
 DB 430 ACCAAGCGCTACAACCTGCAAAATCTATCGTCGGCTTGGGAAACCAAAATACACAGAGT 489
 QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
 DB 490 TTAATGGCATCTGTGAACAGCACCTGTATATGTACACTGACATGCTCTCTAGAGAAAGAA 549
 QY 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGluAsnValLeuGlnIle 180
 DB 550 GAAAGAGATGTACATACATAATGGAGTCCCTCGGAGAGAGGGTAATGTCCTTCAATC 609
 QY 181 PheGlnThrProGluAspGlnLeuThrThrTyrThrCysThrAlaGlnAsnProValSer 200
 DB 610 TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGAGC 669
 QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
 DB 670 AAACAATTTCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCCCAATGGCTTCCGT 729
 QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
 DB 730 ATCCACCAACCGGGTGTGAGCGTGTGCTGGCTATGTTCTTCTGCTTGTCTCATTCG 789
 QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 260
 DB 790 TCTTCAGTCTTTTGTTCGTTGTTTCAAGAGAGAACAAAGATGCTGCTCTCAAGAGAACCC 849
 QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
 DB 850 ATATACACATATATCATGCTTCAAGGAACACCCAGCAGCAGAGTCCAGAAATCTATGAT 909
 QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
 DB 910 GAAATCTTCAGTCCCAAGGTGCTTCTCTCAAGAGAGAGCCAGTGAACACAGTTTATTC 969
 QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320
 DB 970 GAAGTGCAGTTTCTGATAAGATGGGAAAGCCAGCACACAGCAGACAGTAACCTCTCTGG 1029
 QY 321 ThrSerSerTyrGluIleValIle 328
 DB 1030 ACTTCAAGCTATGAAATTTGTGATC 1053
 RESULT 3
 ADQ19066
 ID ADQ19066 standard; DNA; 1067 BP.
 XX
 AC ADQ19066;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1885.
 XX
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 XX WO2004048938-A2.
 XX
 PD 10-JUN-2004.
 XX
 XX 26-NOV-2003; 2003WO-US038193.
 PF
 XX 26-NOV-2002; 2002US-0429739P.
 PR
 XX

(PROT-) PROTEIN DESIGN LABS INC.

Aziz N, Ginsburg WM, Zlotnik A;

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 1885; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,07e-164 Length: 1067
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483 (1-329) x ADQ19066 (1-1067)

QY 1 MetAlaGlnHisLeuTrpIleLeuLeuCysLeuGlnThrTrpProGluAla 20
DB 70 ATGGCTCAGCACACCTATGGATCTGGCTCTTTGCTGCAACCTGGCGGAGCAGCT 129
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 130 CGAAAGACTCAGAAATCTTACAGTGAATGGATCTGGGAGATCAGTCACTTCCCT 189
QY 41 ValAsnIleGlnProArgGlnValIleAlaTrpThrSerLysThrSerVal 60
DB 190 GTAAATATCCAGAACCCAGCGCAAGTAAATCATTTGCTTGGACTTCTAAACATCTGT 249
QY 61 AlaTyValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 250 GCTTATGTAACACCGAGAGACTCAGAAACAGCAGCCGCTAGTCTGACCCACAGAAAT 309
QY 81 TyTyTyGluArgIleHisAlaLeuGlyProAsnTyAsnLeuValIleSerAspLeuArg 100
DB 310 TATTATGACCGATACATGCTTAGTCCGAACTACATCTGGTCAATGAGATCTGAGG 369
QY 101 MetGluAspAlaGlyAspTyIleAlaAspIleAsnThrGlnAlaAspProTyThrThr 120
DB 370 ATGGAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 429
QY 121 ThrLysArgTyAsnLeuGlnIleTyArgArgLeuGlyLysProLysIleThrGlnSer 140
DB 430 ACCAAGCGCTACAACTCGAATCATCTGCGCTTGGGAAACCAAAATATACACAGAT 489
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
DB 490 TTAATGGCATCTGTGAACAGCACCTGTAAATGTCACTGACATGCTCTGTAGAGAAAGAA 549
QY 161 GluLysAsnValThrTyAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180

DB 550 GAAAGAATGTGACATACATAATTTGGAGTCCCTCTGGGAGAGAGGGTAATCTCTCAATC 609
QY 181 PheGlnThrProGluAspGlnLeuLeuThrTyThrCysThrAlaGlnAsnProValSer 200
DB 610 TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCTGTTCAGC 669
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 670 AACAAATCTGACTCCATCTCTGCCGCGAGCTCTGTGAGACATCGCAATGGGCTTCGGT 729
QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
DB 730 ACTACACACCGGTTGCTGAGCGTGTGGCTAGTTCTTCTGCTTGTCTCAATTCG 789
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 260
DB 790 TCTTCAGTGTTTGTTCGTTGTTTCAAGAGAGACAAAGATGCTGCTCAAGAGAAACC 849
QY 261 IleTyThrTyIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyArg 280
DB 850 ATATACATATATATGCTTCAAGGAACACCCAGCAGAGTCAGAAATCTATGAT 909
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTySer 300
DB 910 GAATCTCTGAGTCCAGGTGCTTCCCTCCAGGAGAGCCAGTGAACACAGTTTATTC 969
QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
DB 970 GAAGTGCAAGTTTGCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCGG 1029
QY 321 ThrSerSerTyGluIleValIle 328
DB 1030 ACTTCAAGCTATGAAATGTGATC 1053
RESULT 4
AAV59674
ID AAV59674 standard; DNA; 3173 BP.
XX
AC AAV59674;
XX
DT 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 164 clone HSAWE26.
DE
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
XX WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US004493.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040182P.
PR 07-MAR-1997; 97US-0040183P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040337P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.

Db 231 GCTTATGTAACACGAGGACTCAGAAAACAGCACCGTAGTTACTGTGACCCACAGAAAT 290
Qy 81 TyrTyrGluArgIleHisIleAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 291 TATTATGAACGGATACATCGCTTAGTCGGAACATACTCTGCTCATTAGCGATCTGAGG 350
Qy 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 351 ATGGAAAGACGAGGAGACTTACAAAGCAGACATATAATACACAGCGTGATCCCTACACACC 410
Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyProLysIleThrGlnSer 140
Db 411 ACCAAGCGCTACAACTGCAATCTATCGTCGGCTGGGAAACCAAAATTTACACAGAGT 470
Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 471 TTAATGGCATCTGTGAACAGCACCTGTATGTACACTGCATGCTCTGTAGAGAAAGAA 530
Qy 161 GluLysAsnValThrTyrAsnThrSerProLeuGlyGluGlyAsnValLeuGlnIle 180
Db 531 GAAAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAATGCTTCAAAATC 590
Qy 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db 591 TTCCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCTCTGTACG 650
Qy 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 651 AACAATTTCTGACTCCATCTCTGCCCGGACGCTCTGTGCAGACATCGCAATGGGCTTCCGT 710
Qy 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 240
Db 711 ACTCACACACCGGTTGCTGAGCGGTGCTGGGTATGTTCTTCTGCTGTTCTCAATCTG 770
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 260
Db 771 TCTTCAGTGTGTTTGTTCGTTTGTTCAGAGACAGCAAGATGCTGCTCAAGAAAGAAC 830
Qy 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 831 ATATACACATATATCATGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAAATCTATGAT 890
Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
Db 891 GAAATCCTGCATCCAGGTGCTTCCCTCCAGAGAGAGCCAGTGAACACAGTTTATGCC 950
Qy 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
Db 951 GAAGTGCAGTTTGTCTGATTAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCCTGGG 1010
Qy 321 ThrSerSerTyrGluIleValle 328
Db 1011 ACTTCAAGCTATGAAATTTGTGATC 1034

RESULT 5

ABS73661

ID ABS73661 standard; cDNA; 3173 BP.

XX

AC ABS73661;

XX

DT 15-JAN-2003 (first entry)

XX

DE Human cDNA #1 for novel secreted protein gene 164.

XX

KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.

XX OS Homo sapiens.
XX US6420526-B1.
PN
XX 16-JUL-2002.
PD
XX
PF 08-SEP-1998; 98US-00149476.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.

PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.

(RUBE/) RUBEN S M.
(ROSE/) ROSEN C A.
(SOPP/) SOPPET D R.
(CART/) CARTER K C.
(BEDN/) BEDNARIK D P.
(ENDR/) ENDRESS G A.
(YUGG/) YU G.
(NIJ/) NI J.
(FENG/) FENG P.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERA/) FERRIE A M.
(DUAN/) DUAN D R.
(HUJ/) HU J.
(FLOR/) FLORENCE K A.
(OLSE/) OLSEN H S.
(FISC/) FISCHER C L.
(EBNE/) EBNER R.
(BREW/) BREWER L A.
(MOOR/) MOORE P A.
(SHIY/) SHI Y.
(LAF/) LAFLEUR D W.
(LIYV/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.

XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 2003-521800/49.
PR P-PSDB; ABO34537.

XX New genes and its encoded prostate cancer antigen proteins, useful for
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
PT ischemia.

Claim 4; SEQ ID NO 174; 260bp; English.

XX The present invention relates to the isolation of novel human secreted
CC proteins and the polynucleotide sequences encoding them. The invention
CC also discloses vectors, host cells, antibodies, and recombinant methods
CC for producing human secreted proteins. The polypeptide and polynucleotide
CC sequences for the secreted proteins are useful for preventing, treating,
CC ameliorating or diagnosing medical conditions such as hyperproliferative
CC disorders (e.g. leukemia or breast cancers), wounds, reproductive
CC disorders, blood-related disorders (e.g. haemophilia or
CC thrombocytopenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory
CC disorders, neurological disorders (e.g. Alzheimer's disease or
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsdIDentry.html

XX Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 2,27e-163 Length: 3173
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	99.94%	Indels:	0
DB:	9	Gaps:	0
US-09-882-171-483 (1-329) x ACD82804 (1-3173)			
QY 1 MetAlaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20			
DB 51 ATGGCTCAGCACCACTATGGATCTTGTCTCTCCCTGCAAACTGGCCGGAAGAGCT 110			
QY 21 GlyLysAspSerGluIlePheThrValAenGlyLeuGlyGluSerValThrPhePro 40			
DB 111 GGAAAAGACTCAGAAATCTTACAGTGAATGGGATCTGGGAGAGTCAGTCACTTCCCT 170			
QY 41 ValAenIleGlnGluProArgGlnValLysIleLeuAlaTrpThrSerLysThrSerVal 60			
DB 171 GTAAATATCCAAGAACCAACGCGCAAGTAAATCAATGCTTGGACTTCTAAACATCTGTT 230			
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAen 80			
DB 231 GCTTATGTAACACACAGAGGACTCAGAAACAGCAGCCGCTAGTTACTGTGACCCACAGAAAT 290			
QY 81 TyrTyrGluAtgIleHisAlaLeuGlyProAenTyrAsnLeuValLysSerAspLeuArg 100			
DB 291 TATTATGACGGATACATCCCTTAGTTCGAACTCAATCTGTCATTAGCCGATCTGAGG 350			
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAenThrGlnAlaAspProTyrThrThr 120			
DB 351 ATGGAAGACGCGAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACC 410			
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140			
DB 411 ACCAAGCGCTACAACTGCAATCTATCGTCGGCTTGGGAAACCAAAATATACACAGAGT 470			
QY 141 LeuMetAlaSerValAsnSerThrCysAenValThrLeuThrCysSerValGluLysGlu 160			
DB 471 TTAATGGCATCTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAAAGAA 530			
QY 161 GluLysAenValThrTyrAsnTrpSerProLeuGlyGluGluGlyAenValLeuGlnIle 180			
DB 531 GAAAGAAATGTACATACATAATTTGGAGTCCCTGGGAGAAAGAGGTAAATGCTTCAATC 590			
QY 181 PheGlnThrProGluAspGlnIleLeuThrTyrThrCysThrAlaGlnAenProValSer 200			
DB 591 TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGAACCCCTGTGAGC 650			
QY 201 AsnAenSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220			
DB 651 AACAATTCAGACTCCATCTCTCCCGGAGCTCTGTGCAGACATCCCAATGGCTTCCGT 710			
QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240			
DB 711 ACTCACCAACCCGGGTTGCTGAGCGTGTGGCTATGTTCTTCTGCTTGTCTCAATCTG 770			
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaLysLysLysThr 260			
DB 771 TCTTCACTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 830			
QY 261 IleTyrThrTyrIleMetAlaSerArgAenThrGlnProAlaGluSerArgIleTyrAsp 280			
DB 831 ATATACACATATATCATGCTTCAAGAAACACCCAGCCAGAGATCCAGATCTATGAT 890			
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAenThrValTyrSer 300			
DB 891 GAAATCTGAGCTCCAGAGTCTTCCCTCCAAGAAAGAGCAGTGAACACAGTTTATTC 950			
QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320			
DB 951 GAAGTGCAGTTTGTCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGG 1010			
QY 321 ThrSerSerTyrGluIleValIle 328			
DB 1011 ACTTCAAGCTATGAAATTTGTGATC 1034			

PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2003-898535/82.
DR P-PSDB; ADI23198.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
XX Claim 1; SEQ ID NO 174; 256pp; English.
XX
XX The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a
CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The sequence encodes a novel human secreted
CC protein of the invention.
XX
XX Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores:
Pred. No.: 2,27e-163 Length: 3173
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 10 Gaps: 0

US-09-882-171-483 (1-329) x ADI22889 (1-3173)

QY 1 MetAlaGlnHisHisLeuTrpPileLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20
DB 51 ATGGCTCAGCACACCTATGATCTTCTCTTGGCTGCAACCTGGCGGAAGCAGCT 110
QY 21 GlyLysAspSerGluPheThrValAsnGlyLeuGlyGluSerValThrPhePro 40
DB 111 GGAAGAGACTCAGAAATCTTCACAGTGAATGGGATCTTGGGAGAGTCAGTCACCTTCCCT 170
QY 41 ValAsnIleGlnGluProArgGlnValIleLeuValThrSerLysThrSerVal 60
DB 171 GTAATAATCCAAAGAACCCAGGACTCAGAAACAGCACCCTAGTACTGTGAGCCACAGAAAT 230
QY 61 AlaTrpValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 231 GCATTATGTAACACACGAGAGACTCAGAAACAGCACCCTAGTACTGTGAGCCACAGAAAT 290
QY 81 TyrTrpGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
DB 291 TATTATGAACGATACATACCTTCCGAGTCCGAACTACAACTCTGGTCAATAGCATCTGAGG 350
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
DB 351 ATGGAAGACGAGAGAGACTCAAAAGCAGACATAAATACAGGCTGATCCCTACACACC 410
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
DB 411 ACCAAGCCCTAACCTGCAATCTATCTGCTGGCTTGGAAACCAAAATACACAGAGT 470
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
DB 471 TTAATGGCATCTGTGAACAGCAGCCTGTAAATGTCACATGATCTCTGTAGAGAAAGAA 530

QY 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle 180
DB 531 GAAAGAATGTGACATACATATGGAGTCCCTGGGAGAGAGGGTAATGTCTCTCAAAATC 590
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
DB 591 TTCCAGATCTCTGAGAGCAAGAGCTGACTTACACGTGTACAGCCAGAACCTGTGCAGC 650
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 651 AACATTTCTGACTCCATCTCTGCCCGGAGCTCTGTGCAGACATGCAATGGGCTTCCGT 710
QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
DB 711 ACTCACACACCGGGTGTGTGAGCGTGTGTGCTATGTTCTTCTGCTTCTTCTCATCTG 770
QY 241 SerSerValPheLeuPheArgLeuPheLysArgGlnAspAlaAlaSerLysLysThr 260
DB 771 TCTTCAGTGTGTTTGTTCGTTTGTTCAGAGAGACAGATGCTGCTCAAGAAACC 830
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
DB 831 ATATACACATATATCATGCTTCAAGGAACACCCAGCCAGAGATCCAGAAATCTATGAT 890
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
DB 891 GAAATCTCTGAGTCCCAAGGTGCTTCCCTCAAGGAAGAGCCAGTGAACACAGTTTATTC 950
QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
DB 951 GAAGTGCAGTTTGTCTGATAGATGGGGAAGCCAGGACACACAGGACAGTAACCTCTCTGG 1010
QY 321 ThrSerSerTyrGluIleValIle 328
DB 1011 ACTTCAAGCTATGAATTTGTGATC 1034
RESULT 8
ADH73891
ID ADH73891 standard; cDNA; 3173 BP.
XX
XX ADH73891;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human secreted protein cDNA #164.
DE
XX
XX human; secreted protein; cancer; haematopoietic disorder;
KW endocrine disorder; immune system disease; inflammatory disorder; ss;
KW gene.
XX
XX Homo sapiens.
OS
XX
XX US2003225248-A1.
PN
XX
XX 04-DEC-2003.
PD
XX
XX 10-JUN-2002; 2002US-00164861.
PF
XX
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.

```
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.

PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Dandress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2004-131264/13.
DR P-PSDB; ADH74200.
XX
XX Isolated nucleic acid molecules encoding human secreted proteins, useful
PT for preventing, diagnosing and treating disorders associated with
PT aberrant expression and activity.
XX
XX Claim 3; SEQ ID NO 174; 142pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and the human
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,
CC endocrine disorders, diseases of the immune system, inflammatory
CC disorders and many others. Full details of disorders that may be
CC prevented, diagnosed and/or treated by the above methods are given in the
CC specification. The nucleic acid molecules may be used to produce their
CC proteins. The nucleic acid and it's complementary sequences may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The SPs may also be used
CC as antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of SP expression and activity. The anti-SP
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-SP antibodies may also be used as diagnostic
CC agents for detecting the presence of the proteins in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents a human secreted protein cDNA.
XX
SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores:
Pred. No.: 2.27e-163 Length: 3173
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483 (1-329) x ADH73891 (1-3173)
QY 1 MetAlaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAa 20
DB 51 ATGGCTCAGCACCACTTAAGTCTTGCTCTTGCTTGCAACTGCGGAGAGACACT 110
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 111 GGAAAGAACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCACTTCCTTCCCT 170
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaThrThrSerLysThrSerVal 60
```

```
Db 171 GTAATATCAAGAACCCAGGCAAGTTAAATCATTTGGACTTCTAAACATCTGT 230
Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrHisArgAsn 80
Db 231 GCTTATGTAAACACGAGAGACTCAGAAACAGCACCCTGTACTGTGACCCACAGAA 290
Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 291 TATTATGAACGGATACATGCTTAGGTCCGAACATCAATCTGCTATTAGCGATCTGAGG 350
Qy 101 MetGluAspAlaGlyAspTyrIleValAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 351 ATGGAAGACGACGAGAGACTACAAGACAGACATATAATACACAGGCTGATCCCTACACACC 410
Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 411 ACCAAGCGCTACAACTGCAAACTCTATCGTCGGCTTGGGAACCAAAATTCACAGAGT 470
Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 471 TTAATGGCATCTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAGAAGAA 530
Qy 161 GluLysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGluGluGlnIle 180
Db 531 GAAAAGAAATGTGACATACATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAAATC 590
Qy 181 PheGlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db 591 TTCACAGACTCTGAGGACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCCCTGTGACG 650
Qy 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 651 AACAAATCTGACTCCATCTCTGCCGACGCTCTGTGACAGATCGCAATGGGCTTCCGT 710
Qy 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
Db 711 ACTCACACACCCGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTTGTCTCAATCTG 770
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgGlnAspAlaAlaSerLysLysThr 260
Db 771 TCTTCAGTGTGTTTGTTCGCTTTGTTCAAGAGAGACAAAGATGCTGCTCAAAAGAAACC 830
Qy 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 831 ATATACACATATATCATGCTTTCAGAGAACACCCAGCAGAGTCCAGAACTATGAT 890
Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
Db 891 GAAATCCTGCAGTCCCAAGGTGCTTCCCTCCCAAGGAGAGCCAGTGAACACAGTTTATTC 950
Qy 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320
Db 951 GAAATGCGATTTGCTGATAAGATGGGAAAGCCAGCACAGGACAGTAACCTCTCTGGG 1010
Qy 321 ThrSerSerTyrGluIleValIle 328
Db 1011 ACTTCAAGCTATGAATTTGTATC 1034

RESULT 9
ID ADL82906
XX ADL82906 standard; cDNA; 3299 BP.
AC ADL82906;
XX
DT 17-JUN-2004 (first entry)
DE Human PRO24934 cDNA, SEQ ID 108.
XX
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human; gene; ss.
XX
```

```
OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI: 2004-329389/30.
DR P-PSDB; ADL82907.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 2; Fig 108; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2 4e-163 Length: 3299
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483 (1-329) x ADL82906 (1-3299)
Qy 1 MetAlaGlnHisIleThrIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
Db 45 ATGGCTCAGCACCACTATGATCTTGTCTTGTGCTGCAAACTCGCGGAGCAGCT 104
Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
Db 105 GGAAGAGACTCAGAAATCTTCACAGTGAATGGGATCTTGGGAGAGTCAGTCACCTTCCCT 164
Qy 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaIleAlaIleThrSerVal 60
Db 165 GTAAATATCCAGAACCCAGCCAGTAAATCATTTGCTTGGACTTCTTAAACATCTGTT 224
Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrHisArgAsn 80
Db 225 GCTTATGTAAACACCCAGGAGACTCAGAAACAGCACCCTGTACTGTGAGCCACAGAAAT 284
Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 285 TATTATGAACGAGATACATGCTTAGGTCCGAACTACAATCTGGTCTATTAGCGATCTGAGG 344
```



```
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
DB 345 ATGGAAGCGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACC 404
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
DB 405 ACCAAGCGCTACAACCTGCAATCTATCGTCGGCTGGGAAACCAAAATATACACAGAGT 464
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
DB 465 TTAATGGCATCTGTGACAGCACCTGTGTAATGTACACACTGACATGCTCTGTAGAGAAAGAA 524
QY 161 GluLysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
DB 525 GAAAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAAATGCTCTTCAATC 584
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
DB 585 TTCCAGACTCTCTGAGGACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCCCTGTGAGC 644
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 645 AACAAATTTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 704
QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 240
DB 705 ACTCACACACCGGGTTGCTGAGCGTGTGGGTATGTTCTTCTGCTTGTCTCATTTCTG 764
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerIlylThr 260
DB 765 TCTTCAGTGTGTTTGTTCGGTTGTTTCAAGAGACAGAGAGTGTGCTCAAGAAACCC 824
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
DB 825 ATATACACATATATATGCTGTTCAAGGAACACCCAGCCAGAGTCCAGAAATCTATGAT 884
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
DB 885 GAAATCCTGCAGTCCNAGGTGCTTCCCTCAAGAGAGAGCCAGTGAACACAGTTTATTC 944
QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
DB 945 GAAGTGCAGTTTGTGATAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTCTGG 1004
QY 321 ThrSerSerTyrGluIleValIle 328
DB 1005 ACTTCAAGCTATGAAATTTGTATC 1028
RESULT 10
ADP23942
ID ADP23942 standard; cDNA; 3299 BP.
XX
AC ADP23942;
XX
AC 2.4e-163 Length: 3299
XX 1695.00 Matches: 328
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.94% Indels: 0
XX DB: 13 Gaps: 0
US-09-882-171-483 (1-329) x ADP23942 (1-3299)
QY 1 MetAlaGlnHisHisLeuTyrIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
DB 45 ATGGCTCAGCACCACCTATGATCTTGTCTTCTGCTGCAAACTGCGCGGAGCAGCT 104
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 105 GAAAGAAGACTCAGAAATCTTCACAGTGAATGGGATCTTGGGAGAGTCACTTTCCT 164
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTyrThrSerLysThrSerVal 60
DB 165 GTAATATCCAGAACACCGGCAAGTTAAATCATTTGCTTGGACTTCTTAAACATCTGTT 224
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 225 GCTTATGTAAACCCAGGAGACTCAGAAACAGACCCGCTAGTTACTGTGACCCACAGAAAT 284
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
```

```
PA (GETH ) GENENTECH INC.
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;
PI Wu TD;
XX WPI; 2004-419628/39.
DR P-PSDB; ADP23943.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX Claim 1; SEQ ID NO 1120; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiasthmatic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
```

SQ Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;

```
Alignment Scores:
Pred. No.: 2.4e-163 Length: 3299
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 13 Gaps: 0
```

US-09-882-171-483 (1-329) x ADP23942 (1-3299)

```
QY 1 MetAlaGlnHisHisLeuTyrIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
DB 45 ATGGCTCAGCACCACCTATGATCTTGTCTTCTGCTGCAAACTGCGCGGAGCAGCT 104
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 105 GAAAGAAGACTCAGAAATCTTCACAGTGAATGGGATCTTGGGAGAGTCACTTTCCT 164
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTyrThrSerLysThrSerVal 60
DB 165 GTAATATCCAGAACACCGGCAAGTTAAATCATTTGCTTGGACTTCTTAAACATCTGTT 224
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 225 GCTTATGTAAACCCAGGAGACTCAGAAACAGACCCGCTAGTTACTGTGACCCACAGAAAT 284
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
```

18-NOV-2004 (first entry)

PRO polypeptide encoding cDNA SEQ ID NO:1120.

ss; Gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
immunosuppressive; osteopathic; antidiabetic; dermatological;
antipsoriatic; antiasthmatic; hepatotropic; respiratory;
gene therapy; immune system.

Unidentified.

WO2004041170-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P.

||||| 465 TTAATGGCATCTGTGAACAGCACCTGTAATGTCACTGACATGCTCTGTAGAGAA 524
DB
QY 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
DB 525 GAAAGAATGTGACATACAAATGGAGTCCCTGGGAGAAGAGGGTAATGTCTTCAAAATC 584
QY 181 PheGlnThrProGluAspGlnIleuThrTyrCysThrAlaGlnAsnProValSer 200
DB 585 TTCCAGACTCTCGAGGACCAAGAGTGACTTACACGTGTACAGCCCAAGACCTCTCAGC 644
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 645 AACAAATCTGACTCCATCTCTGCCGGCAGCTCTGTGACACATCGCAATGGCTTCGCT 704
QY 221 ThrHisHisThrGlyLeuSerValLeuAlaMetPhePheLeuValLeuIleLeu 240
DB 705 ACTCACACACCGGGTGTGAGCGTGTGGCTATGTTCTTCTGCTTGTCTCATTTCTG 764
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerIlyslsThr 260
DB 765 TCTTCAGTGTGTTTGTTCGTTGTTCAGAGAGACAGATGCTGCTCAAGAAACCC 824
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
DB 825 ATATACACATATATCATGCTTCAAGGACACCCAGCCAGCAGACTCCAGATCTATGAT 884
QY 281 GluIleLeuGlnSerIlyslsValLeuProSerIlyslsGluGluProValAsnThrValTyrSer 300
DB 885 GAAATCCTGCACTCCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACACAGTTTATTC 944
QY 301 GluValGlnPheAlaAspIlyslsMetGlyLysAlaSerThrGlnAspSerIlyslsProGly 320
DB 945 GAAGTGCAGTTTGTCTGATAAGATGGGAAAGCCAGCACAGAGCAGTAACCTCTGGG 1004
QY 321 ThrSerSerTyrGluIleValIle 328
DB 1005 ACTTCAAGCTATGAAATTTGTATC 1028
RESULT 12
ADQ23399
ID ADQ23399 standard; DNA; 3326 BP.
XX AC ADQ23399;
XX DT 26-AUG-2004 (first entry)
XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6219.
XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX DB.
XX OS Homo sapiens.
XX PN WO2004048938-A2.
XX PD 10-JUN-2004.
XX PF 26-NOV-2003; 2003WO-US038193.
XX PR 26-NOV-2002; 2002US-0429739P.
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PI Aziz N, Ginsburg WM, Zlotnik A;
XX DR WPI; 2004-441208/41.
XX PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX

PS Example 2; SEQ ID NO 6219; 210pp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 3326 BP; 959 A; 802 C; 753 G; 795 T; 0 U; 17 Other;
Alignment Scores:
Pred. No.: 2,42e-163 Length: 3326
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 12 Gaps: 0
US-09-882-171-483 (1-329) x ADQ23399 (1-3326)
QY 1 MetAlaGlnHisHisLeuTyrPheIleLeuLeuLeuCysLeuGlnThrTyrProGluAlaAla 20
DB 72 ATGGCTCAGCACCACTATGGATCTTGCTCTTTGCTGCAACCTGCGGAGACGACT 131
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 132 GGAAGAAGACTCAGAAATCTTCACAGTAGAATGGGATCTGGGAGAGTCACTCACCTTCCCT 191
QY 41 ValAsnIleGlnGluProArgGlnValIlyslsIleAlaTyrThrSerIlyslsSerVal 60
DB 192 GTAAATATCCAAAGAACCCAGCGCAAGTTAAATCATTTGCTTGACTTCTTAAACATCTGTT 251
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 252 GCTTATGTAAACACAGGAGACTCAGAAACACAGCCCGTAGTTACTGTGACCCACAGAAAT 311
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
DB 312 TATTATGAACGGATACATGCTTAGTCCGAACCTACAAATCTGGTCATTAGCGATCTGAGG 371
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
DB 372 ATGGAAGACGAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 431
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
DB 432 ACCAAGCGCTACAACCTGCAATCTATCTGCTGGCTTGGGAAACCCAAAAAATTTACACAGAT 491
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
DB 492 TTAATGGCATCTGTGAACAGACACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGA 551
QY 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle 180
DB 552 GAAAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAAGAGGGTAATGTCTTCAAAATC 611
QY 181 PheGlnThrProGluAspGlnIleuThrTyrCysThrAlaGlnAsnProValSer 200
DB 612 TTCCAGACTCTCGAGGACCAAGAGTGACTTACACGTGTACAGCCCAAGACCTCTCAGC 671
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 672 AACAAATCTGACTCCATCTCTGCCGGCAGCTCTGTGACACATCGCAATGGCTTCGCT 731
QY 221 ThrHisHisThrGlyLeuSerValLeuAlaMetPhePheLeuValLeuIleLeu 240.

Db 732 ACTCACCACCGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTGTTCTCATTCG 791
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaSerLysLysThr 260
Db 792 TCTTCAGTGTGTTTGTTCGCTTGTTCAGAGAAGACAAGAGTCTGCTCCCAAGAAACC 851
Qy 261 IleTyrThrTyrMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 852 ATATACACATATATCATGCTTCAAGGAACACCAGCCAGCAGAGTCCAGATCTATGAT 911
Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
Db 912 GAATCTCTGAGTCCAAAGGTGCTTCCCTCAAGGAAGAGCCAGTGAACACAGTTTATTCC 971
Qy 301 GluValGlnPheAlaSerLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
Db 972 GAAGTGCAGTTTCTGATAGATGGGAAAGCCAGCAGACACAGGACAGTAACCTCCTGGG 1031
Qy 321 ThrSerSerTyrGluIleValIle 328
Db 1032 ACTTCAAGCTATGAAATTTGTGATC 1055

RESULT 13

ACN92105

ID ACN92105 standard; DNA; 3687 BP.

XX AC ACN92105;

XX 02-DEC-2004 (first entry)

XX Breast cancer related marker, seq id 13255.

DE Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX Homo sapiens.

XX US2003099974-A1.

XX 29-MAY-2003.

XX 18-JUL-2002; 2002US-00198846.

XX 18-JUL-2001; 2001US-0306220P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lillie J, Xu Y, Wang Y, Steinmann K;

XX WPI; 2003-787014/74.

XX Novel isolated polypeptide associated with breast cancer, useful for

PT detecting presence of polypeptide in sample, as a marker for breast

PT cancer.

XX Disclosure; SEQ ID NO 13255; 36pp; English.

XX The invention relates to an isolated polypeptide (I) associated with

CC breast cancer which is encoded by a nucleic acid molecule comprising a

CC nucleotide sequence (S1). Further disclosed is an antibody that binds to

CC the polypeptide of the invention. The activity of the polypeptide of the

CC invention may be described as cytostatic. The antibody is useful for

CC detecting the presence of (I) in a sample. Nucleic acid molecules of the

CC invention are useful in the detection of breast tumours. (I) is useful as

CC a marker for breast cancer and in breast cancer therapy. Sequences given

CC in records ACN78851-ACN92934 represent nucleic acid markers associated

CC with breast cancer. Note: The sequence listing does not form part of the

CC specification but may be obtained in electronic format from the USPTO web

CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974

XX Sequence 3687 BP; 1073 A; 881 C; 838 G; 874 T; 0 U; 21 Other;

XX Alignment Scores:

Pred. No.: 2,79e-163 Length: 3687
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 11 Gaps: 0
US-09-882-171-483 (1-329) x ACN92105. (1-3687)
Qy 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAa 20
Db 433 ATGGCTCAGCACACCATATGGATCTTCTTCCTTGGCTGCAAACTGGCGGAGAGCT 492
Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
Db 493 GGAAGAAGACTCAGAAATCTTCACAGTGAATGGATCTTCGGAGAGTCAGTCACTTCCCT 552
Qy 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
Db 553 GTAAATATCCAAGAACACCGCAAGTTAAATCATTTGCTTGGACTTCTTAAACATCTGT 612
Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 613 GCTTATGTAACACACGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAAT 672
Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 673 TATTATGAACGATACATGCTTAGGTCCGAATCAATCTGGTCAATTAGCGATCTGAGG 732
Qy 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 733 ATGGAAGACGACGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACC 792
Qy 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 793 ACCAAGCGCTACAACTGCAAAATCTATGTCGGCTTGGGAAACCAAAATATACACAGT 852
Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 853 TTAAATGGCATCTGTGAACAGCACCTCTGAATGTGCACACTGCATGCTGTGTAGAGAAGAA 912
Qy 161 GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
Db 913 GAAAAGAATGTGACATACAAATTTGGAGTCCCTCGGAGAGAGGGTAAATGCTTCAATC 972
Qy 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db 973 TTCAGACTCCTGAGGACCAAGAGCTGACTTACCGTGTACAGCCCAAGACCTGTCAGC 1032
Qy 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 1033 AACAAATTCGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTTCGT 1092
Qy 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 240
Db 1093 ACTCACACACCGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTGTTGCTCATCTG 1152
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgGlnAspAlaAaSerLysLysThr 260
Db 1153 TCTTTCAGTGTGTTTGTTCCTGTTTGTTCAGAGAAGACAGATGCTGCTCAAGAAAACC 1212
Qy 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 1213 ATATACATATATCATGCTTCAAGGAACACCCAGCAGCAGAGTCCAGAAATCTATGAT 1272
Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
Db 1273 GAAATCTCGAGTCCAAAGGTGCTTCCCTCCAAGAGAGAGGAGTGAACACAGATTTATTC 1332
Qy 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
Db 1333 GAAGTGCAGTTTGTGATAGATGGGAAAGCCAGCACAGGACAGTAAACCTTCTCTGGG 1392

QY	321 ThrSerSerTyrGluIleValIle 328
Db	1393 ACTTCAAGCTATGAATTGTGATC 1416
RESULT 14	
AAL24045	
ID AAL24045 standard; cDNA; 748 BP.	
XX AC	
AC AAL24045;	
XX XX	
DT 07-DEC-2001 (first entry)	
DE Human breast cancer expressed polynucleotide 16502.	
XX KW	
Human; breast cancer; cell marker; cytostatic; ss.	
XX OS	
Homo sapiens.	
PN WO200151628-A2.	
XX PD	
19-JUL-2001.	
XX XX	
10-JAN-2001; 2001WO-US000798.	
XX PF	
14-JAN-2000; 2000US-0176077P.	
PR PR	
14-MAR-2000; 2000US-0189167P.	
PR PR	
24-MAR-2000; 2000US-0192099P.	
PR PR	
29-MAR-2000; 2000US-0193480P.	
PR PR	
15-MAY-2000; 2000US-0205230P.	
PR PR	
09-JUN-2000; 2000US-0211315P.	
PR PR	
25-JUL-2000; 2000US-0220534P.	
XX XX	
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PA Lillie J, Xu Y, Wang Y, Steinmann K;	
XX WPI; 2001-451856/48.	
XX DR	
New peptide useful as a marker for the diagnosis of breast cancer.	
PT Claim 1; Page 3020; 3695pp; English.	
XX PS	
The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity	
CC SQ	Sequence 748 BP; 246 A; 164 C; 164 G; 171 T; 0 U; 3 Other;
Alignment Scores:	
Pred. No.:	Length: 748
Score:	Matches: 100
Percent Similarity:	Conservative: 4
Best Local Similarity:	Mismatches: 20
Query Match:	Indels: 3
DB:	Gaps: 0
US-09-882-171-483 (1-329) x AAL24045 (1-748)	
QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaLa 20 	
Db 378 ATGGCTCAGCACCACTATGATCTTGCTCGTAACCTGGCGGGAAGAGCT 437 	
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40 	
Db 438 GGAAAGACTCAGAATCTTCACAGTAGGAGATCTGGAGAGTCAGTCATTTCCCT 497 	
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60 	

CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 296 BP; 88 A; 74 C; 64 G; 70 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,24e-33 Length: 296
Score: 411.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.23% Indels: 0
DB: 2 Gaps: 0

US-09-882-171-483 (1-329) x AAX41382 (1-296)
QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
DB 60 ATGGCTCAGCACCACTATGGATCTTCTCTTGGCTGCAACCTGGCGGAAGCAGCT 119
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 120 GGAAGAAGACTCAGAAATCTTCACAGTCAATGGGATTCTGGGAGAGTCAGTCACTTTCCCT 179
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
DB 180 GTAAATATCAAGAACCCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTT 239
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHis 78
DB 240 GCTTATGTAAACACAGGAGACTCAGAAACAGACCCGCTAGTTACTGTGACCCAC 293

Search completed: February 5, 2005, 06:54:58
Job time : 712.371 secs

Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2005, 06:13:46 ; Search time 222.449 Seconds
(without alignments)
2420.040 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQTPWRAA.....KASTQDSKPGTSSYEIVIX 329

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlh
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114004_26047/app_query.fasta_1.910
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptn -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09882171@cgn_1_1_93 @runat_04022005_114004_26047 -NCPUS=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	99.9	3173	3	US-09-149-476-174
2	1695	99.9	3296	4	US-09-949-016-1456
3	1695	99.9	3299	4	US-09-949-016-557
4	607	35.8	37475	4	US-09-949-016-12299
5	607	35.8	37492	4	US-09-949-016-13198
6	343	20.2	1140	3	US-09-227-357-53
7	227	13.4	2440	4	US-09-949-016-1036
8	227	13.4	2440	4	US-09-949-016-1454
9	195.5	11.5	1079	1	US-08-348-792-7
10	195.5	11.5	1079	2	US-08-348-792-7
11	195.5	11.5	1079	3	US-09-199-955-7
12	195.5	11.5	1079	3	US-08-880-875-7

13	194	11.4	1716	1	US-08-348-792-1	Sequence 1, Appli
14	194	11.4	1716	2	US-08-462-738-1	Sequence 1, Appli
15	194	11.4	1716	3	US-09-199-955-1	Sequence 1, Appli
16	194	11.4	1716	4	US-08-880-875-1	Sequence 1, Appli
17	194	11.4	1789	3	US-09-023-655-1504	Sequence 1504, Ap
18	187.5	11.1	1852	1	US-08-348-792-3	Sequence 3, Appli
19	187.5	11.1	1852	2	US-08-462-738-3	Sequence 3, Appli
20	187.5	11.1	1852	3	US-09-199-955-3	Sequence 3, Appli
21	187.5	11.1	1852	4	US-08-880-875-3	Sequence 3, Appli
22	187.5	11.1	1852	4	US-09-148-545-258	Sequence 258, App
23	186.5	11.0	1200	1	US-08-348-792-9	Sequence 9, Appli
24	186.5	11.0	1200	2	US-08-462-738-9	Sequence 9, Appli
25	186.5	11.0	1200	3	US-09-199-955-9	Sequence 9, Appli
26	186.5	11.0	1200	3	US-08-880-875-9	Sequence 9, Appli
27	173	10.2	1020	1	US-08-348-792-5	Sequence 5, Appli
28	173	10.2	1020	2	US-08-462-738-5	Sequence 5, Appli
29	173	10.2	1020	3	US-09-199-955-5	Sequence 5, Appli
30	173	10.2	1020	3	US-08-880-875-5	Sequence 5, Appli
31	168	9.9	601	4	US-09-949-016-49958	Sequence 49958, A
32	168	9.9	601	4	US-09-949-016-28967	Sequence 28967, A
33	166.5	9.8	3220	4	US-09-369-248A-1	Sequence 1, Appli
34	165.5	9.8	1140	1	US-08-348-792-11	Sequence 11, Appli
35	165.5	9.8	1140	2	US-08-462-738-11	Sequence 11, Appli
36	165.5	9.8	1140	3	US-09-199-955-11	Sequence 11, Appli
37	165.5	9.8	1140	3	US-08-880-875-11	Sequence 11, Appli
38	161	9.5	448	4	US-09-513-999C-276	Sequence 276, App
39	144.5	8.5	34185	3	US-09-545-481-3	Sequence 3, Appli
40	141.5	8.3	1377	3	US-09-435-956A-2	Sequence 2, Appli
41	140.5	8.3	2839	3	US-08-468-858B-5	Sequence 5, Appli
42	140.5	8.3	2839	3	US-08-468-859A-5	Sequence 5, Appli
43	138.5	8.2	2110	4	US-09-907-794A-319	Sequence 319, App
44	138.5	8.2	2110	4	US-09-905-125A-319	Sequence 319, App
45	138.5	8.2	2110	4	US-09-902-775A-319	Sequence 319, App

ALIGNMENTS

RESULT 1
US-09-149-476-174
; Sequence 174, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23

/	EARLIER APPLICATION NUMBER:	60/056,875
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,862
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,887
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/056,908
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/048,964
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/057,650
/	EARLIER FILING DATE:	1997-09-05
/	EARLIER APPLICATION NUMBER:	60/056,884
/	EARLIER FILING DATE:	1997-08-22
/	EARLIER APPLICATION NUMBER:	60/057,669
/	EARLIER FILING DATE:	1997-09-05
/	EARLIER APPLICATION NUMBER:	60/049,610
/	EARLIER FILING DATE:	1997-06-13
/	EARLIER APPLICATION NUMBER:	60/061,060
/	EARLIER FILING DATE:	1997-10-02

```
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 223 GCTTATGTAAACACAGAGACTCAGAAACAGCACCCTAGTGTACTGTGACCCACAGAAAT 282
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 283 TATTATGAACGGATACATGCTTAGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGG 342
QY 101 MetGluAspAlaGlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 343 ATGGAAGACGACGAGACTACAAAGCAGACATAAATACACAGCGCTGATCCCTACACACC 402
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 403 ACCAAGCGCTACAACTGCAATCTATCGTCGGCTTGGGAAACCAAAATATACACAGAT 462
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 463 TTAATGGCATCTGTGAACAGCACCCTGTAATGTACACACTGACATGCTCTGTAGAAAGAA 522
QY 161 GluLysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
Db 523 GAAAGAATGTGACATACATAAATGGAGTCCCTGGGAGAGAGGTAATGCTCTTCAAAATC 582
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db 583 TTCCAGACTCCTGAGACCAAGAGCTGACTTACAGCTGTACAGCCCAAGAACCTGTGCAGC 642
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 643 AACAAATCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCAATGGCTTCCGT 702
QY 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeuLeu 240
Db 703 ACTCACACACCGGGTGTGAGCGTGTGCTGCTATGTTCTTCTGCTTCTTCTCATCTG 762
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 260
Db 763 TCTTCAGTGTGTTTGTTCGTTTGTTCAGAGAAGCAAGATGCTGCTTCAAGAAACCC 822
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 823 ATATACATATATCATGCTTCAAGAAACCCAGCCAGCAGAGTCCAGAAATCTATGAT 882
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
Db 883 GAAATCCTCGAGTCCAGGTGCTTCCCTCCAAAGGAAGACCCAGTGAACACAGCTTTATTCC 942
QY 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
Db 943 GAAGTGCAGTTGCTGATAGATGGGAAAGCCAGACACAGCAGTAAACCTCTCTGGG 1002
QY 321 ThrSerSerTyrGluIleValIle 328
Db 1003 ACTTCAAGCTATCAAAATTTGTGATC 1026
```

RESULT 3

```
US-09-949-016-557
; Sequence 557, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 3299
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-557

Alignment Scores:
Pred. No.: 1.19e-200 Length: 3299
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 4 Gaps: 0

US-09-882-171-483 (1-329) x US-09-949-016-557 (1-3299)
```

```
QY 1 MetAlaGlnHisHisLeuTyrIleLeuLeuLeuCysLeuGlnThrTyrProGluAlaAla 20
Db 45 ATGGCTCAGCACCACTATGATCTTCTCTTCCCTGCCAACCTGGCCGGAAGACAGCT 104
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
Db 105 GGAAGAAGACTCAGAAATCTTCACAGTGAATGGGATTCCTGGGAGAGTCACTCACTTCCCT 164
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTyrThrSerLysThrSerVal 60
Db 165 GTAAATATCCAAAGAACCAACCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTT 224
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 225 GCTTATGTAACACACAGGAGACTCAGAAACAGCACCCTGAGTGTACTGTGACCCACAGAAAT 284
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 285 TATTATGAACGGATACATGCTTAGTCCGAACTACATCTGGTCAATTAGCGATCTGAGG 344
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 345 ATGGAAGACGCGAGGAGACTACAAAGCAGACATAAATACACAGCGTGTATCCCTACACACC 404
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 405 ACCAAGCGCTCAACCTGCAATCTATCTCGCTTGGGAAACCAAAATATACACAGAT 464
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 465 TTAATGGCATCTGTGAACAGCACCCTGTAATGTCTACACTGACATGCTCTGTAGAGAAAGAA 524
QY 161 GluLysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
Db 525 GAAAGAATGTGACATACAATTTGGAGTCCCTGGGAGAGAGGTAATGTCTCTTCAAAATC 584
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db 585 TTCCAGACTCCTGAGACCAAGAGCTGACTTACAGTGTACAGCCCAAGACCCCTGTGACG 644
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 645 AACAAATCTGACTCCATCTCTGCCCGGAGCTCTGTGCGAGACATCGCAATGGGCTTCCGT 704
QY 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 240
Db 705 ACTCACACACCGGGTGTGAGCGTGTGCTGCTATGTTCTTCTGCTTCTTCTCATCTG 764
QY 241 SerSerValPheLeuPheArgLeuPheLysArgGlnAspAlaAlaSerLysLysThr 260
Db 765 TCTTCAGTGTGTTTGTTCGTTTGTTCAGAGAAGACAAAGATGCTGCTCAAGAAACCC 824
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
Db 825 ATATACATATATCATGCTTCAAGGAACACCCAGCAGAGTCCAGAAATCTATGAT 884
```

Qy 281 GluileuclnSerLysValleuProSerLysGluGluProValaAsnThrValTyrSer 300
Db 885 GAAATCCTGAGTCCAGGCTTCTCCCTCCAGGAAGAGCCAGTGAACAGTTTATTC 944
Qy 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320
Db 945 GAAGTCAGTTTCTGATAGATGGGAAAGCCAGACACAGGACAGTAACCTCTGGG 1004
Qy 321 ThrSerSerTyrGluileValle 328
Db 1005 ACTTCAAGCTATGAAATTTGTATC 1028

RESULT 4
US-09-949-016-12299
; Sequence 12299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12299
; LENGTH: 37475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12299

Alignment Scores:
Pred. No.: 3,96e-63 Length: 37475
Score: 607.00 Matches: 121
Percent Similarity: 81.70% Conservative: 4
Best Local Similarity: 79.08% Mismatches: 6
Query Match: 35.79% Indels: 22
DB: 4 Gaps: 1

US-09-882-171-483 (1-329) x US-09-949-016-12299 (1-37475)
Qy 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuGln----- 14
Db 15623 CTGGGTGAAGTGCATTTGTGGCAGCTCTCAGGAGCTCCAGGCCCAAGATTAGGAA 15682
Qy 15 -----ThrTrpProGlu 18
Db 15683 GTGAAAAGCTGCAACAGTCAGATGGCTACAGTTTCTTTATGTCTCAGGGCCGGAA 15742
Qy 19 AlaAlaGlyLysAspSerGluilePheThrValaAsnGlyileLeuGlyGluSerValThr 38
Db 15743 GCAGCTGGAAAAGACTCAGAAATCTTCACAGTGAATGGGATTTCTGGGAGAGTCAGTCAC 15802
Qy 39 PheProValaAsnIleGlnGluProArgGlnValLysIleleAlaTrpThrSerLysThr 58
Db 15803 TTCCCTGTAAATATCCAGAACCCAGGCAAGTTAAATCATTTGTTGGACTTCTTAAACA 15862
Qy 59 SerValAlaTyrValThrProGlyAspSerGluThrAlaProValThrValThrHis 78
Db 15863 TCTGTTGCTTATGTAACCGGATACATGCTTAGTCCGAACTACAATCTGGTCATTAGCGAT 15922
Qy 79 ArgAsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAsp 98
Db 15923 AGAAATTTATGTAACCGGATACATGCTTAGTCCGAACTACAATCTGGTCATTAGCGAT 15982
Qy 99 LeuArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyr 118
Db 15982 TCTGTTGCTTATGTAACCGGATACATGCTTAGTCCGAACTACAATCTGGTCATTAGCGAT 15982
Qy 99 LeuArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyr 118

Db 15983 CTGAGGATGGAAGACGAGGAGACTACAAAGCAGACATAAATACACAGGCTATCCTAC 16042
Qy 119 ThrThrThrLysArgTyrAsnLeuGlnIleTyrArgArg 131
Db 16043 ACCACACCCAGCGGTACAACTGCANATCTATCTATCGTAAG 16081

RESULT 5
US-09-949-016-13198
; Sequence 13198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13198
; LENGTH: 37492
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13198

Alignment Scores:
Pred. No.: 3,97e-63 Length: 37492
Score: 607.00 Matches: 121
Percent Similarity: 81.70% Conservative: 4
Best Local Similarity: 79.08% Mismatches: 6
Query Match: 35.79% Indels: 22
DB: 4 Gaps: 1

US-09-882-171-483 (1-329) x US-09-949-016-13198 (1-37492)
Qy 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuGln----- 14
Db 15623 CTGGGTGAAGTGCATTTGTGGCAGCTCTCAGGAGCTCCAGGCCCAAGATTAGGAA 15682
Qy 15 -----ThrTrpProGlu 18
Db 15683 GTGAAAAGCTGCAACAGTCAGATGGCTACAGTTTCTTTATGTCTCAGGGCCGGAA 15742
Qy 19 AlaAlaGlyLysAspSerGluilePheThrValaAsnGlyileLeuGlyGluSerValThr 38
Db 15743 GCAGCTGGAAAAGACTCAGAAATCTTCACAGTGAATGGGATTTCTGGGAGAGTCAGTCAC 15802
Qy 39 PheProValaAsnIleGlnGluProArgGlnValLysIleleAlaTrpThrSerLysThr 58
Db 15803 TTCCCTGTAAATATCCAGAACCCAGGCAAGTTAAATCATTTGTTGGACTTCTTAAACA 15862
Qy 59 SerValAlaTyrValThrProGlyAspSerGluThrAlaProValThrValThrHis 78
Db 15863 TCTGTTGCTTATGTAACCGGATACATGCTTAGTCCGAACTACAATCTGGTCATTAGCGAT 15922
Qy 79 ArgAsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAsp 98
Db 15923 AGAAATTTATGTAACCGGATACATGCTTAGTCCGAACTACAATCTGGTCATTAGCGAT 15982
Qy 99 LeuArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyr 118
Db 15983 CTGAGGATGGAAGACGAGGAGACTACAAAGCAGACATAAATACACAGGCTATCCTAC 16042
Qy 119 ThrThrThrLysArgTyrAsnLeuGlnIleTyrArgArg 131
Db 16043 ACCACACCCAGCGGTACAACTGCANATCTATCTATCGTAAG 16081

RESULT 6
US-09-227-357-53
Sequence 53, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
EARLIER FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53
LENGTH: 1140
TYPE: DNA
ORGANISM: Homo sapiens
US-09-227-357-53
Alignment Scores:
Pred. No.: 1,28e-32 Length: 1140
Score: 343.00 Matches: 92
Percent Similarity: 49.83% Conservative: 52
Best Local Similarity: 31.83% Mismatches: 121
Query Match: 20.22% Indels: 24
DB: 3 Gaps: 5
US-09-882-171-483 (1-329) x US-09-227-357-53 (1-1140)
QY 7 TrpIleLeuLeuLeuCysLeu-----GlnThrTrpProGluAla 19
Db 99 TGGCTGCTTCTCTCTCTCTCTCTCCAGGAGGCGAGCCAAAGAGACTCTGGAGATGGGT 158
QY 20 AlaGlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhe 39
Db 159 GGATCCGAGGAA-----GTGGTTGGGTCCTTCAGGAGTCCATCAGCCTC 203
QY 40 ProValAsnIleGlnGluProArgGlnValLysIleIleAlaIleThrSerLysThrSer 59
Db 204 CCCCCTGGGAATACACACAGATGAAGAGTTGAGAACATCATCTGGTCTCTCACAAAAGT 263
QY 60 ValAlaIleValThrProGlyAspSerGluThrAlaProValValThrValHisArg 79
Db 264 CTTCACACTGTGTGTCGCCAGGAAAGAGGACATCCAGCTACCATCATCTGGTACCAATCCA 323
QY 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
Db 324 CACTACACAGGCGCAAGTGAAGCTTCTTGACCCCACTATTCCTGCTCATATCAGCAATCTG 383
QY 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
Db 384 AGCTGGGAGGATTCAGGCGCTTACCAAGCTCAAGTCAACCTGAGAGACATCCAGATCTCT 443
QY 120 ThrThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLys-ProLysIleThrGl 139
Db 444 ACCATGCAGCAGTACAATCTATGTCTTACCGATGGCTGTCCAGAGDCCCAATCACTGT 503
QY 139 nSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu-L 159
Db 504 GAACCTTGAGAGTTCTGGGGAAGGTGCTGAGTATGTCTCTGTGTCTCTGTGGAGRA 563
QY 159 ysGluGluLysAsnValThrTyrAsnTrpSerProLeuGlyGlu----- 173
Db 564 AGCAGGCGATGATATGACCTACAGCTGGCTCTCCCGGGGGATAGCACTTATACATTC 623
QY 174 --GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrC 193
Db 624 ATGAAGGCCCTGTCTCTCAGCACATCTCTGGAGGCCGGGGGACAGTGCCTCTCTACACCT 683
QY 193 ysThrAlaGlnAsnProValSerAsn--AsnSerAspSerIleSerAlaArgGlnLeuC 212
Db 684 GCAGAGCCACACACCCATCAGCAACGCTCAGTTCTTCCCCCATCCCTGATGGGCCCTTCT 743
QY 212 ysAlaAspIleAlaMetGlyPheArgThrHisHisThrGly-----LeuLeuSerV 229
Db 744 ATGCAGATCCTAACTATGCTTCTGAGAAAGCCTTCAACAGCGCTTCTGCTCTCTGCGCAAG 803
QY 229 alLeuAlaMetPhePheLeuLeuValLeuLeuLeuSerSerValPheLeuPheArgLeuP 249
Db 804 GATTGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 863

QY 249 helysargGlnaspAlaalaSerLysIleThrThrTyrrileMetAlaSerA 269
Db 864 AGAAAGACACAAATGCCAAGATGAGAACTCATGAGAAACAGAAATGAAATTGAGGA 923
QY 269 rGAsnThrGlnProAlaGluSer 276
Db 924 AGGAGCAAGCTGGCTCCAGC 946

RESULT 7
US-09-949-016-1036
; Sequence 1036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1036
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1036

Alignment Scores:
Pred. No.: 1,32e-17 Length: 2440
Score: 227.00 Matches: 85
Percent Similarity: 41.67% Conservative: 65
Best Local Similarity: 23.61% Mismatches: 142
Query Match: 13.38% Indels: 68
DB: 4 Gaps: 15

US-09-882-171-483 (1-329) x US-09-949-016-1036 (1-2440)

QY 8 IleLeuLeuCysLeuGlnThrTrp-----ProGluAlaGlyLysAspSerGlu 25
Db 204 ATACTCTCTCTCTCTCAAGGTGTATCAGGCAAGGATGCCAGGATCAGCTGACCAT 263
QY 26 IlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGlnGlu 45
Db 264 GTGGTTAGCATCTCGGGAGTG-----CCTCTTCAGTTACACCA 302
QY 46 -----ProArgGlnValIleAlaTrp-----ThrSerLysThr 58
Db 303 AACAGCATACAGCAAGGTTGACAGCATTCATGGAAGAAGTGTGTCGCCCTCACAAAT 362
QY 59 SerValAlaTyrrValThrProGlyAspSerGluThrAlaProValValThrHis 78
Db 363 GGATTTTCATCATATTGAAGTGGAGAAATGGCTCTTTGCTTCCATATCTCCAAT--- 419
QY 79 ArgAsnTyrrGluArgIleHisAlaLeuGlyProAsnTyrrAsnLeuValIleSerAsp 98
Db 420 -----GATAGATTTCAGTTTATAGTCAGAACTTGAGTCTTCTCATCAGGCA 467
QY 99 LeuArgMetGluAspAlaGlyAspTyrrLysAlaAspIleAsnThrGlnAlaAspProTyrr 118
Db 468 GCTCAGCAGCAGGACAGTGGCTCTACTGCTCGGAGGTC---ACCAGTATATCTGGAATA 524
QY 119 ThrThrThrLysArgTyrrAsnLeuGlnIleTyrrArgArgLeuGlyLysProLysIleThr 138
Db 525 GTTCAGACAGCCAGCTTCCAGGTTTGTATTGATAAGTTGAGAAACCCCGCTACAG 584
QY 139 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 158

Db 585 GGGCAGGGGAAGATCCTGGACAGAGGAGATCCCAAGTGGCTCTGTCTTGTCTGGTCTCC 644
QY 159 LysGluGluLysAsnValThrTyrrAsnTrp-----SerProLeuGlyGluGlu 174
Db 645 AGG---GATGGCAATGTGTCTATCTGGTACAGAGGAGCAAGCTGATCCAGACAGCA 701
QY 175 GlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu----- 189
Db 702 GGGAACTCACCCTACCTG-----GACGAGGAGGTTGACATTAATGGCACT 746
QY 190 ---ThrTyrrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAla 208
Db 747 CACACATATACCTGCAATGTACGAATCTGTAGCTGGAAAGCCACACCTGGAATCTC 806
QY 209 ArgGlnLeuCysAlaAspIleAlaMetGlyPheArgThrHisHisThrGlyLeuLeuSer 228
Db 807 ACTCAGGACTGTCAAGATGCCCATCAGGAATTCAGA----- 842
QY 229 ValLeuAlaMetPhePheLeuLeuValLeuSerSerValPheLeuPheArgLeu 248
Db 843 ---TTTGGCCGTTTGGTGATCATCGTGATTTCTAAGGCGCACTGTCTTGGCACCCCT 899
QY 249 Phe-----LysArgArgGlnAspAlaAlaSerLysLys 259
Db 900 GCCTGCTCTGTGTGTGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
QY 260 -----ThrIleTyrrThrTyrrile-----MetAlaSerArgAsnThrGlnProAla 274
Db 960 GAATTTTGCACAAATTTACGAAGATCTGAAAGAGATCTGAAACCCAGGAGAAATCCAGAGCAG 1019
QY 275 Glu-----SerArgIleTyrrAspGluIleLeuGlnSerLysVal 287
Db 1020 GAGCAGACTTTTCTCGAGGGGGAGACCACTACTCTATGATCCAGTCCCACTTCT 1079
QY 288 LeuProSerLysGluGluProValAsnThrValTyrrSerGluValGlnPheAlaAspLys 307
Db 1080 GCTCCACGCTCACAGAACCTGCATATACATTAATTAATTCAGCCTTCCAGGAAG 1139
QY 308 MetGlyLysAlaSerThrGlnAspSerLysProProGlyThrSerSerTyrrGluIleVal 327
Db 1140 TCTGGATCCAGGAG 1199

RESULT 8

US-09-949-016-1454
; Sequence 1454, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1454
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1454

Alignment Scores:
Pred. No.: 1,32e-17 Length: 2440
Score: 227.00 Matches: 85
Percent Similarity: 41.67% Conservative: 65
Best Local Similarity: 23.61% Mismatches: 142


```
Qy 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
Db 300 ATAGTGTCTTGTATCCATCCGAGGAGCCCTCCACGTTATCTAGGATCGCTACAAG 359
Qy 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
Db 360 TTTTATCTGGAG-----AATCTCACCTGGGATACGGGAAGC 398
Qy 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
Db 399 AGGAAGGAGGATGAGGATGGTACCTTATGACCCCTG-----GAGAAAAATGTT 446
Qy 120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgGluGlyLysProLysIle 137
Db 447 TCAGTTCAGGCGCTTTTGCCTGCGAGTGGCTTTATGACGAGGTCTCCACTCCAGAAAT 506
Qy 138 ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
Db 507 AAAGTTTAAACAGACCCAGGAGAACGGGACCTGCACCTTGATATCTGGGCTGCACAGTG 566
Qy 158 GluLysGluLysAsnValThrTyrAsnTyrSer-----ProLeu 171
Db 567 GAGAAGGGGAC---CATGTGGTTACAGCTGGAGTGAAGCGGGGACCCACCCACCTG 623
Qy 172 -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
Db 624 AACCCAGCCAAAGCTCCACCTCTCTCCCTCACCCTCGGCCCCAGCATGCTGCAAT 683
Qy 190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
Db 684 ATCTACATCTGCACCGTGAGCAACCTTATCAGCAACAATTTCCAGACCTTTCAGCCCGTGG 743
Qy 210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis----- 222
Db 744 CCGGATGC-----AGGACAGACCCCTCAGAAACAAACCATCATG 782
Qy 223 -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
Db 783 GCAGTGTATCTGGGCTGTAGGGGGTGTATCATGATTTCTCATGTTGGTAACTA 842
Qy 241 SerSerValPheLeuPheArgLeuPheLysArg-----GlnAsp 254
Db 843 CAG-----TTGAGAAGAGAGAGTAAACGAAACCATTTACCAGACA 881
Qy 255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg----- 269
Db 882 ACAGTGGAAAAAAGCCCTTACGATCTATGCCCAAGTCCAGAAACAGGTCCTCTTCAG 941
Qy 270 -----AsnThrGlnProAlaGlu-----SerArgIleTyrAspGluIleLeu 283
Db 942 AAGAAACTTGACTCTTCCAGCTCAGACCCCTTGCACCATATAT-----GTTGCT 995
Qy 284 GlnSerValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
Db 996 GCCACAGACCTGTGCCAGAGTCTGTCCAGGAACAATTCATCATCAGCTATGCTAGT 1055
Qy 302 Val 302
Db 1056 GTG 1058
```

```
RESULT 10
US-08-462-738-7
; Sequence 7, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
```

```
; NAME/KEY: CDS
; LOCATION: 153..1073
; US-08-462-738-7
```

```
Alignment Scores:
Pred. No.: 3,02e-14 Length: 1079
Score: 195.50 Matches: 80
Percent Similarity: 39.88% Conservative: 56
Best Local Similarity: 23.46% Mismatches: 124
Query Match: 11.53% Indels: 81
DB: 2 Gaps: 17
```

```
US-09-882-171-483 (1-329) x US-08-462-738-7 (1-1079)
Qy 12 CysLeuGlnThrTrpProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly 31
Db 129 TGCCTGTGTGAGTGG-----GGTGGCGCATGATGAACCTGCCCAAGATTTCTCCGG 179
Qy 32 IleLeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluPro 46
Db 180 CAGTTGGGAAGCAAGTGTGTGCTCCCTCAGCATATGAAGGATAAATAAGAGCATGAAC 239
Qy 47 ArgGlnValLysIleIleAlaTrpThrSerLysThr-----Ser 59
Db 240 AAAAGCATCCACATTTGCTGCATCGCAATGGCAAAATCACTGGGAGAACAGTGTGAGAACAA 299
Qy 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
Db 300 ATAGTGTCTTGTATCCATCCGAGGAGCCCTCCACGTTATCTAGGAGATCGCTACAAG 359
Qy 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
Db 360 TTTTATCTGGAG-----AATCTCACCTGGGATACGGGAAGC 398
Qy 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
Db 399 AGGAAGGAGGATGAGGATGGTACCTTATGACCCCTG-----GAGAAAAATGTT 446
Qy 120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgGluGlyLysProLysIle 137
Db 447 TCAGTTCAGGCGCTTTTGCCTGCGAGTGGCTTTATGACGAGGTCTCCACTCCAGAAAT 506
```


447 TCAGTTCAGCGCTTTGGCTGCGAGTGGCTTTATGAGCAGGCTCCACCTCCAGAAATT 506
138 ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
507 AAAGTTTAAACAGAGACCCAGGAGACCGGACCTTGACCTTGATGCGCTGCACAGTG 566
158 GluLysGluGluLysAsnValThrTyrAsnTyrSer-----ProLeu 171
567 GAGAGAGGGGAC---CATGTGGCTTACAGTGGAGTGAAGAGGGGGCCACCCACCTTG 623
172 -----GlyGluGluGluAsnValThrLeuGlnLeuPheGlnThrProGluAspGlnGluLeu 189
624 AACCCAGCCACAGCTCCACCTCTGCTCCCTCACCCTGCGCCGCCAGCATGCTGACAAT 683
190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerLeuSerAlaArg 209
684 ATCTACATCTGCACCGTGCAGCAACCTTATCAGCAACAATTCCAGACCTTCAGCCCGTGG 743
210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis----- 222
744 CCCGGATGC-----AGGACAGACCCCTCAGAAACAAACACCATGG 782
223 -----HisThrGlyLeuLeuSerValLeuAlaMetPheLeuLeuValLeuLeuLeu 240
783 GCAGTGATGCTGGGCTTTAGGGGGTGTCTCATGATTCATCATGTTGGTGGTAATCTA 842
241 SerSerValPheLeuPheArgLeuPheLysArg-----GlnAsp 254
843 CAG-----TTGAGAGAGAGAGGTTAAACAGAACCATTTACACAGACA 881
255 AlaAlaSerLysLysThrIleTyrThrIleMetAlaSerArg----- 269
882 ACAGTGGAAAAAAGAGCTTACGATCTATGCCCCAGTCCAGAACCCAGTCTCTTCAG 941
270 -----AsnThrGlnProAlaGlu-----SerArgIleTyrAspGluLeuLeu 283
942 AAGAACTTGACTCTTCCTCCAGCTCAGGACCCCTTGACACCATATAT-----GTTGCT 995
284 GlnSerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
996 GCCACAGAGCTGTCCAGAGTGTGTCAGGAAACAAATTCATCATCAGTCTATGCTAGT 1055
302 val 302
1056 GTG 1058

RESULT 11
US-09-199-955-7
Sequence 7, Application US/09199955
Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1073
US-09-199-955-7
Alignment Scores:
Pred. No.: 3,02e-14 Length: 1079
Score: 195.50 Matches: 80
Percent Similarity: 39.88% Conservative: 56
Best Local Similarity: 23.46% Mismatches: 124
Query Match: 11.53% Indels: 81
DB: 3 Gaps: 17
US-09-882-171-483 (1-329) x US-09-199-955-7 (1-1079)
QY 12 CysLeuGlnThrTrpProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly 31
Db 129 TGCCTGTGTGAGTGG-----GGTGGGGCATGATGAACTGCCCAAGATTCTCCGG 179
QY 32 IleLeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluPro 46
Db 180 CAGTTGGGAAGCAAGTGTCTGCTGCCCTGCATATGAAAGGATAAATAAGAGCATGAAC 239
QY 47 ArgGlnValLysIleAlaTrpThrSerLysThr-----Ser 59
Db 240 AAAGCATCCACATTGTCTCACAATGGCAAAATCACTGAGAACAGTGTGCGAACAAC 299
QY 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
Db 300 ATAGTGTCTCTTGATCCATCCGAAGCAGGCGCTCCACGTTATCTAGGAGATCGCTACAAG 359
QY 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
Db 360 TTTTATCTGGAG-----AATCTCACCTGGGGATACGGGAAAGC 398
QY 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
Db 399 AGNAGAGGAGTGGAGGTGTTACCTTATGACCCCTG-----GAGAAAATGTT 446
QY 120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIle 137
Db 447 TCAGTTTCAGCGCTTTTGGCTGCGAGTGGCTTTATGAGCAGGCTCCACTCCAGAAATT 506
QY 138 ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
Db 507 AAAGTTTTAAACAGAGACCCAGGAGACCGGACCTGCACCTTGATGCTGCGCTGCACAGTG 566
QY 158 GluLysGluGluLysAsnValThrTyrAsnTyrSer-----ProLeu 171
Db 567 GAGAGAGGGGAC---CATGTGGCTTACAGTGGAGTGAAGAGGGGGCCACCCACCTCTG 623
QY 172 -----GlyGluGluGluAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189

624 AACCCAGCCAAAGCTCCACCTCTCTGTCCTCCCTCGGCCCCAGCATGCTGACAAAT 683
190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
684 ATCTACATCTGCACCGTGGAGCAACCTATCAGCAACAATTCAGAGACCTTCAGCCCGTGG 743
210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis----- 222
744 CCGGATGC-----AGGACAGACCCCTCAGAAACAAACCATCGG 782
223 -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
783 GCAGTGTATGCTGGGCTGTAGGGGTGTCATCATCTCATCTCATCTGTTGGTAACTA 842
241 SerSerValPheLeuPheArgLeuPheLysArg-----GlnAsp 254
843 CAG-----TTGAGAGAGAGAGAGGTTAAACGAAACCATACAGACA 881
255 AlaAlaSerLysLysThrIleTyrThrIleMetAlaSerArg----- 269
882 ACAGTGGAAAAAAGAGCTTACGATCTATGCCCCAGTCCAGAAACCCAGTCTCTTCAG 941
270 -----AsnThrGlnProAlaGlu-----SerArgIleTyrAspGluIleLeu 283
942 AAGAAACTTGACTCTTCCAGCTCAGGACCTTGCACCAACCATATAT-----GTTGCT 995
284 GlnSerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
996 GCCACAGAGCTGTCCAGAGTGTCTCCAGGAAACAAATTCATCAGTCTATGCTAGT 1055
302 Val 302
1056 GTG 1058

RESULT 12
US-08-880-875-7
Sequence 7, Application US/08880875
Patent No. 639065

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153...1073
US-08-880-875-7

Alignment Scores:
Pred. No.: 3,02e-14 Length: 1079
Score: 195.50 Matches: 80
Percent Similarity: 39.8% Conservative: 56
Best Local Similarity: 23.4% Mismatches: 124
Query Match: 11.5% Indels: 81
DB: 3 Gaps: 17

US-09-882-171-483 (1-329) x US-08-880-875-7 (1-1079)

QY 12 CysLeuGlnThrTyrProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly 31
DB 129 TGCCTGTGTGAGTGG-----GGTGGGCGCATGATGAAGTGCCTCCCAAGATTTCTCCGG 179
QY 32 IleLeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluPro 46
DB 180 CAGTTGGGAAGCAAGTGTCTGCTGCCCTGACATATGAAGGANTAAATAAGCATGAAC 239
QY 47 ArgGlnValLysIleAlaTyrThrSerLysThr-----Ser 59
DB 240 AAAAGCATCCACATTTGCTGCAATGGCAAAATCACTGGAGAACAGTGTGAGAACAAA 299
QY 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
DB 300 ATAGTGTCTCTTGCATCCATCCGAAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAG 359
QY 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
DB 360 TTTTATCTCGAG-----AATCTCACCTGGGGATACCGGAAAGC 398
QY 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
DB 399 AGGAAGAGAGTGGAGGATGTTACCTTATGACCCCTG-----GAGAAAAATGTT 446
QY 120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIle 137
DB 447 TCAGTTTCAGCGCTTTTGGCTGTCAGTGTGAGGCTTTATGAGCAGGCTCTCCACTCCAGAAAT 506
QY 138 ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
DB 507 AAAGTTTAAACAAGACCCAGGAGAACGGAGCTTACCTTGATATCTGGGCTGCACAGTG 566
QY 158 GluLysGluGluLysAsnValThrTyrAsnTyrSer-----ProLeu 171
DB 567 GAGAGGGGGAC---CATGTGGCTTACAGCTGGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 623
QY 172 -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGlnLeu 189
DB 624 AACCCAGCCAAAGCTCCACCTCTCTGCTCCCTCCCTCGGCCCCAGCATGCTGACAAT 683
QY 190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
DB 684 ATCTACATCTGCACCGTGGAGCAACCTTATCAGCAACAATTCAGAGACCTTCAGCCCGTGG 743
QY 210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis----- 222
DB 744 CCGGATGC-----AGGACAGACCCCTCAGAAACAAACCATCGG 782
QY 223 -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240

Db 783 GCAGTGTATGCTGGCGGTGTAGGGGTGTATCATCATGATTCTCATCATGTTGGTAAATACTA 842
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArg-----GlnAsp 254
Db 843 CAG-----TTGAGAGAGAGAGGTAAACGAAACCAATTACCCAGACA 881
Qy 255 AlaAlaSerLysLysThrIleThrTyrIleMetAlaSerArg----- 269
Db 882 ACAGTGGAAAAAAGCCCTTACCATCTATGCCCAAGTCCAGAAACAGAGTCTCTTTCAG 941
Qy 270 -----AenThrGlnProAlaGlu-----SerArgIleTyrAspGluIleLeu 283
Db 942 AAGAAACTTGACTCTTCCAGCTTCAGGACCCCTTGACACCACTATAT-----GTTGCT 995
Qy 284 GlnSerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
Db 996 GCCACAGAGCTGTCAGAGTCTGTCCAGGAACAAATTCATCAGACTATGCTAGT 1055
Qy 302 Val 302
Db 1056 GTG 1058

RESULT 13

US-08-348-792-1
; Sequence 1, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1716 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1065
US-08-348-792-1

Alignment Scores: 9.83e-14 Length: 1716
Pred. No.: 194.00 Matches: 76
Score: 40.62% Conservative: 54
Percent Similarity:

Best Local Similarity: 23.75% Mismatches: 112
Query Match: 11.44% Indels: 78
DB: 1 Gaps: 16
US-09-882-171-483 (1-329) x US-08-348-792-1 (1-1716)
Qy 33 LeuGlyGluSerValThrPhePro-----ValAsnIleGlnIleProArg 47
Db 175 ITGGAGAGCAAAAGTCTGCTGCCCTGACATATGAAGAGATAAATAAGCATGAACAA 234
Qy 48 GlnValLysIleIleAlaIleThrSerLysThr-----SerVal 60
Db 235 ACATCCACATTTGCTGCTCAATGCAAAATCATCTGGAGAACAGTGTGAGAACAAATA 294
Qy 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 295 GTGTCTCTTGATCCATCCGAAAGCAGCGCCCTCCACGTTATCTAGGAGATCGCTACAAGTTT 354
Qy 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
Db 355 TATCTGGAG-----AATCTCACCCCTGGGGATACGGGAAGCAGG 393
Qy 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Db 394 AAGGAGGATGAGGATGCTTATGACCTG-----GAGAAATGTTTCA 441
Qy 121 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 138
Db 442 GTTCAGCGCTTTTGCCTGAGTTGAGGCTTTATGAGCAGGTTCTCACTCCAGAAATTA 501
Qy 139 GlnSerLeuMetAlaSerValAsnSerTyrCysAsnValThrLeuThrCysSerValGlu 158
Db 502 GTTTTAAACAAGACCCAGGAGACGGGACCTTGACCTTGATACTGCTGCGCATGTGAG 561
Qy 159 LysGluGluLysAsnValThrTyrAsnTyrSer-----ProLeu--- 171
Db 562 AAGGGGAC---CATGTGGCTTACAGCTGGAGTGAAGGGGGGACCCACCCACTGAAC 618
Qy 172 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 190
Db 619 CCAGCCAACAGCTCCACCTCTGCTCCCTCCGCCCCCAGCATGTGTCACATATC 678
Qy 191 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210
Db 679 TACATCTGCACCGTGACCAACCTTATCAGCAACAATTCACAGCTTCCAGCCCTGCGCC 738
Qy 211 LeuCysAlaAspIleAlaMetGlyPheArgThrHis----- 222
Db 739 GGATGC-----AGGACAGACCCCTCAGAAACAAACCAACCATGGCA 777
Qy 223 ---HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer 241
Db 778 GTGTATGCTGGGTGTAGGGGTGTCATCATGATTCTCATGTGGTGGTAAATACTACAG 837
Qy 242 SerValPheLeuPheArgLeuPheLysArgArg-----GlnAspAla 255
Db 838 -----TTGAGAGAGAGAGGTAAACGAAACCACTTACCAGACACA 876
Qy 256 AlaSerLysLysThrIleTyrThrIleMetAlaSerArg----- 269
Db 877 GTGGAAGAAAAAGCCCTTACGATCTATGCCCAAGTCCAGAAACCAAGCTCTCTTCAAG 936
Qy 270 -----AsnThrGlnProAlaGlu-----SerArgIleTyrAspGluIleLeuGln 284
Db 937 AAATTGACTCTTCCAGCTCAGGACCTTGACCAACCACTATAT-----GTTGCTGCC 990
Qy 285 SerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGluVal 302
Db 991 ACAGAGCTGTCGCCAGAGTCTGTCCAGGAACAAATTCATCAGACTGTATGCTAGTGTG 1050
RESULT 14
US-08-462-738-1
; Sequence 1, Application US/08462738


```

, APPLICATION NUMBER: US/09/199,955
, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/461,473
, FILING DATE: 05-JUN-1995
, APPLICATION NUMBER: US 08/348,792
, FILING DATE: 02-DEC-1994
, ATTORNEY/AGENT INFORMATION:
, NAME: Ching, Edwin P.
, REGISTRATION NUMBER: 34,090
, REFERENCE/DOCKET NUMBER: DX0436GC
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415-852-9196
, TELEFAX: 415-496-1200
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 1716 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 61..1065
US-09-199-955-1

```

Alignment Scores:		
Pred. No.:	9.83e-44	Length:
Score:	194.00	Matches:
Percent Similarity:	40.62%	Conservative:
Best Local Similarity:	23.75%	Mismatches:
Query Match:	11.44%	Indels:
DB:	3	Gaps:
		16
		1716

US-09-882-171-483 (1-329) x US-09-199-955-1 (1-1716)

QY	33	LeuGlyGluservValthrPhePro-----ValAsnIleGlnGluProArg	47
Db	175	TTTTGGAGCAAGAAGTCTGCTGCCCTGCATCATGAAGGATAAATAGACATGAACAA	234
QY	48	GlnVallylleAlaAtipThrSerIysThr-----ServAl	60
Db	235	AGCATCCCATNTGTCTCACAATGGCAAAATCACTGGAGAACAGTGTCGGAACAACAAATA	294
QY	61	AlaTyrvAlThrProGlyAspSerGluThralaProValValThrValThrHisArgasn	80
Db	295	GTGTCCTTTGATTCCATCCGAGACGAGGCCCTCCACGTTATCTAGGAGATCGTCAAGATT	354
QY	81	TyTyvTyGluArgIleHisAlaLeuGlyProAsnTyvRsnLeuValIleSerAspLeuArg	100
Db	355	TATCTGGAG-----AATCTCACCTGGGGNATCGGHAACACGAG	393
QY	101	MetGluAspAlagLyAspTyLysAlaaspIleAsnthrGlnAlaaspProTyvThrThr	120
Db	394	AAGGAGGATGAGGATGGTGACTTATGACCCTG-----GAGAAAATGTTTCA	441
QY	121	ThrIysAisgTyvRsnLeuGln-----IleTyvArgargLeuGlyysProllysileThr	138
Ddb	442	GTTCAGCGCTTTGCTTCGCTGCACTTGAGCGCTTTATGAGCAGGTCTCCA	501
QY	139	GlnSerLeuMetAlaServAlasnSerThrCysAsnValThrLeuthrCysSerValGlu	158
Ddb	502	GTTTTPAAACAAGACCCAGGAGAACGGGACCTGCACCTTGATACTGCGCTGCACAGTGAG	561
QY	159	LysGluGluLysAsnValThrTyvAsnTrpSer-----ProLeu-----	171
Ddb	562	AAGGGGAC---CATGTGGCTTACAGCTGGAGTGMAAAGCGGGGACCACCACCTAGAAC	618
QY	172	--GlyGluGluGlyAsnValLeuGlnIlepheGlnThrProGluAspGlnGluLeuthr	190
Db	619	CGAGCCAAACAGCTCCCACCTCTGTCCCTCACCTCGGGCCCCAGCATGCTGCACATATC	678

Qy	191	TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln	210
Db	679	TACATCTGCACCGTGAGCAACCTTATCAGCAACAATTCACAGACCTTCAGCCCGTGGCC	738
Qy	211	LeuCysAlaAspIleAlaMetGlyPheArgThrHis	222
Db	739	GGATGC-----AGGACAGACCCCTCAGAAACAAACCAATGGGCA	777
Qy	223	---HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer	241
Db	778	GTGTATGCTGGCGTGTAGGGGTGTCATCATGATTCTCATCATGGTGGTAACTACTACAG	837
Qy	242	SerValPheLeuPheArgLeuPheLysArgArg-----GlnAspAla	255
Db	838	-----TTGAGAAGAAGAGGTAAACGAACCATTTACCAGACAACA	876
Qy	256	AlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg-----	269
Db	877	GTGGAAAAAAGCCCTTACGATCTATGCCAAGTCCAGAAACACAGTCTCTTCAGAAG	936
Qy	270	-----AsnThrGlnProAlaGlu-----SerArgIleTyrAspGluIleLeuGln	284
Db	937	AAACTGTGACTCTTCCAGCTCAGGACCCCTTGACACCACTATAT-----GTTGCTGCC	990
Qy	285	SerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGluVal	302
Db	991	ACAGAGCCTGTCCAGAGTCTGTCCAGGAACAATAATCCATCAGCTATGCTAGTGTG	1050

Search completed: February 5, 2005, 11:31:47
Job time : 239.449 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 5, 2005, 09:29:36 ; Search time 700.371 Seconds
(without alignments)
2703.765 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWLLCLQIWPEAA.....KASTQDSKPPGSSSEIVIX 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114005_26092/app_query.fasta_1.910
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=ext -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09882171.qcgn_1_1582@runat_04022005_114005_26092
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US12_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1695	99.9	1040	16	US-10-436-523-29	Sequence 29, Appl
2	1695	99.9	1067	18	US-10-723-860-1885	Sequence 1885, Ap
3	1695	99.9	3173	10	US-09-809-391-174	Sequence 174, App
4	1695	99.9	3173	10	US-09-882-171-174	Sequence 174, App
5	1695	99.9	3173	17	US-10-164-861-174	Sequence 174, App
6	1695	99.9	3226	18	US-10-723-860-6219	Sequence 6219, Ap
7	1695	99.9	3687	14	US-10-138-846-13255	Sequence 13255, A
8	382.5	22.6	1849	17	US-10-471-449-20	Sequence 20, Appl
9	382.5	22.6	2286	10	US-09-860-836B-12	Sequence 12, Appl
10	374	22.1	2448	18	US-10-310-612-1	Sequence 1, Appl
11	374	22.1	2448	18	US-10-328-538-1	Sequence 1, Appl
12	373	22.0	870	16	US-10-436-523-75	Sequence 75, Appl
13	373	22.0	1139	16	US-10-436-523-74	Sequence 74, Appl
14	373	22.0	1139	17	US-10-170-385-132	Sequence 132, App
15	373	22.0	1423	15	US-10-220-946-17	Sequence 17, Appl
16	370.5	21.8	1225	14	US-10-104-943-40	Sequence 40, Appl
17	370.5	21.8	1463	17	US-10-471-449-17	Sequence 17, Appl
18	370.5	21.8	1868	14	US-10-245-752-75	Sequence 75, Appl
19	370.5	21.8	1868	14	US-10-245-859-75	Sequence 75, Appl
20	370.5	21.8	1868	14	US-10-245-103-75	Sequence 75, Appl
21	370.5	21.8	1868	14	US-10-245-107-75	Sequence 75, Appl
22	370.5	21.8	1868	14	US-10-245-143-75	Sequence 75, Appl
23	370.5	21.8	1868	14	US-10-245-171-75	Sequence 75, Appl
24	370.5	21.8	1868	14	US-10-245-851-75	Sequence 75, Appl
25	370.5	21.8	1868	14	US-10-245-883-75	Sequence 75, Appl
26	370.5	21.8	1868	14	US-10-237-535-75	Sequence 75, Appl
27	370.5	21.8	1868	14	US-10-238-183-75	Sequence 75, Appl
28	370.5	21.8	1868	14	US-10-238-283-75	Sequence 75, Appl
29	370.5	21.8	1868	14	US-10-238-370-75	Sequence 75, Appl
30	370.5	21.8	1868	14	US-10-245-055-75	Sequence 75, Appl
31	370.5	21.8	1868	14	US-10-245-147-75	Sequence 75, Appl
32	370.5	21.8	1868	14	US-10-245-730-75	Sequence 75, Appl
33	370.5	21.8	1868	14	US-10-245-739-75	Sequence 75, Appl
34	370.5	21.8	1868	14	US-10-246-210-75	Sequence 75, Appl
35	370.5	21.8	1868	14	US-10-239-196-75	Sequence 75, Appl
36	370.5	21.8	1868	14	US-10-243-024-75	Sequence 75, Appl
37	370.5	21.8	1868	14	US-10-243-409-75	Sequence 75, Appl
38	370.5	21.8	1868	14	US-10-245-621-75	Sequence 75, Appl
39	370.5	21.8	1868	14	US-10-245-880-75	Sequence 75, Appl
40	370.5	21.8	1868	14	US-10-245-033-75	Sequence 75, Appl
41	370.5	21.8	1868	14	US-10-243-095-75	Sequence 75, Appl
42	370.5	21.8	1868	14	US-10-245-185-75	Sequence 75, Appl
43	370.5	21.8	1868	14	US-10-245-427-75	Sequence 75, Appl
44	370.5	21.8	1868	14	US-10-245-473-75	Sequence 75, Appl
45	370.5	21.8	1868	14	US-10-245-770-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-436-523-29
; Sequence 29, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-436-523-29

Alignment Scores:

Pred. No.: 1.16e-203 Length: 1040
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 16 Gaps: 0

US-09-882-171-483 (1-329) x US-10-436-523-29 (1-1040)

Qy 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20
Db 42 ATGGCTCAGCACCACTATGATCTTGGCTTGGCTGCAAACTGGCGGAGAGCT 101
Qy 21 GlyLysAspSerGluLeuPheThrValAsnGlyLeuGlyGluSerValThrPhePro 40
Db 102 GGAAGAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACTTCCCT 161
Qy 41 ValAsnIleGlnProArgGlnValLysIleAlaThrThrSerLysThrSerVal 60
Db 162 GTAAATATCCAGAACACCGCAAGTTAAATCAITGCTTGAGCTTCTAAACATCTGT 221
Qy 61 AlaTyValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 222 GCTTATGTAAACACCGAGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAAT 281
Qy 81 TyrTyGluArgIleHisAlaLeuGlyProAsnTyAsnLeuValLysSerAspLeuArg 100
Db 282 TATATGAACGGGATACATCCCTTAGTCCGAACTACAATCTGGTCAATAGCGATCTGAGG 341
Qy 101 MetGluAspAlaGlyAspTyLysAlaAspIleAsnThrGlnAlaAspProTyThrThr 120
Db 342 ATGGAAGACGAGGAGACTACAAAGCAGACATATAACACAGCTGTATCCCTACACCACC 401
Qy 121 ThrLysArgTyAsnLeuGlnIleTyArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 402 ACCAAGCGGTACAACTGCAAAATCTATCTCGCTTGGGAAACCAAAATTAACAGAGT 461
Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 462 TTAATGGCATCTGTGACAGACCTCTGTAATGTACACTGACATGCTGTGTAGAGAAAGAA 521
Qy 161 GluLysAsnValThrTyAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle 180
Db 522 GAAAGAAATGTACATACAAATTTGGAGTCCCTGGGAGAGAGGTAATGTCTTCAATC 581
Qy 181 PheGlnThrProGluAspGlnLeuThrTyThrCysThrAlaGlnAsnProValSer 200
Db 582 TTCCAGACTCTCCGAGACCAAGAGCTGACTTACAGCTGTACAGCCCAAGACCCCTGTGAGC 641
Qy 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
Db 642 AACAAATCTGACTCTCTCCCGGAGCTCTGTGAGACATCGCAATGGGCTTCCGT 701
Qy 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuValLeuIleLeu 240
Db 702 ACTCACCAACCGGGTGTGAGCGGTGTGATGTTCTTCTGTTCTTCTCATCTG 761
Qy 241 SerSerValPheLeuPheArgGluPheLysArgArgGlnAspAlaAlaSerLysIleThr 260
Db 762 TCTTCAGTGTCTTGTGCTCGTTGTCAAGAGAGACAGAGATGCTGCTCAAGAAAGAAC 821
Qy 261 IleTyThrTyIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyAsp 280
Db 822 ATATACATATATCATGGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAAATCTATGAT 881
Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTySer 300
Db 882 GAAATCTCTGCATCCAGGTGCTTCCCTCCCAAGGAAGAGCCAGTGAACACAGAGTTATTC 941
Qy 301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProGly 320

Db 942 GAAGTGCAGTTTGCCTGATAAGATGGGAAAGCCAGACACAGGACAGTAAACCTCTCTGGG 1001
Qy 321 ThrSerSerTyGluIleValIle 328
Db 1002 ACTTCAAGCTATGAATTTGTGATC 1025
RESULT 2
US-10-723-860-1885
; Sequence 1885, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1885
; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1885
Alignment Scores:
Pred. No.: 1.21e-203 Length: 1067
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 18 Gaps: 0
US-09-882-171-483 (1-329) x US-10-723-860-1885 (1-1067)

Qy 1 MetAlaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaA 20
Db 70 ATGGCTCAGCACCACTATGATCTTGGCTTGGCTGCAAACTGGCGGAGAGCT 129
Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
Db 130 GGAAGAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACTTCCCT 189
Qy 41 ValAsnIleGlnProArgGlnValLysIleAlaThrThrSerLysThrSerVal 60
Db 190 GTAAATATCCAGAAACACCGCAAGTTAAATCATCTTGGACTTCTAAACATCTGTT 249
Qy 61 AlaTyValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
Db 250 GCTTATGTAAACACCGAGAGACTCAGAAACAGCACCGCTAGTGTACTGTGACCCACAGAAAT 309
Qy 81 TyrTyGluArgIleHisAlaLeuGlyProAsnTyAsnLeuValLysSerAspLeuArg 100
Db 310 TATATGAACGGATACATGCTTAGTCCGAACTACAACTGCTGATTCAGCATCTGAGG 369
Qy 101 MetGluAspAlaGlyAspTyLysAlaAspIleAsnThrGlnAlaAspProTyThrThr 120
Db 370 ATGGAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 429
Qy 121 ThrLysArgTyAsnLeuGlnIleTyArgArgLeuGlyLysProLysIleThrGlnSer 140
Db 430 ACCAAGCGCTACAACTGCAAAATCTATCTGCTCGGCTTGGGAAACCAAAATTAACAGAGT 489
Qy 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db 490 TTAATGGCATCTGTGAACAGACCTCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAA 549
Qy 161 GluLysAsnValThrTyAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle 180

[illegible]


```
101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
121 ThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSer 140
141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
161 GluLysAsnValThrTyrAsnThrProSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysThr 260
261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300

; NAME/KEY: misc feature
; LOCATION: 1, 2, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677,
; LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13255

Alignment Scores:
Pred. No.: 8,93e-203 Length: 3687
Score: 1695.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 14 Gaps: 0

US-09-882-171-483 (1-329) x US-10-198-846-13255 (1-3687)
QY 1 MetAlaGlnHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAa 20
DB 433 ATGGCTCAGCACACCTATGGATCTTGCTTCCTTGGCTGCAACCTGGCGGAGAGCT 492
QY 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
DB 493 GGAAGAAGACTCAGAATCTTCACAGTGAATGGGATCTCGGAGAGTCAGTCACCTTCCCT 552
QY 41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
DB 553 GTAAATATCAAGAACACCGCAAGTTAAATCAATTCCTGGACTTCTAAACCATCTGTT 612
QY 61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
DB 613 GCTTATGTAAACACCGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAAT 672
QY 81 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 100
DB 673 TATTAAGACGGATACATGCTTAGCTCGAAGTCAATCTGCTCATTAGCGATCTGAGG 732
QY 101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
DB 733 ATGGAAGACGACGAGGACTACAAAGCAGACATAAATACACAGGCTGATCCTACACACC 792
QY 121 ThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSer 140
DB 793 ACCAAGCGCTACAACTCTATCGTCGGCTTGGGAAACCAAAATTTACACAGAT 852
QY 141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
DB 853 TTAATGGCATCTGTGAACAGCACCTGTATGTCACACTGACATGCTCTGTAGAGAAAGAA 912
QY 161 GluLysAsnValThrTyrAsnThrProSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
DB 913 GAAAGAAATGTGACATACAAATTTGGAGTCCCTCGGAGAGAGGGTAAATGCTTCAATC 972
QY 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
DB 973 TTCAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACGCCAGACCCCTGTGAGC 1032
QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
DB 1033 ACAAATCTGACTCCATCTCTGCCGCGACGCTCTGTGCAGACATCGCAATGGGCTCCGT 1092
QY 221 ThrHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuLeu 240
DB 1093 ACTCACACACCGGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTTGTCTCATCTG 1152
QY 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysThr 260
DB 1153 TCTTCAGTGTCTTGTTCCTGTTGTTTCAAGAGAGACCAAGATGCTGCTTCAAGAAAC 1212
QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
DB 1213 ATATACATATATCATGGCTTCAAGGAACACCCAGCAGCAGTCCAGATCTATGAT 1272
QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
```

RESULT 7

```
US-10-198-846-13255
; Sequence 13255, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13255
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```



```
Db 817 CCAGTACCCTGCCACTTGCCTCCAGCCTCCGGGACACACAGAGGTTGTCTGGTTG 876
Qy 246 PheArg-----LeuPheLysArgArgGlnAspAlaAlaSerLysLysThrIleTyr 262
Db 877 TTTAACACATCCATCATTTAGCAAGAGAGGGAAGAGCAGCAACGGGAGATCCACTCAT 936
Qy 263 ThrTyrIleMetAlaSerArgAnthrGlnProAlaGluSerArgIleTyr 279
Db 937 -----AAATCCAGGATCCTTACCAAGAACAGGGTGTGG 969

RESULT 11
US-10-328-538-1
; Sequence 1, Application US/10328538
; Publication No. US20040109863A1
; GENERAL INFORMATION:
; APPLICANT: Emage, Peter
; TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
; FILE REFERENCE: HVS-68CP
; CURRENT APPLICATION NUMBER: US/10/328,538
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 10/310,612
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-328-538-1

Alignment Scores:
Pred. No.: 5,36e-36 Length: 2448
Score: 374.00 Matches: 98
Percent Similarity: 52.86% Conservative: 59
Best Local Similarity: 33.00% Mismatches: 104
Query Match: 22.05% Indels: 36
DB: 18 Gaps: 10

US-09-882-171-483 (1-329) x US-10-328-538-1 (1-2448)
Qy 3 GlnHisHleuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAlaGlyLys 22
Db 127 CAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 174
Qy 23 AspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsn 42
Db 175 GACTCAGCCCCAACAGTGGTGTGAGGGATCTTCTAGGGGGTCTCCGCTGACTCTCCCTTAAAC 234
Qy 43 IleGlnGluProArgGlnValLysIleAlaTrpThrSer---LysThrSerValAla 61
Db 235 ATCTCAGTAGACACAGAGATTGGAACGTCATCTGGATTGGTCCCAAAAATCTCTTGTCT 294
Qy 62 TyrValThrProGlyAspSerGluThrAlaProValThrValThrHisArgAnthr 81
Db 295 TTTCGACGCTCCCAAGAAAAT-----GTAAACATTATGTGTCAAAAGCTAC 339
Qy 82 TyrGluArgIleHisAlaLeuGlyProAnthrValLeuValIleSerAspLeuArgMet 101
Db 340 CTGGGCGGAGTACATACACCAAGTGGAGTTACTCCCTGTGATCAGCAATCTGACTCTG 399
Qy 102 GluAspAlaGlyAspTyrLysAlaAspIleAnthrGlnAlaAspProTyrThrThr 121
Db 400 AATGATGAGGATCTTACAAAGCCAGATAAACCAAGGAATTTTGAAGTCCACCACTGAG 459
Qy 122 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 141
Db 460 GAGGAATTCACCTTGTCTATGAGCAGCTGCAGAGGCCCAAGTCCACCAAGTCT 519
Qy 142 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 161
Db 520 GTGAGGTTCTGAGAACTTCTGTAAACATCACTCTTAATGTCTCCGTGAAGGGGCAGAG 579
```

```
Qy 162 LysAsnValThrTyrAsnTrpSerProLeu-----GlyGluGluGly 175
Db 580 AAAAGTGTCTCTACAGCTGGACCCCAAGGAACCCCATGCTTCTGAGTCCAATGGAGGC 639
Qy 176 AsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAla 195
Db 640 TCCATTCCTACCGTCTCCGAAACACCATGTGACCCAGACCTGCCATACATCTGCACAGCC 699
Qy 196 GlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCysAlaAsp 214
Db 700 CAGAACCCCGTCAGCCACAGAGAGTCCCTCCCTGTCATGTTGGGCGAGTCTGTACAGAT 759
Qy 215 -----IleAlaMetGlyPheArgThrHisHisThrGlyLeuLeuSerValLeuAlaMet 232
Db 760 CCAGGAGCCTCCAGAGAGGAGGAACAACGGGGGAGACT---GTGGTAGGGGTCTCTGGAGAG 816
Qy 233 PhePheLeuValLeuIleLeuSerSer-----ValPheLeu 245
Db 817 CCAGTCACTCCCTGCCACTTGCCTCCAGCCTCCGGGACACACAGAGGTTGTCTGGTTG 876
Qy 246 PheArg-----LeuPheLysArgArgGlnAspAlaAlaSerLysLysThrIleTyr 262
Db 877 TTTAACACATCCATCATTTAGCAAGAGAGGGAAGAGCAGCAACGGGAGATCCACTCAT 936
Qy 263 ThrTyrIleMetAlaSerArgAnthrGlnProAlaGluSerArgIleTyr 279
Db 937 -----AAATCCAGGATCCTTACCAAGAACAGGGTGTGG 969

RESULT 12
US-10-436-523-75
; Sequence 75, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-523-75

Alignment Scores:
Pred. No.: 1.35e-36 Length: 870
Score: 373.00 Matches: 92
Percent Similarity: 50.87% Conservative: 54
Best Local Similarity: 32.06% Mismatches: 119
Query Match: 21.99% Indels: 22
DB: 16 Gaps: 5

US-09-882-171-483 (1-329) x US-10-436-523-75 (1-870)
Qy 7 TrpIleLeuLeuLeuCysLeu-----GlnThrTrpProGluAla 19
Db 16 TGGCTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 75
Qy 20 AlaGlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhe 39
Db 76 GGATCCGAGAA-----GTGGTTGGGTCTCTTCCAGGAGTCCATCAGCCTC 120
Qy 40 ProValAsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSer 59
Db 121 CCGCTGGAATATCACACAGATGAAGAGTTGAGAAATCATCTGCTCTCTCAAAAAGT 180
Qy 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValThrValThrHisArg 79
```

```
Db 181 CTTGCCACTGTGTGCGCCAGGAAAGGAGGACATCCAGCTACCATCATGTGTGACCAATCCA 240
      ::::: ||| ||||| ::| |||||:::
Qy 80 AsnTyrTyGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 241 CACTACAGGGCCCAAGTGTCTCCCTGGAGCCCGAGCTATTCCTGTGATATCAGCAATCG 300
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 301 AGCTGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 360
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 120 ThrThrLysArgTyrAsnLeuGlnIleTyrArgLysGlyLysProLysIleThrGln 139
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 361 ACCATCAGCAGTACATCTATGTCTACCGATGCTGTGCAGAGCCCGAGATCACTGTG 420
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 140 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 159
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 421 AACTTTGAGAGTTCTGGGGAAGGTGCTGCAGTATGTCCCTGTGTGCTGTGGGAAG 480
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 160 GluGluLysAsnValThrTyrAsnTyrSerProLeuGlyGlu----- 173
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 481 GCAGGATGATATGATACCTACAGCTGCTCTCCCGGGGGATAGCACTTATATATCCAT 540
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 174 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 193
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 541 GAAGGCCCTGTCTCAGCACATCTCTGAGGCGCGGGGACAGTCCCTCTCTCTACACTGC 600
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 194 ThrAlaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 601 AGAGCCCAACACCCCATCAGCAACGTCAGTCTTGGCCCATCCCTGATGGGCCCTTCTAT 660
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 213 AlaAspIleAlaMetGlyPheArgThrHisThrGly-----LeuLeuSerVal 229
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 661 GCAGATCTCACTATGCTTCTGAGAGCCCTTCAACAGCCCTTCTGCTCTCTGGCCAGGGA 720
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 230 LeuAlaMetPhePheLeuValLeuIleLeuSerSerValPheLeuPheArgLeuPhe 249
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 721 TTGCTCATCTTCTGCTCTTGTGTAATCTGGCCATGGGACTCTGGGTATCCGAGTCCAG 780
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 250 LysArgGlnAspAlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg 269
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 781 AAAAGACACAAATGCCAAGATGAAGAACTCATGAGAAACAGAAATGAAATGAGGAAG 840
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 270 AsnThrGlnProAlaGluSer 276
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 841 GAGGCAAGGCTGGCTCCAGC 861
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
```

RESULT 13

```
US-10-436-523-74
; Sequence 74, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-523-74

Alignment Scores:
Pred. No.: 2 09e-36 Length: 1139
Score: 373.00 Matches: 92
Percent Similarity: 50.87% Conservative: 54
```

```
Best Local Similarity: 32.06% Mismatches: 119
Query Match: 21.99% Indels: 22
DB: 16 Gaps: 5
US-09-882-171-483 (1-329) x US-10-436-523-74 (1-1139)
Qy 7 TrpIleLeuLeuLeuCysLeu-----GlnThrTrpProGluAla 19
      ::::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 100 TGGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 159
      ::::: |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 20 AlaGlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhe 39
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 160 GGATCCGAGGAA-----GTGGTTGGGTCTCTTCAGAGTCCATCAGCCCTC 204
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 40 ProValAsnIleGlnGluProArgGlnValIleIleAlaThrPheThrSerLysThrSer 59
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 205 CCCCTGGAAATACCCAGATGAAGAGGTTGAGAACATCATCTGTGCTCTCACAAGT 264
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 265 CTTGCCACTGTGTGCGCCAGGAAAGGAGGACATCCAGCTACCATCATGTGTGACCAATCCA 324
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 80 AsnTyrTyGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 325 CACTACAGGCGCCAGTGTGAGTCTTCCAGCCCGAGCTATTCCTGTGATATCAGCAATCTG 384
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 385 AGCTGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 444
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 120 ThrThrLysArgTyrAsnLeuGlnIleTyrArgLysGlyLysProLysIleThrGln 139
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 445 ACCATCAGCAGTACATCTATGTGTCTACCGATGCTGTGCAGAGCCCGAGATCACTGTG 504
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 140 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 159
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 505 AACTTTGAGAGTTCTGGGGAAGGTGCTGCAGTATGTCCCTGTGTGCTCTGTGGGAAG 564
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 160 GluGluLysAsnValThrTyrAsnTyrSerProLeuGlyGlu----- 173
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 565 GCAGGATGATATGATACCTACAGCTGCTCTCCCGGGGGATAGCACTTATATATCCAT 624
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 174 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 193
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 625 GAAGGCCCTGTCTCAGCACATCTCTGAGGCGCGGGGACAGTGCCTCTCTCTACACCTGC 684
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 194 ThrAlaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 685 AGAGCCCAACACCCCATCAGCAACGTCAGTCTTGGCCCATCCCTGTGATGGGCCCTTCTAT 744
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 213 AlaAspIleAlaMetGlyPheArgThrHisThrGly-----LeuLeuSerVal 229
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 745 GCAGATCTCACTATGCTTCTGAGAGCCCTTCAACAGCCCTTCTGCTCTCTGGCCAAAGGA 804
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 230 LeuAlaMetPhePheLeuValLeuIleLeuSerSerValPheLeuPheArgLeuPhe 249
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 805 TTGCTCATCTTCTGCTCTTGTGTAATCTGGCCATGGGACTCTGGGTATCCGAGTCCAG 864
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 250 LysArgGlnAspAlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg 269
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 865 AAAAGACACAAATGCCAAGATGAAGAACTCATGAGAAACAGAAATGAAATGAGGAAG 924
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Qy 270 AsnThrGlnProAlaGluSer 276
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
Db 925 GAGGCAAGGCTGGCTCCAGC 945
      ::::: ::::: ||| |||||::: |||||::: |||||::: |||||::: |||||:::
RESULT 14
US-10-170-385-132
; Sequence 132, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
```



```
QY 20 AlaGlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhe 39
Db 160 GGATCCGAGAA-----GTGGTTGGCTCTTCAGGAGTCCATCAGCCTC 204
QY 40 ProValAsnIleGlnGluProArgGlnValLysIleAlaThrPheSerLysThrSer 59
Db 205 CCCCTGGAATACCACAGATGAAGAGTTGAGACATCATCTGTGCTCTCACAAAGT 264
QY 60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValHisArg 79
Db 265 CTTCACACTGTGTGGTGAAGAGGAGGACATCCAGATACCATCATGTGTACCAATCCA 324
QY 80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu 99
Db 325 CACTACAGGGCCAGTGGAGCTTCCTGGACCCAGCTATTCCTCGCATATCAGCATCTG 384
QY 100 ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
Db 385 AGCTGGGAGGATTCAAGGCTTTACCAAGCTCAAGTCAAGCTCAAGTCAAGTCAAGTCTCT 444
QY 120 ThrThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGln 139
Db 445 ACCATGCAGCAGTACATCTATGTCTACCGATGCTGTCAGAGCCCGAGATCCTGTG 504
QY 140 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 159
Db 505 AACTTTGAGAGTTCTGGGGAGGTGCTGTCAGATATGTCCCTGTGTGCTCTGTGGAGAG 564
QY 160 GluGluLysAsnValThrTyrAsnTyrSerProLeuGlyGlu----- 173
Db 565 GCAGGCATGGATGATGACTACAGTGGCTCTCCCGGGGGATAGCACTTATACATTCCAT 624
QY 174 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 193
Db 625 GAAGGCCCTCTCCTCAGCACATCCTGGAGGCCGGGGGACAGTGCCTCTCTACACCTGC 684
QY 194 ThrAlaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
Db 685 AGAGCCCAACACCCATCAGAACCTGAGTCTTGCCCCATCCCTGATGGGCCCTTCTAT 744
QY 213 AlaAspIleAlaMetGlyPheArgThrHisHisThrGly-----LeuLeuSerVal 229
Db 745 GCAGATCTTAATATGCTTCTGAGAGCCTTCAACAGCCTTCTGCCTCTCTGGCCAGGGA 804
QY 230 LeuAlaMetPhePheLeuValLeuIleLeuSerSerValPheLeuPheArgLeuPhe 249
Db 805 TTGCTCATCTCTTGTCTCTTGTAAATCTGGCCATGGGACTCTGGGTCTATCCGAGTCCAG 864
QY 250 LysArgArgGlnAspAlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg 269
Db 865 AAAAGACACAAATGCCAAGATGAAGAACTCATGAGAAACAGAAATGAATTCAGGAGAG 924
QY 270 AsnThrGlnProAlaGluSer 276
Db 925 GAGGCAAGCTGTGCTCCAGC 945
```

Search completed: February 5, 2005, 14:07:54
Job time : 707.371 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 5, 2005, 03:27:31 ; Search time 4338.06 Seconds
(without alignments)
2886.805 Million cell updates/sec

Title: US-09-882-171-483
Perfect score: 1696
Sequence: 1 MAQHLLWILLCLQTWPEAA.....KASTQDSKPPGTSYEIVIX 329

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114004_26033/app_query.fasta_1.910
-Db=EST -OPM=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09882171@cgn 1.1.4385 @runat 04022005_114004_26033 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	99.9	987	9 AY408981	AY408981 Homo sapi
2	1676	98.8	987	9 AY408982	AY408982 Pan trogl
3	1071	63.1	608	7 CV023928	CV023928 1001 Full
4	1030.5	60.8	1074	4 BG106937	BG106937 602291349
5	1008	59.4	582	5 BP303350	BP303350 BP303350
6	886	52.2	923	9 AY408983	AY408983 Mus muscu
7	853	50.3	739	6 CB467388	CB467388 733129 MA
8	852	50.2	535	2 BF754299	BF754299 PMO-CT054
9	829	48.9	837	5 BP159730	BP159730 BP159730

10	818	48.2	582	5 BP303194	BP303194 BP303194
11	732	43.2	788	4 BI151764	BI151764 602915927
12	717	42.3	466	5 BU927996	BU927996 AGENCOURT
13	705.5	41.6	671	6 BY748483	BY748483 BY748483
14	683	40.3	402	2 AW013969	AW013969 UI-H-BIO-
15	627	37.0	389	2 AK408076	AK408076 UI-HF-BMO
16	596.5	35.2	651	6 BY724459	BY724459 BY724459
17	595	35.1	519	4 BM089070	BM089070 502719 NA
18	588	34.7	677	9 AG090451	AG090451 Pan trogl
19	576	34.0	719	7 CK772231	CK772231 960749 MA
20	498.5	29.4	721	6 CB530813	CB530813 737641 NA
21	492	29.0	322	1 AL597403	AL597403 DKFZ63131L
22	419	24.7	322	6 AL597429	AL597429 BY749229
23	382.5	22.6	2030	3 CR590858	CR590858 full Leng
24	378.5	22.3	660	2 BB630528	BB630528 BB630528
25	378.5	22.3	1090	3 AK040694	AK040694 Mus muscu
26	378.5	22.3	3377	3 AK037385	AK037385 Mus muscu
27	378	22.3	584	5 BP302120	BP302120 BP302120
28	377.5	22.3	634	2 BB636608	BB636608 BB636608
29	377.5	22.3	2131	3 BC027920	BC027920 Homo sapi
30	376.5	22.2	426	5 BY181022	BY181022 BY181022
31	376	22.2	767	1 AU141507	AU141507 AU141507
32	373.5	22.0	1133	5 BM922555	BM922555 AGENCOURT
33	372.5	22.0	406	5 BY207872	BY207872 BY207872
34	371	21.9	233	1 AA355777	AA355777 EST64278
35	369.5	21.8	1671	9 AY413809	AY413809 Pan trogl
36	368	21.7	1303	3 AK090041	AK090041 Mus muscu
37	367	21.6	759	4 BI907423	BI907423 603063795
38	367	21.6	1100	3 AK009505	AK009505 Mus muscu
39	366	21.6	912	5 BX388160	BX388160 BX388160
40	364	21.5	1671	9 AY413808	AY413808 Homo sapi
41	363	21.4	580	5 BP300475	BP300475 BP300475
42	363	21.4	1017	1 AL561509	AL561509 AL561509
43	354	20.9	951	1 AL561522	AL561522 AL561522
44	351	20.7	2099	3 AK088815	AK088815 Mus muscu
45	348	20.5	366	5 BY199370	BY199370 BY199370

ALIGNMENTS

RESULT 1
AY408981
LOCUS Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 15-DEC-2003
DEFINITION Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY408981
VERSION AY408981.1 GI:39764949
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 987)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
Location/Qualifiers
1..987


```
Db      301 ATGGAAGACGACGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 360
QY      121 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
Db      361 ACCAAGCGCTACAACTGCAAACTTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT 420
QY      141 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 160
Db      421 TTAATGGCATCTGTGAACGACACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA 480
QY      161 GluLysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
Db      481 GAAAGAAGATGTGACATACAAATTTGAGTCCCTGGGAGAGAGGGTAAATGCTTCAAATC 540
QY      181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200
Db      541 TTCACAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAAGAACCTGTGCAGC 600
QY      201 AsnAsn 202
Db      601 AACAAAT 606
```

```
RESULT 4
BG106937 602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
LOCUS 1074 bp mRNA linear EST 30-JAN-2001
DEFINITION mRNA sequence.
ACCESSION BG106937
VERSION 1 GI:12600783
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1074)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA library Prepared by: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10068 row: b column: 14
High quality sequence stop: 638.
FEATURES
Location/Qualifiers
1..1074
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4385965"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
Note="Organ: lymph; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
```

FEATURES

```
Source
1..1074
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4385965"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
Note="Organ: lymph; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
```

```
RESULT 5
BP303350 582 bp mRNA linear EST 17-SEP-2004
LOCUS BP303350 Sugano cDNA library, macrophage Homo sapiens cDNA clone
DEFINITION MP08190, mRNA sequence.
ACCESSION BP303350
VERSION BP303350.1 GI:52232310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 582)
JOURNAL Suzuki, Y., Yamashita, R., Hirota, M., Sakakibara, Y., Chiba, J.,
COMMENT Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
```


O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CT0547-091000-001-a04&t3=2000-10-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 533.

FEATURES

Location/Qualifiers
 1..535
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CT0547"
 /notes="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORFEST PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 2,28e-90 Length: 535
 Score: 852.00 Matches: 165
 Percent Similarity: 98.80% Conservative: 0
 Best Local Similarity: 98.80% Mismatches: 1
 Query Match: 50.24% Indels: 1
 DB: 2 Gaps: 0

US-09-882-171-483 (1-329) x BF754299 (1-535)

Qy 1 MetAlaGlnHisHisLeuTrrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAala 20
 |||||
 Db 35 ATGGCTCAGCACCACTATGATCTTCTTTCCTTGCCTTGAACCTGGCGGAGCAGCT 94
 |||||
 Qy 21 GlyLysAspSerGluIlePheThrVal-AsnGlyIleLeuGlyGluSerValThrPhePr 40
 |||||
 Db 95 GGAAGAAAGCTCAGAAATCTTCACAGTGAATGGATCTCTGGAGAGTCAGTCACTTTCCC 154
 |||||
 Qy 40 ovalAsnIleGlnGluProArgGlnValIleAlaTrpThrSerLysThrSerVa 60
 |||||
 Db 155 TGTAAATATCCAGAACACCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGT 214
 |||||
 Qy 60 lAlaTyThrValThrProGlyAspSerGluThrAlaProValValThrHisArgAs 80
 |||||
 Db 215 TGCTTATGTAAACACGAGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAA 274
 |||||
 Qy 80 nTyThrGluArgIleHisAlaLeuGlyProAsnTyrrAsnLeuValIleSerAspLeuAr 100
 |||||
 Db 275 TTATTATGAAGGATACATGCTTAGTCCGAACTACATCTGTCATTAGCGATCTGAG 334
 |||||
 Qy 100 gMetGluAspAlaGlyAspTyrrLysAlaAspIleAsnThrGlnAlaAspProTyThrTh 120
 |||||
 Db 335 GATGGAAGACCGCAGGAGACTCAAGACAGACAGATAAATACACAGGCTGATCCCTACACAC 394
 |||||
 Qy 120 rThrLysArgTyrrAsnLeuGlnIleTyrrArgArgLeuGlyLysProLysIleThrGlnSe 140
 |||||

Db 395 CACCAAGCGCTACAACTGCAAAATCTATCGCGGCTTGGGAACCAAAATTTACAGAG 454
 |||||
 Qy 140 rLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysG1 160
 |||||
 Db 455 TTTATATGCACTCTGTGAACACAGCAGCTGTAAATGTACACATGCTCTGTAGAGAAAGA 514
 |||||
 Qy 160 uGluLysAsnValThrTyr 166
 |||||
 Db 515 AGAAAAGAAATGTGACATAC 533
 |||||
 RESULT 9
 BP159730 837 bp mRNA linear EST 30-DEC-2003
 BP159730 full-length enriched swine cDNA library, adult thymus Sus
 scrofa cDNA clone THY010074A04 5', mRNA sequence.
 ACCESSION BP159730
 VERSION BP159730.1 GI:40409203
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 837)
 Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
 Okumura, N., Hamasima, N. and Awata, T.
 PEDE (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 Contact: Hirohide Uenishi
 National Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
 FEATURES
 Location/Qualifiers
 1..837
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="THY010074A04"
 /tissue_type="thymus"
 /dev_stage="adult"
 /clone_lib="full-length enriched swine cDNA library, adult
 thymus"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,44e-87 Length: 837
 Score: 829.00 Matches: 165
 Percent Similarity: 79.22% Conservative: 37
 Best Local Similarity: 64.71% Mismatches: 49
 Query Match: 48.88% Indels: 4
 DB: 5 Gaps: 3
 US-09-882-171-483 (1-329) x BP159730 (1-837)
 Qy 1 MetAlaGlnHisHisLeuTrrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAala 20
 |||||
 Db 61 ATGGCTCATCGCACACATGATCTTCTTTCCTTCAAAACCCGCTGGGAGCAGTT 120
 |||||
 Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
 |||||
 Db 121 GGAAGCAACACAGACATCACTATAGTAATGGGATCTGGGGGAGTCAGTCACTTTTCC 180
 |||||

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1179 row: e column: 07
High quality sequence stop: 782.
Location/Qualifiers

FEATURES

1..788
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5066478"
/tissue type="spontaneous tumor, metastatic to mammary."
Stem cell origin."
/lab_host="PH108"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:
Pred. No.: 7,43e-76 Length: 788
Score: 732.00 Matches: 151
Percent Similarity: 74.50% Conservative: 36
Best Local Similarity: 60.16% Mismatches: 59
Query Match: 43.16% Indels: 6
DB: 4 Gaps: 3

US-09-882-171-483 (1-329) x BI151764 (1-788)

QY 5 HisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaGlyAspSer 24
DB 6 CATCTCTGGATCTGGTTCTTCCTGCTACAACTGCTGAGCAGCAGCAAGATGCA 65
QY 25 GluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGln 44
DB 66 GACCCGGTGAATGAGTGGTCTGGGAGTCTGATCTTCTCTTAATATTCAA 125
QY 45 GluProArgGlnValIleLeuThrSerIleThrSerIleThrSerValAlaIleValThr 64
DB 126 GAACCAAGAAATTCGACCAATTCCTGGATCTCAATCATCTGCTTCTTTATAAAA 185
QY 65 ProGlyAspSerGluThrAlaProValThrValThrHisArgAsnTyrTyrGluArg 84
DB 186 CCAGGAGTCAATAAAGCTGAA-----GTTACCATTAACCCAGGCCTTATAAGACGA 239
QY 85 IleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAla 104
DB 240 ATAGAAATCATAGATCAGAGTATGACCTGCTGATGAGACCTGAGATGGAAGATGCA 299
QY 105 GlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThrIleAspGlyTyr 124
DB 300 GGAACCTTACAAAGCAGACATCAATGAAGAAGATGAGAA---ACCATCACAAGATCTAC 356
QY 125 AsnLeuGlnIleTyrArgArgLeuGlyLeuGlyProIleThrGlnSerLeuMetAlaSer 144
DB 357 TACCTTTCATATCTACCGTTCGACTTAAACACCAAAATTCACAGAGTTTGAATCATCT 416
QY 145 ValAspSerThrCysAsnValThrLeuThrCysSerValGluGlyGluGlyAsnVal 164
DB 417 TTGAACAATACCTGTAATATTACACTGACATGCTCTGTGGAAGAGGAGGAAGGATGTC 476
QY 165 ThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePheGlnThrPro 184
DB 477 ACATATAGCTGGATCTCTTTGGAGAGAAAGCAATGCTTCAATCGTCCACTCCCCC 536
QY 185 GluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnPro-ValSerAsnAsnSerAs 204
DB 537 ATGACCAAAACTGACCTACATGATGATGATGATGATGATGATGATGATGATGATGAT 596
QY 204 pSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArgThrHisHisTh 224

DB 597 CTCCTGCTACATGTCCAGCAGCCATGTACAGAC---ACTCCAAGCTTCCATCTCGCATCC 653
QY 224 rClyLeuLeuSerValLeuAlaMetPhePheLeuValLeuValLeuLeuSerValPh 244
DB 654 TGTGTGTCCAGGAGGATGGCGGTCTCTTCTTCTGTTATGCTCATTCGATGTGGCAT 713
QY 244 eLeuPheArgLeuPheLeuArgArgGlnAsp 254
DB 714 TCTGTTCGTTG-TATAAGAGAAGCGGAGAC 743

RESULT 12

LOCUS BU927996 466 bp mRNA linear EST 18-OCT-2002
DEFINITION AGENCOURT 10434334 NIH MGC 126 Homo sapiens cDNA clone
IMAGE:6653558 5', mRNA sequence.

ACCESSION BU927996
VERSION BU927996.1 GI:24116726
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 466)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov

Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2903 row: m column: 14
High quality sequence stop: 437.

FEATURES

Location/Qualifiers

source

1..466
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6653558"
/tissue type="mixed (pool of 40 RNAs)"
/lab_host="PH108 (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggcgctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AACCTAGGTATCAGCAGATGGCGGCGGCGG-3' and
5'-ATTCTAGGCGGCGGCGGCGGCGGCGGCGGCGG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected using the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.02e-74 Length: 466
Score: 717.00 Matches: 135
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.28% Indels: 0
DB: 5 Gaps: 0

RESULT 15
 AW408076
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AW408076 389 bp mRNA linear EST 16-FEB-2000
 UI-HF-BM0-adu-d-01-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone
 IMAGE:3062832 5', mRNA sequence.
 AW408076
 AW408076.1 GI:6927133
 EST.
 Homo sapiens (human)
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward

FEATURES

Location/Qualifiers
 1..389
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3062832"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 38"
 /note="Vector: p77f3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (2.5-3.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. library preparation by Maria de Fatima
 Bonaudo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Alignment Scores:
 Pred. No.: 7.54e-64 Length: 389
 Score: 627.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.21% Mismatches: 0
 Query Match: 36.97% Indels: 0
 DB: 2 Gaps: 0

US-09-882-171-483 (1-329) x AW408076 (1-389)

QY 201 AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
 ::::|||||
 Db 7 GACATTCTGATCCATCTCTGCCCGGACGCTCTGTGCACACATCGCAATGGGCTTCGT 66
 :|||
 QY 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuValLeuLeu 240
 :|||
 Db 67 ACTCACACACCGGGTGTGTCAGCGTGTGGGTATGTTCTTCTGCTTCTCATTCG 126
 :|||
 QY 241 SerSerValPheLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeu 260
 :|||
 Db 127 TCTTCAGTGTGTTGTTCGCTTGTTCAGAGAGACAGATGCTGCCTCAAGAAACC 186
 :|||
 QY 261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp 280
 :|||
 Db 187 ATATACACATATATCATGCTTCAGGAACACCCAGCCAGCAGAGTCCAGATCTATGAT 246
 :|||
 QY 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300
 :|||

Search completed: February 5, 2005, 11:25:35
 Job time : 4346.06 secs

Db 247 GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCC 306
 :|||
 QY 301 GluValGlnPheAlaAspIleMetGlyLysAlaSerThrGlnAspSerLysProGly 320
 :|||
 Db 307 GAAGTGCAGTTTGTCTGATAAGATGGGAAAGCCAGCAGACACAGGACAGTAACCTCTCTGGG 366
 :|||
 QY 321 ThrSerSerTyrGluIleVal 327
 :|||
 Db 367 ACTTCAAGCTATGAAATTGTG 387
 :|||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2005, 03:24:06 ; Search time 3491.17 Seconds
(without alignments)
2761.994 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220

Perfect score: 1039

Sequence: 1 KDSBFTVNGILGESVTFPV.....NNSDSISARQLCADIANGFR 199

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

. Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DBV=xlh
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114004_26025/app_query.fasta_1.910
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09882171 @CGN_1_1_4930 @runat_04022005_114004_26025 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1039	100.0	967	9 AF054817	AF054817 Homo sapi
2	1039	100.0	984	9 CR541847	CR541847 Homo sapi
3	1039	100.0	1040	6 AX474268	AX474268 Sequence
4	1039	100.0	1040	9 HSU82988	U82988 Human leuko

5	1039	100.0	1067	9 AF054815	AF054815 Homo sapi
6	1039	100.0	1100	9 HSLDADC084	Y12632 H.sapiens m
7	1039	100.0	1118	9 AF054816	AF054816 Homo sapi
8	1039	100.0	1299	9 HSU96627	U96627 Homo sapien
9	1039	100.0	3173	6 BD191209	BD191209 186 human
10	1039	100.0	3173	6 AX924719	AX924719 Sequence
11	1039	100.0	3278	9 BC020063	BC020063 Homo sapi
12	1039	100.0	3296	6 CQ718714	CQ718714 Sequence
13	1039	100.0	3299	9 HSAJ3324	AJ223324 Homo sapi
14	1003	96.5	858	9 AF054818	AF054818 Homo sapi
15	610.5	58.8	1132	10 AF043445	AF043445 Mus muscu
16	571	55.0	1088	9 HSLDAL	AF101030 Homo sapi
17	571	55.0	175386	9 AL138930	AL138930 Human DNA
18	571	55.0	176698	2 AL355996	AL355996 Homo sapi
19	571	55.0	179614	2 AC012471	AC012471 Homo sapi
20	571	55.0	189057	2 AC027082	AC027082 Homo sapi
21	439	42.3	584	9 HSLDA2	AF101031 Homo sapi
22	439	42.3	70557	2 AC090143	AC090143 Homo sapi
23	439	42.3	70557	2 AC090143	AC090143 Homo sapi
24	439	42.3	179614	2 AC012471	AC012471 Homo sapi
25	352	33.9	2286	6 AX357541	AX357541 Sequence
26	352	33.9	2286	9 HUMLY9	L42621 Homo sapien
27	346	33.3	1350	6 CQ723314	CQ723314 Sequence
28	346	33.3	2334	6 CQ718717	CQ718717 Sequence
29	343.5	33.1	2448	9 AF244129	AF244129 Homo sapi
30	339	32.6	1847	9 AY007142	AY007142 Homo sapi
31	335	32.2	220349	2 AC118856	AC118856 Rattus no
32	335	32.2	232173	2 AC134805	AC134805 Rattus no
33	335	32.2	237455	2 AC096815	AC096815 Rattus no
34	332	32.0	652	6 AX474323	AX474323 Sequence
35	332	32.0	711	6 AX474326	AX474326 Sequence
36	332	32.0	870	6 AX474314	AX474314 Sequence
37	332	32.0	870	6 AX474332	AX474332 Sequence
38	332	32.0	870	6 AX474334	AX474334 Sequence
39	332	32.0	941	9 BC074754	BC074754 Homo sapi
40	332	32.0	1062	6 CQ728586	CQ728586 Sequence
41	332	32.0	1139	6 AX474313	AX474313 Sequence
42	332	32.0	1139	9 AF275725	AF275725 Homo sapi
43	332	32.0	1170	9 AY034613	AY034613 Homo sapi
44	332	32.0	1423	6 AX357479	AX357479 Sequence
45	331	31.9	870	6 AX474331	AX474331 Sequence

ALIGNMENTS

RESULT 1	AF054817	967 bp	mRNA	linear	PRI 01-JAN-2000
LOCUS	Homo sapiens leukocyte differentiation antigen CD84 isoform CD84d				
DEFINITION	(CD84) mRNA, complete cds.				
ACCESSION	AF054817				
VERSION	AF054817.1	GI:6650109			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 967)				
AUTHORS	Falou, E., Sole, J., Pirotto, F. and Gaya, A.				
TITLE	Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic,				
JOURNAL	Villarreal 170, Barcelona 08036, Spain				
FEATURES	Location/Qualifiers				
source	1..967				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
gene	1..967				
	/gene="CD84"				
CDS	70..888				
	/gene="CD84"				
	/codon_start=1				
	/product="leukocyte differentiation antigen CD84 isoform				

CD84d"
/protein_id="AAF21723.1"
/db_xref="GI:6650110"
/translation="MAQHHLWILLCLQTPPEAAGKDSIEFTVNGILGESVTFPVNIQ
EPQVKIATWTSKTSVAVYTPGDSPTAVVTVTHRYVERIHALGPNVNLVSLRME
DAGYKADINTQADPYTTTKRYNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
EKNTVNSPLGEENVLQIFQTPEDQELTYCTAQNPFVNSNDSISARQLCADTAMG
FRTHHTGLSVLANFFLLVLLSVFLFRFKRQGLQGRASHSLSFRSAVC"

ORIGIN

Alignment Scores:
Pred. No.: 1,14e-104 Length: 967
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AF054817 (1-967)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 133 AAAGACTCAGAAATCTTACAGTGAATGGATCTGGAGAGTCAGTCACATTCCTGTA 192
QY 21 AsnIleGlnGluProArgGlnValIleIleAlaTTPThrSerIysThrSerValAla 40
Db 193 AATATCCAGAACCCAGCGCAAGTTAAATCATTTGCTTGACTTCTAAACATCTGTGCT 252
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 253 TATGTAAACACGAGGACTCAGAAACAGACCCGCTAGTTACTGTGACCCACAGAAATAT 312
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 313 TATGAACGGATACATGCTTAGCTCGAATCAATCTGCTTGGAAACCAAAATATACACAGATT 372
QY 81 GluAspAlaGlyAspTyrIlyAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 373 GAAGACGCGAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACC 432
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 433 AAGCGCTACAACCTGCAATCATCTCGCTTGGAAACCAAAATATACACAGATT 492
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluGluGlu 140
Db 493 ATGGCATCTGTGAACAGCACCTGTAATGTACACTGACATGCTGCTGAGAGAAAGAA 552
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
Db 553 AAGATGTGACATACAAATTGGAGTCCCTGGAGAGAGGGTAATGTCCTTCAAAATCTTC 612
QY 161 GlnThrProGluAspGlnLeuLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 613 CAGACTCCTGAGACCAAGAGCTGACTACAGTGTACAGCCAGAACCTGTCTCAGCAAC 672
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 673 AATTCTGACTCATCTCTGCCCGGAGCTCTGTGAGACATCGCAATGGGCTTCGCT 729

RESULT 2

CR541847
LOCUS CR541847
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834H0132D for
gene CD84, CD84 antigen (leukocyte antigen); complete cds, without
stopcodon.

ACCESSION

CR541847.1 GI:49456648

VERSION

Full ORF shuttle clone, Gateway(TM), complete cds.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.REFERENCE
AUTHORS

1 (bases 1 to 984)
Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

TITLE

Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 984)

AUTHORS

Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

TITLE

Direct Submission

JOURNAL

Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer

COMMENT

Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD; RZPD0834H0132D, ORFNO 3790
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTCTT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_003874 (GI:4502686) we found
AA exchange(s) at position (first base of changed triplet):
880 (pro->ser)
Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES
source

1..984
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834H0132D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attPL; Site_2: attP2"

gene

1..984

CDS

1..->984
/gene="CD84"
/codon_start=1
/protein_id="CAG46645.1"
/db_xref="GI:49456649"
/translation="MAQHHLWILLCLQTPPEAAGKDSIEFTVNGILGESVTFPVNIQ
EPQVKIATWTSKTSVAVYTPGDSPTAVVTVTHRYVERIHALGPNVNLVSLRME
DAGYKADINTQADPYTTTKRYNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
EKNTVNSPLGEENVLQIFQTPEDQELTYCTAQNPFVNSNDSISARQLCADTAMG
FRTHHTGLSVLANFFLLVLLSVFLFRFKRQGLQGRASHSLSFRSAVC"
RIYDEILQSKVLPSKESVNTVYSEVQFADKMGKASTQDSKPPGTSYSYEIV"

ORIGIN

Alignment Scores:
Pred. No.: 1,16e-104 Length: 984
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0


```
US-09-882-171-483_COPY_22_220 (1-199) x CR541847 (1-984)
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 64 AAAGACTCAGAAATCTTACAGTGAATGGGATCTTGGAGAGTCACTTTCCTGTA 123
QY 21 AsnIleGlnGluProArgGlnValIleAlaTTPThrSerIysThrSerValAla 40
DB 124 AATATCCAAGAACCCAGCGCAAGTAAATCAATCTTGGACTTCTAAACATCTGTGCT 183
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 184 TATGTAAACACCAAGGACTCAGAAACAGACCGTAGTACTTGTGACCCACAGAAATTA 243
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 244 TATGAACGGATACATCGCTTAGCTCGCAATCTAATCTGGTCAATAGCGATCTGAGGATG 303
QY 81 GluAspAlaGlyAspTyrIysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 304 GAAGACGCGAGGACTACAAAGCAGACATAAATACAGCGCTGATCCCTACACCACC 363
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyIleProIysIleThrGlnSerLeu 120
DB 364 AAGCGTACAACTCGCAATCTATCGTCGGCTTGGGAAACCAAAATTAACAGAGTTTA 423
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluIysGlu 140
DB 424 ATGGCATCTGTGAACAGCACCTGTAATGTGCACACTGACATGCTCTCTAGAGAAAGAA 483
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGluValLeuGlnIlePhe 160
DB 484 AAGAATGTGCATACAAATGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAAAATCTTC 543
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 544 CAGACTCTGAGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTGTGCAGAAC 603
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 604 AATTCTGACTCCATCTCTGCGCGAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 660

RESULT 3
AX474268 1040 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 29 from Patent EP1223218.
DEFINITION AX474268
ACCESSION AX474268.1 GI:22213881
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Fraser, C.C.
AUTHORS Cd2000 and cd2001 molecules and uses thereof
TITLE Patent: EP 1223218-A 29 17-JUL-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source 1..1040
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1.25e-104 Length: 1040
Pred. No.: 1039.00 Matches: 199
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
```

```
CDS
42. 1028
/note="member of immunoglobulin superfamily"
/codon_start=1
/product="leukocyte antigen CD84"
/protein_id="AAB84364.1"
/db_xref="GI:2618740"
/translation="NAQHLLWILLCLQTPWPAAGKDSIEFTVNGILGESVTFPVNIO
EPROVKIANTSKTSVAVYTPGDSAPVTVTHRYNRYERHALGPNVNLVTSLRME
DAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITOSLMASVNSTCNVTITCSVEKE
EKNVTYNSPLGEEGNVLQIFQTPEDQELTYCTAONPVSNNSDISAROLCADIAMG
FRTHHTGLLSVLAMFLLVILSSVFLFKRRQDAASKKTIYIIMASNTQPAES
RIYDEILQSKVLPSKEEFPVNTVSYVQFADKMGKASTQDSKPPGTSSYEIV"
ORIGIN
1
LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
105
AAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTA 164
21
AsnIleGlnGluProArgGlnValIleLeuAlaThrThrSerLysThrSerValAla 40
165
AATATCCAGAACACCGGCAAGTAAATCAATCTGGACITCTAAACATCTGTGCT 224
41
TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
225
TATGTAACACACGAGACTCAGAAACAGCACCGCTAGTCTGTGACCCACACCAATAT 284
61
TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
285
TATGACCGATACATGCTTAGTTCGAACTCAATCTGGTCAATGAGATCTGAGGATG 344
81
GluAspAlaGlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
345
GAAGACGACGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 404
101
LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
405
AAGCGCTACAACTGCAATCTATCGTCGGCTTGGAAACCAAAAATATACACAGATTTA 464
121
MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
465
ATGGCATCTGTGAACAGACCTGTATGTACACTGACATGCTCTGTAGAGAAAGAGAA 524
141
LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
525
AAGAATGTGACATACAAATGGAGTCCCTGGGAGAAGAGGTAATGTCTTCAATCTTC 584
161
GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
585
CAGACTCTCTAGGACCAAGAGCTGACTTACAGCTGTACAGCCCAAGACCTCTGCAAC 644
181
AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
645
AATCTGACTCCTATCTTGCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCCGT 701
RESULT 5
AF054815
LOCUS
DEFINITION
Homo sapiens leukocyte differentiation antigen CD84 isoform CD84c
ACCESSION
AF054815
VERSION
AF054815.1
GI:6650105
KEYWORDS
Homo sapiens (human)
```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Palou.E., Sole.J., Piroto,F. and Gaya.A.
TITLE Direct Submision
JOURNAL Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
FEATURES
Location/Qualifiers
1..1067
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1067
/gene="CD84"
70..1056
/gene="CD84"
/codon_start=1
/product="leukocyte differentiation antigen CD84 isoform CD84c"
/protein_id="AAF21721.1"
/db_xref="GI:6650106"
/translation="MAQHLLWILLCLQTPWPAAGKDSIEFTVNGILGESVTFPVNIO
EPROVKIANTSKTSVAVYTPGDSAPVTVTHRYNRYERHALGPNVNLVTSLRME
DAGDYKADINTQADPYTTTKRYNLQIYRRLGPKKITOSLMASVNSTCNVTITCSVEKE
EKNVTYNSPLGEEGNVLQIFQTPEDQELTYCTAONPVSNNSDISAROLCADIAMG
FRTHHTGLLSVLAMFLLVILSSVFLFKRRQDAASKKTIYIIMASNTQPAES
RIYDEILQSKVLPSKEEFPVNTVSYVQFADKMGKASTQDSKPPGTSSYEIV"

Alignment Scores:
Pred. No.: 1,25e-104 Length: 1040
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x HSU82988 (1-1040)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 105 AAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTA 164
QY 21 AsnIleGlnGluProArgGlnValIleLeuAlaThrThrSerLysThrSerValAla 40
Db 165 AATATCCAGAACACCGGCAAGTAAATCAATCTGGACITCTAAACATCTGTGCT 224
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 225 TATGTAACACACGAGACTCAGAAACAGCACCGCTAGTCTGTGACCCACACCAATAT 284
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 285 TATGACCGATACATGCTTAGTTCGAACTCAATCTGGTCAATGAGATCTGAGGATG 344
QY 81 GluAspAlaGlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
Db 345 GAAGACGACGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 404
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 405 AAGCGCTACAACTGCAATCTATCGTCGGCTTGGAAACCAAAAATATACACAGATTTA 464
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
Db 465 ATGGCATCTGTGAACAGACCTGTATGTACACTGACATGCTCTGTAGAGAAAGAGAA 524
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 525 AAGAATGTGACATACAAATGGAGTCCCTGGGAGAAGAGGTAATGTCTTCAATCTTC 584
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 585 CAGACTCTCTAGGACCAAGAGCTGACTTACAGCTGTACAGCCCAAGACCTCTGCAAC 644
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 645 AATCTGACTCCTATCTTGCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCCGT 701

US-09-882-171-483_COPY_22_220 (1-199) x AF054815 (1-1067)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 133 AAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTA 192
QY 21 AsnIleGlnGluProArgGlnValIleLeuAlaThrThrSerLysThrSerValAla 40
Db 193 AATATCCAGAACACCGGCAAGTAAATCAATCTGGACTTCTAAACATCTGTGCT 252
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 253 TATGTAACACACGAGAGACTCAGAAACAGCACCGCTAGTCTGTGACCCACAGAAATAT 312
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 313 TATGACCGATACATGCTTAGTTCGAACTCAATCTGGTCAATGAGATCTGAGGATG 372
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
Db 373 GAAGCGCAGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 432
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 433 AAGCGCTACAACTGCAATCTATCGTCGGCTTGGAAACCAAAAATATACACAGATTTA 492
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
Db 493 ATGGCATCTGTGAACAGACCTGTATGTACACTGACATGCTCTGTAGAGAAAGAGAA 552
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 553 AAGAATGTGACATACAAATGGAGTCCCTGGGAGAAGAGGTAATGTCTTCAATCTTC 612
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180

```

613 CAGACTCTGAGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGCAGAAC 672
|||||
181 AnSerAspSerIleSerAlaArgGlnLeuGlyAlaAspIleAlaMetGlyPheArg 199
|||||
673 AATTCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 729
|||||

RESULT 6
HSLDACD84      1100 bp  mRNA  linear  PRI 04-JAN-2002
LOCUS          H. sapiens mRNA for leukocyte differentiation antigen CD84.
DEFINITION
ACCESSION      Y12632
VERSION        Y12632.1 GI:18073112
KEYWORDS       leukocyte differentiation antigen.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS       Gaya, A.
JOURNAL       Unpublished
2 (bases 1 to 1100)
AUTHORS       Gaya, A.
TITLE         Direct Submission
JOURNAL       Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
FEATURES
source
1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="leukocyte"
/clone_lib="lambda gt10"
70..1089
/codon_start=1
/product="leukocyte differentiation antigen CD84"
/protein_id="CAA73181.1"
/db_xref="GI:18073113"
/db_xref="Uniprot/TREMBL:Q8WW18"
/translation="MAQHLLWLLLCLOTWPEAGKDSEIFTVNGILGSVTPPVNIQ
EPQVKIIAINTSKTSVAYVTPGSETAPVTVTHRYNRYERIHAGPNYNLVISDLRME
DAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSLMASVNSCTNVLTCSEVEKE
EKVNTYNSPLBEGNVLOI FOTPEOELTYTCTAQNPSVNSDSISARQLCADIANG
FRTHYTGLLSLVAMFLLVILSSVFLRLFKRQGRIPPEGSCLTFTKNPYAASKKIYTYI
MASRNTQPAESRIYDEILQSKVLPSPKEEPVNTYVSEVQFADKMGKASTQDSKPTGTS
YEIVI"
sig_peptide   70..132
mat_peptide   133..1086
/product="leukocyte differentiation antigen CD84"

ORIGIN
Alignment Scores:
Pred. No.:      1.34e-104      Length:      1100
Score:          1039.00        Matches:      199
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:              9           Gaps:        0

US-09-882-171-483_COPY_22_220 (1-199) x HSLDACD84 (1-1100)

Qy      1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
|||||
Db      133 AAAGACTCAGAAATCTTCACAGTGAATGGGATTTCTGGAGAGTCAGTCATTTCCCTGTA 192
|||||

Qy      21 AsnIleGlnIleProArgGlnValIleIleAlaTrpThrSerLysThrSerValAla. 40
|||||
Db      193 AATATCCAGAACACCGCAAGTTAAATCATCTCTGGACTTCTAAACATCTGTGCT 252
|||||

Qy      41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
|||||
Db      253 TATGTAACACCCAGGAGACTCAGAAACAGCACCCCGCTAGTTACTGTGACCCAGAAATAT 312
|||||

```

```

Qy      61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
|||||
Db      313 TATGAACGGATACATCGCTTAGGTCGAACTCAATCTGGTCATTAGCGATCTGAGGATG 372
|||||

Qy      81 GluAspAlaGlyAspTyrIlyslAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
|||||
Db      373 GAAGACGGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 432
|||||

Qy      101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
|||||
Db      433 AAGCGCTACACCTGCAATCTATCTGCGCTGGGAACCAAAATATACACAGAGTTTA 492
|||||

Qy      121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlnLysGluGlu 140
|||||
Db      493 ATGGCATCTGTGAACAGCACCTGTAATGTCACTGACATGCTCTGTAGAGAAAGAGAA 552
|||||

Qy      141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGluValLeuGlnIlePhe 160
|||||
Db      553 AAGAATGTGACATACAAATTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTTC 612
|||||

Qy      161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
|||||
Db      613 CAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGCAGAAC 672
|||||

Qy      181 AnSerAspSerIleSerAlaArgGlnLeuGlyAlaAspIleAlaMetGlyPheArg 199
|||||
Db      673 AATTCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 729
|||||

RESULT 7
AF054816      1118 bp  mRNA  linear  PRI 01-JAN-2000
LOCUS          Homo sapiens leukocyte differentiation antigen CD84 isoform CD84a
DEFINITION
ACCESSION      AF054816
VERSION        AF054816.1 GI:6650107
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1118)
AUTHORS       Palou, E., Sole, J., Piroto, F. and Gaya, A.
TITLE         Direct Submission
JOURNAL       Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
FEATURES
source
1..1118
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1118
/gene="CD84"
70..1107
/gene="CD84"
/codon_start=1
/product="leukocyte differentiation antigen CD84 isoform
CD84a"
/protein_id="AAF21722.1"
/db_xref="GI:6650108"
/translation="MAQHLLWLLLCLOTWPEAGKDSEIFTVNGILGSVTPPVNIQ
EPQVKIIAINTSKTSVAYVTPGSETAPVTVTHRYNRYERIHAGPNYNLVISDLRME
DAGDYKADINTQADPYTTTKRYNLQIYRRLGPKITQSLMASVNSCTNVLTCSEVEKE
EKVNTYNSPLBEGNVLOI FOTPEOELTYTCTAQNPSVNSDSISARQLCADIANG
FRTHYTGLLSLVAMFLLVILSSVFLRLFKRQGRIPPEGSCLTFTKNPYAASKKIYTYI
TIITYIMASRNTQPAESRIYDEILQSKVLPSPKEEPVNTYVSEVQFADKMGKASTQDSK
PPTGTSYEIVI"
ORIGIN
Alignment Scores:
Pred. No.:      1.37e-104      Length:      1118
Score:          1039.00        Matches:      199
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```


Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H.
 186 human secreted proteins
 Patent: JP 2002510192-A 173 02-APR-2002;
 HUMAN GENOME SCIENCES INC
 COMMENT
 PN JP 2002510192-A/173
 PD 02-APR-2002
 PF 06-MAR-1998 JP 1998538883
 PR 07-MAR-1997 US 60/040162, 07-MAR-1997 US 60/040333 PR
 07-MAR-1997 US 60/038621, 07-MAR-1997 US 60/040161 PR
 07-MAR-1997 US 60/040626, 07-MAR-1997 US 60/040334 PR
 07-MAR-1997 US 60/040336, 07-MAR-1997 US 60/040163 PR
 11-APR-1997 US 60/043580, 11-APR-1997 US 60/043568 PI
 STEVEN
 M RUBEN, CRAIG A ROSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI
 KENNETH C CARTER, DANIEL P BEDNARIK, GREGORY
 A ENDRESS, GUO LIANG
 PI YU, JIAN NI,
 PI PING FENG, PAUL E YOUNG, JOHN M GREENE, ANN
 M FERRIE, ROXANNE DUAN,
 PI JING SHAN HU, KIMBERLY A FLORENCE, HENRIK
 S OLSEN, REINHARD EBER, PI
 LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI
 , YI LI, ZHIZHEN ZENG,
 PI HLA KVAM
 PC C12N15/12, C12N5/10, C12N1/21, C07K14/47, C07K16/18, C12Q1/68, PC
 G01N33/50,
 PC G01N33/53, G01N33/68, A61K38/17
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers.
 FEATURES
 source
 1. .3173
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.24e-104 Length: 3173
 Score: 1039.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-882-171-483_COPY_22_220 (1-199) x BD191209 (1-3173)
 QY 1 LysAspSerGluThrValAsnGlyLeuGluSerValThrPheProVal 20
 DB 114 AAGACTCAGAAATCTTCACAGTGAATGGATCTGGAGAGTCAGTCACATTTCCCTGTA 173
 QY 21 AsnIleGlnGluProArgGlnValIleAlaTrpThrSerLysThrSerValAla 40
 DB 174 AATATCCAAGAACCCAGCGCAAGTTAAATCATTTGGACTTCTAAACATCTGTGCT 233
 QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
 DB 234 TATGTAACACAGGAGACTCAGAACACGACCCGCTAGTTACTGTGACCCACAGAAATAT 293
 QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 DB 294 TATGAACGGATACATGCTTAGTGCCGAATCACTCAATCTGGTCAATACCGATCTGAGATG 353
 QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
 DB 354 GAAGACGACGAGACTCAAGACAGACATAAATACACAGGCTGATCCTACACCACC 413
 QY 101 LysArgTyrAsnLeuGlnIleTyrArgGluGlyLysProLysIleThrGlnSerIeu 120
 DB 414 AAGCGCTACAACTGCAAACTATCTCGTGGCTTGGGAAACCAAAAATTTACACAGATT 473
 QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 DB 474 ATGGCATCTGTGAACAGACACCTGTAAATGTCTACATGTACATCTCTGTAGAGAAAGAGAA 533
 QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
 DB 534 AAGAATGTGACATACATAATTTGGAGTCCCTGGGAGAGAGGGTAAATGCTCTTCAATCTTC 593
 QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
 DB 594 CAGACTCTCTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTGTTCAGCAAC 653
 QY 181 AsnSerAspSerIleSerAlaArgGlnIleuCysAlaAspIleAlaMetGlyPheArg 199
 DB 654 AATTCTGATCTCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCCT 710
 RESULT 10
 AX924719 3173 bp DNA linear PAT 19-DEC-2003
 LOCUS
 DEFINITION Sequence 174 from Patent EP1352962.
 ACCESSION AX924719
 VERSION AX924719.1 GI:40242664
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified
 unclassified
 REFERENCE
 1 Olsen, H.S., Yu, G.L., Endress, G.A., Bednarik, D.P., Carter, K.C.,
 Feng, P., Soppet, D.R., Young, P.E., Duan, D.R., Florence, K.A.,
 Greene, J.M., Fischer, C.L., Hu, J.S., Ruben, S.M., Ebner, R.,
 Brewer, L.A., Ferrie, A.M., Moore, P.A., Ni, J., Shi, Y., Lafleur, D.W.,
 Li, Y., Zeng, Z., Kyaw, H. and Rosen, C.A.
 186 human secreted proteins
 Patent: EP 1352962-A 174 15-OCT-2003;
 HUMAN GENOME SCIENCES, INC. (US)
 TITLE
 JOURNAL
 FEATURES
 source
 1. .3173
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.24e-104 Length: 3173
 Score: 1039.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-882-171-483_COPY_22_220 (1-199) x AX924719 (1-3173)
 QY 1 LysAspSerGluThrValAsnGlyLeuGluSerValThrPheProVal 20
 DB 114 AAGACTCAGAAATCTTCACAGTGAATGGATCTGGAGAGTCAGTCACATTTCCCTGTA 173
 QY 21 AsnIleGlnGluProArgGlnValIleAlaTrpThrSerLysThrSerValAla 40
 DB 174 AATATCCAAGAACCCAGCGCAAGTTAAATCATTTGGACTTCTAAACATCTGTGCT 233
 QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
 DB 234 TATGTAACACAGGAGACTCAGAACACGACCCGCTAGTTACTGTGACCCACAGAAATAT 293
 QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 DB 294 TATGAACGGATACATGCTTAGTGCCGAATCACTCAATCTGGTCAATACCGATCTGAGATG 353
 QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
 DB 354 GAAGACGACGAGACTCAAGACAGACATAAATACACAGGCTGATCCTACACCACC 413
 QY 101 LysArgTyrAsnLeuGlnIleTyrArgGluGlyLysProLysIleThrGlnSerIeu 120
 DB 414 AAGCGCTACAACTGCAAACTATCTCGTGGCTTGGGAAACCAAAAATTTACACAGATT 473
 QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 DB 474 ATGGCATCTGTGAACAGACACCTGTAAATGTCTACATGTACATCTCTGTAGAGAAAGAGAA 533

QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 Db |||||
 474 ATGGCATCTGTGAACAGCACCTGTATGTACACAGTGTCTGTAGAGAAAGAA 533
 QY 141 LysAsnValThrTyxAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
 Db |||||
 534 AAGATGTGACATACATAATTTGGAGTCCCTGGGAGAGAGGTAATGTCTCAATCTTC 593
 QY 161 GlnThrProGluAspGlnGluLeuThrTyxThrCysThrAlaGlnAsnProValSerAsn 180
 Db |||||
 594 CAGACTCTCTAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGACCCCTGTACGCAAC 653
 QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
 Db |||||
 654 AATTCGTCTCCATCTCTCCCGGAGCTCTGTGAGACATCGCAATGGCTTCCT 710

RESULT 11
 BC020063
 LOCUS 3278 bp mRNA linear PRI 29-JUN-2004
 DEFINITION Homo sapiens CD84 antigen (leukocyte antigen), mRNA (cDNA clone
 MGC:21324 IMAGE:4385965), complete cds.
 ACCESSION BC020063
 VERSION BC020063.1 GI:18043042
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 3278)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Uscin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

TITLE
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 2 (bases 1 to 3278)
 REFERENCE Strausberg, R.
 AUTHORS Direct Submission
 TITLE Submitted (19-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue procurement: Lou Staudt
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: ang@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Ioulesged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 26 Row: 0 Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4502686.

FEATURES

Location/Qualifiers
 source
 1..3278
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:21324 IMAGE:4385965"
 /tissue_type="Lymph, Lymphoma"
 /clone_lib="NIH_MGC_85"
 /lab_hosts="DH10B"
 /note="Vector: PCMV-SPORT6"
 gene
 1..3278
 /gene="CD84"
 /note="synonyms: SLAMF5, hCD84, mCD84, LY9B"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 25..1011
 /gene="CD84"
 /codon_start=1
 /product="CD84 antigen (leukocyte antigen)"
 /protein_id="AAH20063.1"
 /db_xref="GI:18043043"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 /translation="MAQHHLWLLLCLOTWPEAAKGDSBIFTVNGILGESVTFPNIQ
 EPRQVKIANTSKTSVAYTPVTPGDSAPVTVTHRYVYRIHALGPNVNLVSLRME
 DAGYKADINTQADPTTKRYNLQIVYRLGPKITQSLMASVNSCTNVTITCSVEKE
 EKNVTYVNSPLGESEGNVLQIQTPEDELTCTTAONPVSNNSDISARQICADIAMG
 FRTHHTGLLSVLAMFFLLVLLSVFRLFKRQDAASKKTIYTIMASNTQPAES
 RIYDEILQSLKPLSKPEPVNTVSEVQFADKMGKASTQDSKPKTSSYEIVL"

ORIGIN

Alignment Scores:
 Pred. No.: 5,46e-104 Length: 3278
 Score: 1039.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-882-171-483_COPY_22_220 (1-199) x BC020063 (1-3278)
 QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
 Db 88 AAAGACTCAGAAATCTTCACAGTGAATGGGATTCCTGGGAGAGTCAGTCACATTCCTCTGTA 147
 QY 21 AsnIleGlnGluProArgGlnValIleIleAlaTrpThrSerLysThrSerValAla 40
 Db 148 AATATCCAAAGAACCCAGCAAGTAAATCAATTCCTTGGACTTCATAAACATCTGTGCT 207
 QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
 Db 208 TATGTAAACACAGGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 267
 QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 Db 268 TATGAACGGATACATGCTTAGCTCCGAACTACAACTCTGGTCAATAGCATCTAGGATG 327
 QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
 Db 328 GAAGACGGAGAGACTCAAAAGCAGACATAAATACACAGGCTGATCCCTACACCAACCACC 387
 QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
 Db 388 AAGCGCTACACCTGCAATCTATCGTCGGCTTGGGAAACCAAAATATACACAGAGTTTA 447
 QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 Db 448 ATGGCATCTGTGAACAGCACCTGTAAATGTACATGTCACATGCTCTGTAGAGAAAGAA 507

QY 141 LysAsnValThrTyrrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 508 AAGAATGTGACATACATAATGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTC 567
QY 161 GlnThrProGluAspGlnGluLeuThrTyrrThrCysThrAlaGlnAsnProValSerAsn 180
Db 568 CAGATCTCTGAGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCTGTGCAGAAC 627
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 628 AATTCTGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTTCCT 684
RESULT 12
LOCUS CQ718714 3296 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 4648 from Patent WO02068579.
ACCESSION CQ718714
VERSION CQ718714.1 GI:42279571
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 4648 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1. 3296
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 5.5e-104 Length: 3296
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-882-171-483_COPY_22_220 (1-199) x CQ718714 (1-3296)
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 106 AAGACTCAGAAATCTTCACAGTGAATGGGATCTCGGAGAGTCAGTCATCTCCCTGTA 165
QY 21 AsnIleGlnGluProArgGlnValIleAlaTrpThrSerTyrrSerValAla 40
Db 166 AATATCAAGAACCAACGCGCAAGTTAAATCATCTCTGGACTCTAAACATCTGTGTCT 225
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 226 TATGTAACACCCAGAGAGACTCAGAAACAGCACCCCGTAGTTACTGTGACCCACAGAAATAT 285
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 286 TATGACGGATACATGCTTAGTCCGAACTACAACTCATCTGTCATTACCGATCTGAGATG 345
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
Db 346 GAACACGACGAGACTCAAGACAGACATAAATACACAGGCTGATCCTACACCAACC 405
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerIleu 120
Db 406 AAGCGCTACACCTGCAAATCTATCGCGCTTGGAAACCAAAATATACACAGAGTTTA 465
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140

Db 466 ATGGCATCTGTGACAGCACCTGTAAATGTGCACACTGCATGCTCTGTAGAGAAAGAA 525
QY 141 LysAsnValThrTyrrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 526 AAGAATGTGACATACATAATGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTC 585
QY 161 GlnThrProGluAspGlnGluLeuThrTyrrThrCysThrAlaGlnAsnProValSerAsn 180
Db 586 CAGATCTCTGAGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCTGTGCAGAAC 645
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 646 AATTCTGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTTCCT 702
RESULT 13
LOCUS HSAJ3324 3299 bp mRNA linear PRI 07-APR-2000
DEFINITION Homo sapiens mRNA for MAX.3 cell surface antigen.
ACCESSION AJ223324
VERSION AJ223324.1 GI:3392916
KEYWORDS cell surface antigen; glycoprotein; MAX.3 antigen.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Andreessen, R., Bross, K.J., Osterholz, J. and Emrich, F.
TITLE Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens
JOURNAL Blood 67 (5), 1257-1264 (1986)
MEDLINE 86188202
PUBMED 3008886
REFERENCE 2
AUTHORS Krause, S.W., Rehli, M., Heinz, S., Ebner, R. and Andreessen, R.
TITLE Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with CD84
JOURNAL Biochem. J. 346 Pt 3, 729-736 (2000)
MEDLINE 20164057
PUBMED 10698700
REFERENCE 3 (bases 1 to 3299)
AUTHORS Krause, S.W.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1998) Krause S.W., Hematology, University of Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042, GERMANY
FEATURES
source Location/Qualifiers
1. 3299
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HDPFF19"
/cell_type="dendrite"
45. 1031
/codon_start=1
/evidence=experimental
/product="MAX.3 cell surface antigen"
/protein_id="CAAL1264.1"
/db_xref="GI:3392917"
/db_xref="GOA:O15430"
/translation="MAQHLMLLLCLQWPEAAGKDSSEIFTVNGILGESVTPPVNIQEPQVKIIAWTSKTSVAYTPGDSFAPVTVTHRYRIHALGPNYNIASDLRME DAGDYKADINTQADPYTKRYNLQIYRIGKPKITQSLMASVNSTCNVTLTCSVEKE EKNYTNWSPGLGEENVLQIFQTPDELTYYTCTAQNPVSNNSDSISARQLCADIAMG FRTHYTGLLSVLAMFLLVILSSVFLFRLFKRRQDAASKKTIYTIMASRNTQPAES RIYDEILQSKVLPSPKEPVNTVYSEVQFADKMGKASTQDSKPPGTSSEYIVI"
45. 107
sig_peptide
mat_peptide 108. 1028
/product="MAX.3 cell surface antigen"
ORIGIN

Alignment Scores:
 Pred. No.: 5,51e-104 Length: 3299
 Score: 1039.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x HSAJ3324 (1-3299)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
 DB 108 AAAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTA 167
 QY 21 AsnIleGlnGluProArgGlnValIleAlaThrThrSerLysThrSerValAla 40
 DB 168 ATATCCAGAACACCGCAAGCTTAATCATTTGCTTGGACTTCTAAACATCTGTGCT 227
 QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
 DB 228 TATGTAAACACAGGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 287
 QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 DB 288 TATGAACGGATACATCGCTTAGGTCGGAACATACTAGTCAATGAGGATCTGAGGATG 347
 QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
 DB 348 GAAGACGACGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACC 407
 QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
 DB 408 AAGCGCTACAACTCGCAATCTATCGTCGGCTTGGGAAACCAAAATATACACAGAGTTTA 467
 QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 DB 468 ATGGCATCTGTGAACAGCACCTGTATGTCACACTGACATGCTCTGTAGAGAAAGAGAA 527
 QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyGluAsnValLeuGlnIlePhe 160
 DB 528 AAGAATGTGACATACAAATGGAGTCCCTGGGAGAGAGGGTAAATGTCCTCAAAATCTTC 587
 QY 161 GlnThrProGluAspGlnIleuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
 DB 588 CAGACTCCTGAGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGAGCAAC 647
 QY 181 AsnSerAspSerIleAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
 DB 648 AATCTGACTCCATCTCTGCCGGCAGCTCTGTGACAGACATCGCAATGGGCTTCGGT 704

RESULT 14
 AF054818 858 bp mRNA linear PRI 01-JAN-2000
 LOCUS Homo sapiens leukocyte differentiation antigen CD84 isoform CD84s
 DEFINITION (CD84) mRNA, complete cds.

ACCESSION AF054818
 VERSION AF054818.1 GI:6650111

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 858)

Palou,E., Sole,J., Pirotto,F. and Gaya,A.

Direct Submission

Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic,

Villarreal 170, Barcelona 08036, Spain

Location/Qualifiers

1..858

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

RESULT 15

AF043445

LOCUS

Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.

DEFINITION

AF043445

ACCESSION

AF043445.1 GI:4105142

VERSION

KEYWORDS

gene

CDS

1..858

/gene="CD84"

70..795

/gene="CD84"

/codon_start=1

/product="leukocyte differentiation antigen CD84 isoform

CD84s"

/protein_id="AAP21724.1"

/db_xref="GI:6650111"

/translation="MAQHLEWILLCLQWPEAGKDSIEFTVNGILGESVTFPNIQ

EPKVKLIATWTSKTSVAIVTPGDSAPVTVTHRYVRIHALGPNVNLVLSRME

DAGYKADINTQADPYTKRYNLQIYRRLGPKKITQSLMASVNSTCNVLTCSVKE

EKNVYVNSPLGEGNVLOIFOTPEDQLFTVCTAQNPFVSNNSDSISARQLCAGNQLC

PSLLVSLRDSHEELQGLNVGHIL"

ORIGIN

Alignment Scores:

Pred. No.: 9.01e-101 Length: 858

Score: 1003.00 Matches: 192

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 96.54% Indels: 0

DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AF054818 (1-858)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
 DB 133 AAAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTA 192
 QY 21 AsnIleGlnGluProArgGlnValIleAlaThrThrSerLysThrSerValAla 40
 DB 193 AATATCCAGAACACCGCAAGTAAATCATTTGCTTGGACTTCTAAACATCTGTGCT 252
 QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
 DB 253 TATGTAAACACCGAGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 312
 QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 DB 313 TATGAACGGATACATGCTTAGGTCGGAACATAATACACAGGCTGATCCCTACACACCACC 372
 QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
 DB 373 GAAGACGACGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACC 432
 QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
 DB 433 AAGCGCTACAACTCGCAATCTATCGTCGGCTTGGGAAACCAAAATATACACAGAGTTTA 492
 QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 DB 493 ATGGCATCTGTGAACAGCACCTGTAAATGTACATGACATGCTCTGTAGAGAAAGAGAA 552
 QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyGluAsnValLeuGlnIlePhe 160
 DB 553 AAGATGTGACATACAAATGGAGTCCCTGGGAGAGAGGGTAAATGTCCTCAAAATCTTC 612
 QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
 DB 613 CAGACTCCTGAGGACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCCCTGTGAGCAAC 672
 QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAla 192
 DB 673 AATCTGACTCCATCTCTGCCGGCAGCTCTGTGACAGACATCGCAATGGGCTTCGGT 708

RESULT 15

AF043445

LOCUS

Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.

DEFINITION

AF043445

ACCESSION

AF043445.1 GI:4105142

VERSION

KEYWORDS

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1132)
 de la Fuente, M.A., Tovar, V., Pizcueta, P., Nadal, M., Bosch, J. and Engel, P.
 TITLE Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell surface molecules
 JOURNAL Immunogenetics 49 (4), 249-255 (1999)
 MEDLINE 99180614
 PUBMED 10079287
 REFERENCE 2 (bases 1 to 1132)
 de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.
 AUTHORS Direct Submission
 TITLE Submitted (17-JAN-1998) Immunology Unit, Department of Cellular Biology, Medical School, University of Barcelona, Casanova 143, Barcelona 08036, Spain
 JOURNAL Location/Qualifiers
 FEATURES
 Source
 1..1132
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /chromosome="1"
 /map="close to ly-9"
 /cell_type="macrophage"
 /tissue_type="peritoneum"
 1..1132
 /gene="CD84"
 55..1044
 /gene="CD84"
 /codon_start=1
 /product="CD84 leukocyte antigen"
 /protein_id="AAD02273.1"
 /db_xref="GI:4105143"
 /translations="MAQRHLWIFLCIQTWSAAGKADPVMVNGILGESVTFLLNIQ
 EPKIDNIANTSSVAFIKPGVNAEVIITQGYKRIEIIDQYDLVIRDLRMEDA
 GYTKADINEENETITKIYHLIYRLKTPKITQSLISLNNCTNITLCSVEKEKD
 VTVSFPFEEKSVLQIVHSMDQKLTITTAQNPVSNSSDVTVOQPCDTIPSPHPR
 HAVLPGLAVFLILLIPLMLFLRLYKRDRIVLEADVDVSKKTVYAVVSRNAQPT
 SRIYDEIPQSKMLSKCKDPVTITTYSSVQLSEKMKETNMKDRSLPKALGNEIVV"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,18e-57 Length: 1132
 Score: 610.50 Matches: 119
 Percent Similarity: 78.24% Conservative: 32
 Best Local Similarity: 61.66% Mismatches: 39
 Query Match: 58.76% Indels: 3
 DB: 10 Gaps: 2
 US-09-882-171-483_COPY_22_220 (1-199) x AF043445 (1-1132)
 Qy 1 LysAspSerGluThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
 Db 118 AAGATCGACCGCGGTGAATGAATGGGATCTTGGGAGTCAGTACTTTCCTT 177
 Qy 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
 Db 178 AATATTCAAGACCAAGAAATTTGACACATTCCTGGACTTCTCAATCATCTGTGCT 237
 Qy 41 TyrValThrProGlyAspSerGluThrAlaProValThrValThrHisArgAsnTyr 60
 Db 238 TTTATAAACACGAGGTCATTAAGCTGAA-----GTTACCATTAACCCAGGCGACTTAT 291
 Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
 Db 292 AAGGACGATAGAAATCATAGATCAGAGATGACCTGGTCTATTAGACCTGAGGATG 351
 Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
 Db 352 GAAGATCGAGGACCTTACAAAGCAGACATCAATGAAGAGAATGAGGAA---ACCATCACC 408

Qy 101 LysAspGlyTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
 Db 409 AAGATCTACTACTCTCATATCTACCGTCGACTTAAACACCAAAATATACACAGATTTG 468
 Qy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
 Db 469 ATATCATCTTTTGAACAATACCTGTAAATATACACACTGACATGCTCTGTGGAAGGAAGAA 528
 Qy 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
 Db 529 AAGGATGTACATATAGCTGGAGTCCCTTTGGAGAGAAAGCAATGCTCTTCAATTCGTC 588
 Qy 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
 Db 589 CACTCCCCCATCGACCAAAACTGACCTACACATGTACAGCCCAAGAACCTGTTCAGCAAC 648
 Qy 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAsp 193
 Db 649 AGTTCTGACTCTGTCACTGTCCAGCAGCCATGTACAGAC 687

Search completed: February 5, 2005, 09:29:31
 Job time : 3495.17 secs

Blank (uspio)

XX EP1223218-A1.
PN
XX
PD 17-JUL-2002.
XX
PF 02-NOV-2001; 2001EP-00309339.
XX
XX 03-NOV-2000; 2000US-00706167.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Fraser CC;
PI
XX WPI: 2002-620680/67.
XX P-PSDB; AAE26238.
DR
XX
XX Novel isolated polypeptide containing immunoglobulin and immunoglobulin-like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders.
PT
PT
XX
XX Disclosure; Page 76; 139pp; English.
XX
XX The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. asthma and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in gene therapy. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 DNA used in the invention
XX
SQ Sequence 1040 BP; 308 A; 256 C; 231 G; 245 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.75e-106 Length: 1040
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AAD43563 (1-1040)

QY 1 LysAspSerGluLeuPheThrValAlaGlnIleLeuGlyGluSerValThrPheProVal 20
Db 105 AAAGACTCAGAAATCTTACAGTGAATGGGATCTTGGGAGAGTCAGTCACTTCCCTGTA 164
QY 21 AsnIleGlnGluProArgGlnValIleAlaTrpThrSerIysThrSerValAla 40
Db 165 AATATCCAAGAACCCAGGCAAGTTAAATCATTTGTTGGACTTCTAAACATCTGTGCT 224
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValHisArgAsnTyr 60
Db 225 TATGTAAACACAGGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAATAT 284
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 285 TATGAACGGATCATGCTTGGTCCGAACACTCAATCTGGTCATTAGCGATCTGAGGATG 344
QY 81 GluAspAlaGlyAspTyrIysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

Db 345 GAAGCGCAGGAGACTACAAAGCAGACATAAATACAGAGGTGATCCCTACACCACCACC 404
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 405 AAGCGCTACAACTGCAATCTATCGTCGGCTTGGGAAACCAAAATTTACACAGAGTTTA 464
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 465 ATGGCATCTGTGAACAGACACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAGAA 524
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 525 AAGAATGTGACATACATAATTGGAGTCCCTGGGAGAGAGGGTAATGTCTCTCAATCTTC 584
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 585 CAGACTCTCTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCGACAGACCTGTCTCAGCAAC 644
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 645 AATCTGACTCAATCTCTGCGCGGAGCTCTGTGCGACATCGCAATGGGCTTCCGT 701

RESULT 2
ADO05707
XX ID ADO05707 standard; DNA; 1067 BP.
XX AC ADO05707;
XX DT 15-JUL-2004 (first entry)
XX DE Human leukocyte differentiation antigen CD84 encoding DNA.
XX KW T cell; antiallergic; immunosuppressive; virucide; antibacterial;
KW antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds;
KW leukocyte differentiation antigen.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 70..1056
FT /*tag= a
FT /product= "CD84"
XX WO2004032867-A2.
XX PD 22-APR-2004.
XX PF 09-OCT-2003; 2003WO-US032065.
XX PR 09-OCT-2002; 2002US-0417102P.
PR 09-OCT-2002; 2002US-0417103P.
PR 09-OCT-2002; 2002US-0417243P.
PR 18-OCT-2002; 2002US-0419575P.
PR 08-NOV-2002; 2002US-0424777P.
PR 08-NOV-2002; 2002US-0424881P.
XX (TOLE-) TOLERRX INC.
PA Rao P, Szymanska G;
XX WPI: 2004-340801/31.
DR P-PSDB; ADO05708.
DR GENBANK; 6650105.
XX
PT Treating a condition that benefits from modulating regulatory or effector
PT T cell function comprises administering an agent that modulates the
PT expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbeta1,
PT Jagged-1 or GPR-32).
XX Example; SEQ ID NO 7; 161pp; English.
XX The invention relates to treating a subject having a condition that

CC benefits from modulating the balance of regulatory T cell function
CC relative to effector T cell function, or vice versa, in a subject. The
CC method involves administering an agent that modulates the expression or
CC activity of a molecule selected from PTGER2 and TGFbeta1, or Jagged-1,
CC GPR-32, CD84, CD89, serotonin R, BY55, serotonin R2C, GPR63,
CC histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-
CC 3-related kinase to the subject, such that treatment occurs. The methods
CC are useful for diagnosing, preventing or treating conditions
CC characterized by a too-vigorous or weak effector T cell or regulatory T
CC cell response to antigens associated with the condition, such as in an
CC allergic response, an autoimmune disorder, a viral infection, a microbial
CC infection, a parasitic infection or a tumour. The present sequence
CC represents a DNA encoding a human leukocyte differentiation CD84 antigen,
CC preferentially expressed in regulatory T cells.

XX
SQ Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.02e-106 Length: 1067
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AD005707 (1-1067)

QY 1 LysAspSerGluLeuPheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 133 AAAGACTCAGAAATCTTCACAGTGAATGGGATCTCGGAGAGTCAGTCATCTTCCCTGTA 192
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 193 AATATCCAGAACACCGGCAAGTTAAATCATTTGGTGGACTTCTAAACATCTGTGCT 252
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 253 TATGTAACACGAGAGCTCAGAACAGCACCCTGTAGTACTGTGACCCACAGAAATAT 312
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 313 TATGAACGGATACATGCTTAGTCCGAACTACAACTCATCTGGTCAATAGCGATCTCAGGATG 372
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 373 GAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACC 432
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 433 AAGCGCTACAACTCGCAAACTATCTGCTGGCTGGGAAACCAAAATACACAGAGTTTA 492
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
DB 493 ATGGCATCTGTGAACAGACACCTGTAATGTGCACACTGACATGCTCTGTAGAGAAAGAGAA 552
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 553 AAGAATGTGACATACAAATGGAGTCCCTCGGAGAGAGGGGTAAATGCTTCAAAATCTTC 612
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 613 CAGACTCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCCGAACCCTGTGTCAGCAAC 672
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 673 AATTCTGACTCCATCTCTGCGCGGCGAGCTCTGTGCAGACATGCAATGGGCTCCGT 729
RESULT 3
ID ADQ19066
XX ADQ19066 standard; DNA; 1067 BP.
AC
XX ADQ19066;

DT 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 1885.
DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
KW Homo sapiens.
OS
XX WO2004048938-A2.
PN 10-JUN-2004.
PD 26-NOV-2003; 2003WO-US038193.
PF 26-NOV-2002; 2002US-0429739P.
PR (PROT-) PROTEIN DESIGN LABS INC.
PA Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
DR Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 1885; 210pp; English.
PS The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual,
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.02e-106 Length: 1067
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x ADQ19066 (1-1067)

QY 1 LysAspSerGluLeuPheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 133 AAAGACTCAGAAATCTTCACAGTGAATGGGATCTCGGAGAGTCAGTCATCTTCCCTGTA 192
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 193 AATATCCAGAACACCGGCAAGTTAAATCATTTGGTGGACTTCTAAACATCTGTGCT 252
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 253 TATGTAACACGAGAGACTCAGAACAGCACCCTGTAGTACTGTGACCCACAGAAATAT 312
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 313 TATGAACGGATACATGCTTAGTCCGAACTACAACTCATCTGGTCAATAGCGATCTCAGGATG 372
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

Db	373	GAAGACGAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACACC	432	PR	23-MAY-1997;	97US-0047492P.
Qy	101	LyAsGtYrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu	120	PR	23-MAY-1997;	97US-0047500P.
Db	433	AAGCGCTACACCTGCAATCTATCGTGGCTTGGAAACCAAAATACACAGATTTA	492	PR	23-MAY-1997;	97US-0047501P.
Qy	121	MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlyLysGluGlu	140	PR	23-MAY-1997;	97US-0047503P.
Db	493	ATGGCATCTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA	552	PR	23-MAY-1997;	97US-0047581P.
Qy	141	LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe	160	PR	23-MAY-1997;	97US-0047582P.
Db	553	AAGAATGTGACATACAAATGGAGTCCCTGGGAGAGAGGGTAATGTCCTTCAATCTTC	612	PR	23-MAY-1997;	97US-0047583P.
Qy	161	GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn	180	PR	23-MAY-1997;	97US-0047584P.
Db	613	CAGACTCTGAGACCAAGAGTGACTTACAGGTGTACAGCCAGAACCTGTGCAGCAAC	672	PR	23-MAY-1997;	97US-0047585P.
Qy	181	AsnSerAspSerIleSerAlaArgGlnIleuCysAlaAspIleAlaMetGlyPheArg	199	PR	23-MAY-1997;	97US-0047586P.
Db	673	AATCTGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTTCGGT	729	PR	23-MAY-1997;	97US-0047587P.

RESULT 4
AAV59674
ID AAV59674 standard; DNA; 3173 BP.
AC AAV59674;
DT 19-JAN-1999 (first entry)
XX Human secreted protein gene 164 clone HSAWPF26.
DE XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98WO-US004493.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040337P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043368P.
PR 11-APR-1997; 97US-0043369P.
PR 11-APR-1997; 97US-0043376P.
PR 11-APR-1997; 97US-0043378P.
PR 11-APR-1997; 97US-0043380P.
PR 11-APR-1997; 97US-0043386P.
PR 11-APR-1997; 97US-0043370P.
PR 11-APR-1997; 97US-0043371P.
PR 11-APR-1997; 97US-0043372P.
PR 11-APR-1997; 97US-0043374P.

PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI: 1998-506364/43.
DR P-PSDB; AAW74891.
XX
PT New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 402-404; 721pp; English.
XX
CC This sequence represents a nucleic acid molecule designated Gene 164 from
CC the human cDNA clone HSAW26 (deposited as clone ATCC 97903 and ATCC
CC 209049) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAW74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)
XX
SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores:
Pred. No.: 3-5e-105 Length: 3173
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-882-171-483_COPY_22_220 (1-199) x AAV59674 (1-3173)
QY 1 LysAspSerGluLeuPheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 114 AAGAGCTCAGAAATCTTCACAGTGAATGGGATCTTGGGAGAGTCAGTCACTTTCCCTGTA 173
QY 21 AsnIleGlnGluProArgGlnValLysIleIleAlaThrPheSerLysThrSerValAla 40
Db 174 AATATCCAGAACACACGCGAAGTAAATCATTCCTGGAGCTTCTAAACATCTGTGCT 233
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 234 TATGTAACACGAGAGACTCAGAAACAGACCCGCTAGTCTACTGTGACCCACAGAAATAT 293
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 294 TATGAACGGATACATGCTTAGTCCGAACCTACAACTACAACTAGCTATGATCTGAGGATG 353
QY 81 GluAspIleGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 354 GAAGACGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCC 413
QY 101 LysArgTyrAsnLeuGlnIleTyrArgGluLeuGlyLysProLysIleThrGlnSerLeu 120
Db 414 AAGCGCTACACCTGCAAACTATCTCGTCGGCTTGGGAAACCAAAATACACAGAGTTTA 473

QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 474 ATGGCATCTGTGAACAGCACCTGTAATGTGCACACTGACATGCTCTGTAGAGAAAGAA 533
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 534 AAGATGTGACATACAAATGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTC 593
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 594 CAGACTCTCTGAGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTCTCAGCAAC 653
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 654 AATTCTGACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 710
RESULT 5
ABS73661
ID ABS73661 standard; cDNA; 3173 BP.
XX
AC ABS73661;
XX
XX 15-JAN-2003 (first entry)
DT
DE Human cDNA #1 for novel secreted protein gene 164.
XX
KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
KW Rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW Preservative; nutritional.
XX
OS Homo sapiens.
XX
PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
XX 08-SEP-1998; 98US-00149476.
XX
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040826P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.

Db 414 AAGCGCTACACCTGCATATCTATCGTCGGCTTGGGAAACAAAATTACACAGATTTA 473
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluIysGluGlu 140
Db 474 ATGGCATCTGTGAACAGCACCTGTAATGTACACTGCATGTGTGTAGAGAAAGAAGAA 533
QY 141 LysAsnValThrTyraAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
Db 534 AAGAATGTACATACATATGGAGTCCCTCCCTGGGAGAGAGGGTAAATGTCTTCATATCTTC 593
QY 161 GlnThrProGluAspGlnGluLeuThrTyThrCysThrAlaGlnAsnProValSerAsn 180
Db 594 CAGACTCCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGACCCCTGTCTCAGCAAC 653
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 654 AATCTTGACTCCATCTCTGCCCGCAGCTCTGTGCAGCATCGCAATGGGCTTCGGT 710

RESULT 6
ACD82804
ID ACD82804 standard; cDNA; 3173 BP.
XX
AC ACD82804;
XX
DT 22-SEP-2003 (first entry)
XX
DE cDNA sequence #164 containing coding region of a human secreted protein.
XX
KW Human; secreted protein; hyperproliferative disorder; leukaemia;
KW breast cancer; wound; reproductive disorder; blood-related disorder;
KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;
KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;
KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;
KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;
KW angina pectoris; cerebral ischaemia; congenital heart defect;
KW respiratory disorder; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; inflammation; Crohn's disease; vulnery;
KW immunosuppressive; antibacterial; haemostatic; thrombolytic;
KW anticoagulant; neuroprotective; thyromimetic; antiallergic;
KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;
KW cerebroprotective; cardiant; nootropic; antiparkinsonian;
KW antiinflammatory; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003049618-A1.
XX
XX 13-MAR-2003.
XX
PF 16-MAR-2001; 2001US-00809391.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.

11-APR-1997; 97US-0043674P.
23-MAY-1997; 97US-0047492P.
23-MAY-1997; 97US-0047500P.
23-MAY-1997; 97US-0047501P.
23-MAY-1997; 97US-0047502P.
23-MAY-1997; 97US-0047503P.
23-MAY-1997; 97US-0047581P.
23-MAY-1997; 97US-0047582P.
23-MAY-1997; 97US-0047583P.
23-MAY-1997; 97US-0047584P.
23-MAY-1997; 97US-0047585P.
23-MAY-1997; 97US-0047586P.
23-MAY-1997; 97US-0047587P.
23-MAY-1997; 97US-0047588P.
23-MAY-1997; 97US-0047590P.
23-MAY-1997; 97US-0047592P.
23-MAY-1997; 97US-0047593P.
23-MAY-1997; 97US-0047594P.
23-MAY-1997; 97US-0047595P.
23-MAY-1997; 97US-0047596P.
23-MAY-1997; 97US-0047597P.
23-MAY-1997; 97US-0047598P.
23-MAY-1997; 97US-0047599P.
23-MAY-1997; 97US-0047600P.
23-MAY-1997; 97US-0047601P.
23-MAY-1997; 97US-0047612P.
23-MAY-1997; 97US-0047613P.
23-MAY-1997; 97US-0047614P.
23-MAY-1997; 97US-0047615P.
23-MAY-1997; 97US-0047617P.
23-MAY-1997; 97US-0047618P.
23-MAY-1997; 97US-0047632P.
23-MAY-1997; 97US-0047633P.
06-JUN-1997; 97US-0048964P.
13-JUN-1997; 97US-0048974P.
13-JUN-1997; 97US-0049610P.
16-JUL-1997; 97US-0052874P.
18-AUG-1997; 97US-0055724P.
22-AUG-1997; 97US-0056630P.
22-AUG-1997; 97US-0056631P.
22-AUG-1997; 97US-0056632P.
22-AUG-1997; 97US-0056636P.
22-AUG-1997; 97US-0056637P.
22-AUG-1997; 97US-0056662P.
22-AUG-1997; 97US-0056664P.
22-AUG-1997; 97US-0056845P.
22-AUG-1997; 97US-0056862P.
22-AUG-1997; 97US-0056864P.
22-AUG-1997; 97US-0056872P.
22-AUG-1997; 97US-0056874P.
22-AUG-1997; 97US-0056875P.
22-AUG-1997; 97US-0056876P.
22-AUG-1997; 97US-0056877P.
22-AUG-1997; 97US-0056878P.
22-AUG-1997; 97US-0056879P.
22-AUG-1997; 97US-0056880P.
22-AUG-1997; 97US-0056881P.
22-AUG-1997; 97US-0056882P.
22-AUG-1997; 97US-0056884P.
22-AUG-1997; 97US-0056886P.
22-AUG-1997; 97US-0056887P.
22-AUG-1997; 97US-0056888P.
22-AUG-1997; 97US-0056889P.
22-AUG-1997; 97US-0056892P.
22-AUG-1997; 97US-0056893P.
22-AUG-1997; 97US-0056894P.
22-AUG-1997; 97US-0056903P.
22-AUG-1997; 97US-0056908P.
22-AUG-1997; 97US-0056909P.
22-AUG-1997; 97US-0056910P.
22-AUG-1997; 97US-0056911P.

```
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 12-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJU/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJU/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFI/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP,
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 2003-521800/49.
DR P-PSDB; ABO34537.
XX
PT New genes and its encoded prostate cancer antigen proteins, useful for
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
PT ischemia.
XX
PS Claim 4; SEQ ID NO 174; 260pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC proteins and the polynucleotide sequences encoding them. The invention
CC also discloses vectors, host cells, antibodies, and recombinant methods
CC for producing human secreted proteins. The polypeptide and polynucleotide
CC sequences for the secreted proteins are useful for preventing, treating,
CC ameliorating or diagnosing medical conditions such as hyperproliferative
CC disorders (e.g. leukaemia or breast cancers), wounds, reproductive
CC disorders, blood-related disorders (e.g. haemophilia or
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
CC pectoris, cerebral ischaemia or congenital heart defects), respiratory
CC disorders, neurological disorders (e.g. Alzheimer's disease or
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipdbIDentry.html
XX
SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
```

Alignment Scores:

Pred. No.: 3.5e-105 Length: 3173
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 9

US-09-882-171-483_COPY_22_220 (1-199) x ACD82804 (1-3173)

```
Oy 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 114 AAAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGAGAGTCACTTCCTCCGTGA 173
Oy 21 AsnIleGlnGluProArgGlnValLysIleIlealaItrPheSerLysThrSerValala 40
Db 174 AATATCCAAGAACCCAGCGCAAGTTAAATCATTTCTTGGACTTCTAAACATCTGTTGCT 233
Oy 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 234 TATGTAACACCAGGAGACTTCAAAACAGACCCCGTAGTTACTGTGACCCAGAAATAT 293
Oy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 294 TATGACGGATACATGCTTAGGTCCGAACCTACAATCTGGTCAATAGCGATCTGAGGATG 353
Oy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
Db 354 GAAGACGCGAGAGACTACAAGACAGACATAAATACACAGGCTGATCCCTACACCACCACC 413
Oy 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 414 AAGCGCTACAACCTGCGAAATCTATCGTCGGCTTGGAAACCCAAAAATATACACAGATT 473
Oy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 474 ATGGCATCTGTGAACAGCACCTGTAATGTGCACACTGCATCTCTGTAGAGAAAGAGAA 533
Oy 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 534 AAGAAATGTGACATACAATTTGGAGTCCCTCGGAGAGAGGGTAATGTCTTCAATCTTC 593
Oy 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 594 CAGACTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGACCCCTGTGAGCAAC 653
Oy 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 654 AATCTGACTCCTCTCTCCCGCGAGCTCTGTGACAGACATCGCAATGGGCTTCGGT 710
```

RESULT 7

AD122889
ID AD122889 standard; cDNA; 3173 BP.

XX AC AD122889;

XX DT 22-APR-2004 (first entry)

XX DE CDNA encoding novel human secreted protein seq id 174.

XX KW cytosolic; gene therapy; cancer; human; secreted protein; gene; ss.

XX OS Homo sapiens.

XX PN US2003175858-A1.

XX PD 18-SEP-2003.

XX PF 18-JUN-2001; 2001US-00882171.

XX PR 07-MAR-1997; 97US-0038621P.

XX PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 23-MAY-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056883P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056885P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US0004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R. R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Andreas GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2003-898535/82.
DR P-PSDB; ADI23198.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
PS Claim 1; SEQ ID NO 174; 256pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a

CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The sequence encodes a novel human secreted
CC protein of the invention.
XX

SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores:
Pred. No.: 3,5e-105 Length: 3173
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x ADI22889 (1-3173)

QY 1 LysAspSerGluLeuPheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 114 AAAGACTCAGAATCTTACAGTGAATGGATCTGGAGAGTCAGTCACCTTCCCTGTA 173
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
Db 174 AATATCCAGAACACCGGCAAGTTAAATCATTTGTCGACTTCTAAACATCTGTGT 233
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrHisArgAsnTyr 60
Db 234 TATGTAACACAGGAGACTCAGAAACAGACCCGCTAGTTACTGTGACCCACAGAAATAT 293
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 294 TATGAACGGATACATCCCTTAGCTCGAACTCAATCTGGTTCATTAGCAATCTGAGATG 353
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
Db 354 GAAGACGACGAGGACTTACAAAGCAGACATAAATACACAGCTGATCCCTTACACCACC 413
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProIleValThrGlnSerLeu 120
Db 414 AAGCGCTACAACTGCAATCTATCTGCTGGCTTGGAAACCAAAATTTACAGAGTTTA 473
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
Db 474 ATGGCATCTGTGAACAGCACCTGTAAATGTCACACTGACATGCTGTAGAGAAAGAGAA 533
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 534 AAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAAATGCTTCAATCTTC 593
QY 161 GlnThrProGluAspGlnGluLeuThrTyrCysThrAlaGlnAsnProValSerAsn 180
Db 594 CAGACTCCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCCAAGACCCCTGTCAACA 653
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 654 AATTCGATCCATCTCTGCCCGGACGCTGTGTGCAGACATCGCAATGGGCTTCCT 710

RESULT 8
ID ADH73891
ID ADH73891 standard; cDNA; 3173 BP.
XX
AC ADH73891;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human secreted protein cDNA #164.
XX
KW human; secreted protein; cancer; haematopoietic disorder;
KW endocrine disorder; immune system disease; inflammatory disorder; ss;
XX

OS Homo sapiens.
XX US2003225248-A1.
XX 04-DEC-2003.
PD
XX
XX 10-JUN-2002; 2002US-00164861.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051928P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.

PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 22-AUG-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Peng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2004-131264/13.
DR P-PSDB; ADH74200.
XX
XX Isolated nucleic acid molecules encoding human secreted proteins, useful
PT for preventing, diagnosing and treating disorders associated with
PT aberrant expression and activity.
XX
XX Claim 3; SEQ ID NO 174; 142pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and the human
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,
CC endocrine disorders, diseases of the immune system, inflammatory
CC disorders and many others. Full details of disorders that may be
CC prevented, diagnosed and/or treated by the above methods are given in the
CC specification. The nucleic acid molecules may be used to produce their
CC proteins. The nucleic acid and it's complementary sequences may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The SPs may also be used
CC as antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of SP expression and activity. The anti-SP
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-SP antibodies may also be used as diagnostic
CC agents for detecting the presence of the proteins in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)). The present sequence
CC represents a human secreted protein cDNA.

XX SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
Alignment Scores: 3.5e-105 Length: 3173
Pred. No.: 1039.00 Matches: 199
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 12
US-09-882-171-483_COPY_22_220 (1-199) x ADH73891 (1-3173)
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 114 AAGACTCAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCACTCAGTTCCTCCCTGTA 173
QY 21 AsnIleGlnGluProArgGlnValIysIleIleAlaThrThrSerLysThrSerValAla 40
DB 174 AATATCCAAGAACCCACGCGCAAGTTAAATCAATGCTTGGACTTCTAANAACATCTGTGCT 233
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 234 TATGTAACACACGAGAGACTCAGAAACAGACCCCGTAGTCTGTGACCCACAGAAATAT 293
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 294 TATGAACGGATACATGCTTAGTCCGAACACTACAATCTGGTCAATAGCGATCTGAGGATG 353
QY 81 GluAspAlaGlyAspTyrIysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 354 GAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACC 413
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 414 AAGCGCTCAACCTGCAATCTATCTCGCTTGGGAAACCAAAATTAACACAGATTTA 473
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
DB 474 ATGGCATCTGTGCAACAGCACCTGTAAATGTCACTGACATGCTCTGTAGAGAAAGAA 533
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
DB 534 AAGAATGTGACATACAATTTGGAGTCCCTGGGAGAAGAGGGTAATGTCTCTCAATCTTC 593
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 594 CAGACTCTCGAGGACCAAGAGCTTGACTTACAGCTGTACAGCCAGAACCCCTGTCAAC 653
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 654 AATCTGACTCTCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCCTG 710

RESULT 9
ADL82906
ID ADL82906 standard; cDNA; 3299 BP.
XX
XX ADL82906;
AC
XX
XX 17-JUN-2004 (first entry)
DT
XX
XX Human PRO24934 cDNA, SEQ ID 108.
DE
XX
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004024097-A2.
FN
XX
XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US029097.
PF
XX
XX 16-SEP-2002; 2002US-0411392P.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
PI
XX WPI; 2004-329389/30.
DR P-PSDB; ADL82907.
XX
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX Claim 2; Fig 108; 695pp; English.
XX
XX The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IGG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
XX Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 3299 Length: 3299
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x ADL82906 (1-3299)

QY 1 LysAspSerGluLeuPheThrValAlaGlyIleLeuGlyGluSerValThrPheProVal 20
DB 108 AAAGCTCGAATCTTCACTGATGGATCTGGGAGATGTCAGTCACTTCCCTGTA 167
QY 21 AsnIleGlnGluProArgGlnValLysIleIleAlaTTPThrSerIlysthrSerValAla 40
DB 168 AATATCCAAGACCAACCGCAAGTAAATCAATCTGCTGGACTCTAAACATCTGTGCT 227
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgSerTyr 60
DB 228 TATGTAACACAGGAGACTCAGAAACAGACCCGCTAGTTACTGTGACCCACACAAATTAT 287
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 288 TATGACGGATACATGCTTAGTTCGAACTCAATCTGGTCAATAGCGATCTGAGGATG 347
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 348 GAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACC 407
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 408 AAGCGCTACAACTCGCAATCTATCGTCGGCTTGGAAACCAAAATATACACAGATTTA 467
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140

DB 468 ATGGCATCTGTGAACAGCACTGTAAATGTCACTGACATGCTCTGTAGAAAGAA 527
QY 141 LysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLysGlnIlePhe 160
DB 528 AAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTC 587
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 588 CAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCTGTGTAGAAC 647
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 648 AATCTGACTCCATCTCTGCCGCGAGCTCTGTGACAGACATCGCAATGGGCTTCGCT 704
RESULT 10
ADP23942
ID ADP23942 standard; cDNA; 3299 BP.
XX
XX AC ADP23942;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE PRO polypeptide encoding cDNA SEQ ID NO:1120.
XX
XX KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX
XX OS Unidentified.
XX
XX PN WO2004041170-A2.
XX
XX PD 21-MAY-2004.
XX
XX PF 30-OCT-2003; 2003WO-US034312.
XX
XX PR 01-NOV-2002; 2002US-0423394P.
XX
XX (GETH) GENENTECH INC.
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-419628/39.
DR P-PSDB; ADP23943.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematosis, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 1; SEQ ID NO 1120; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplant-associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
SQ Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,68e-105 Length: 3299
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x ADP23942 (1-3299)

QY 1 LysAspSerGluLeuPheThrValAsnGlyLeuGlySerValThrPheProVal 20
DB 108 AAAGACTCAGAAATCTTCACAGTGAATGGGATTCGGAGAGTCAGTCACTTCCCTGTA 167
QY 21 AsnIleGlnProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 168 AATATCCAGAACCCAGGCAAGTTAAATCATTTGGACTTCTAAACATCTGTGCT 227
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 228 TATGTAAACACGAGAGACTCAGAAACAGCACCCTAGTCTAGTCCACAGAAATAT 287
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 288 TATGAACGGATACATGCTTAGTCCGAACTCAATCTGCTCAATAGCGATCTGAGGATG 347
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 348 GAAGACGCGAGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACC 407
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 408 AAGCGCTACAACTGCAATCTATCTGCGCTGGGAAACCAAAATACACAGAGTTTA 467
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
DB 468 ATGGCATCTGTGAACACAGCAGCTGTAAATGTCCACACTGACATGCTGTAGAGAAAGAGAA 527
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
DB 528 AAGAATGTGACATACAAATTTGAGTCCCTGGGAGAGAGGGTAAATGTCCTCAAAATCTTC 587
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 588 CAGACTCTGTAGGACCAAGAGCTGACTTACAGTGTACAGCCAGACCTGTGTCAGAAC 647
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuGlyCysAlaAspIleAlaMetGlyPheArg 199
DB 648 AATTCTGACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGGTCCGT 704

RESULT 11

ID AA172383
AA172383 standard; cDNA; 3300 BP.

XX
AC AA172383;

XX 02-MAY-2002 (first entry)

XX CD84 coding sequence.

XX SCZ; gene; CD84; platelet; monocyte; circulating B cell; schizophrenia;

KW allele; polymorphic marker; chromosome 1q22; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
CDS 45..1031
/*tag= a
/product= "SCZ"

PN WO200202054-A2.

XX 10-JAN-2002.

XX 23-APR-2001; 2001WO-US013040.

XX 21-APR-2000; 2000US-0198873P.

PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.

PI Brzustowicz LM, Bassett AS;

XX WPI; 2002-171605/22.

DR P-PSDB; AAB47878.

XX Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by
PT determining presence or absence of an allele of a linked polymorphic
PT marker present on chromosome 1q22, were the marker is linked to a variant
PT form of the SCZ gene.

XX Claim 19; Page 68-70; 82pp; English.

XX This sequence was isolated using the method of the invention as the SCZ
CC gene. This sequence has been previously identified as CD84, GenBank
CC accession No: NM_003874. CD84 is a 73 kDa antigen present on platelets,
CC monocytes and circulating B cells. The proteins encoded by this sequence
CC may be involved in the processes by which the brain responds to
CC biological stimuli. Therefore they may provide targets for therapeutic
CC intervention in the treatment of schizophrenia. The SCZ sequence may be
CC used in a new method of diagnosing susceptibility to schizophrenia in a
CC patient. The method comprises determining the presence or absence of an
CC allele of a linked polymorphic marker in the DNA of the patient. The
CC polymorphic marker is present in chromosome 1q22 and is linked to a gene
CC (SCZ) having a variant form associated with a phenotype of schizophrenia
XX
SQ Sequence 3300 BP; 957 A; 802 C; 750 G; 791 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,69e-105 Length: 3300
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AA172383 (1-3300)

QY 1 LysAspSerGluLeuPheThrValAsnGlyLeuGlySerValThrPheProVal 20
DB 108 AAAGACTCAGAAATCTTCACAGTGAATGGGATTCGGAGAGTCAGTCACTTCCCTGTA 167
QY 21 AsnIleGlnProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 168 AATATCCAGAACCCAGGCAAGTTAAATCATTTGGACTTCTAAACATCTGTGCT 227
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 228 TATGTAAACACGAGAGACTCAGAAACAGCACCCTAGTCTAGTCCACAGAAATAT 287
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 288 TATGAACGGATACATGCTTAGTCCGAACTCAATCTGCTCAATAGCGATCTGAGGATG 347
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

XX (MILL-) MILLENNIUM PHARM INC.
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2003-787014/74.
XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
XX Disclosure; SEQ ID NO 13255; 36pp; English.
XX
XX The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumors. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
XX Sequence 3687 BP; 1073 A; 881 C; 838 G; 874 T; 0 U; 21 Other;
SQ

Alignment Scores:
Pred. No.: 4 28e-105 Length: 3687
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x ACN92105 (1-3687)

QY 1 LysAspSerGluLeuPheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
Db 496 AAAGACTCAGAAATCTTCACAGTGAATGGGATTCCTGGAGAGTCAGTCACTTCCCTGTA 555

QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
Db 556 AATATCCAGAACACCGCGAAGTAAATCATTTGCTGGACTTCAAAACATCTGTGCT 615

QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 616 TATGTAACACCGAGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATTAT 675

QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
Db 676 TATGAACGGATACATGCTTAGTTCGCAACTCAAACTCTGTCATTCGCGATCTGAGGATG 735

QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 736 GAAGACCGAGAGACTCAAAAGCAGACATTAATACACAGCGTGTATCCCTACACACACC 795

QY 101 LysArgTyrAsnLeuGlnIleTyrArgGluGlyLysProLysIleThrGlnSerLeu 120
Db 796 AAGCGCTACAACTGCAAAATCTATCGTCGGCTTGGGAAACCAAAATTCACACAGAGTTTA 855

QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 856 ATGCACTCTGTGAACAGACACCTGTAATGTTCACACTGACATGCTCTGTAGAGAAAGAGAA 915

QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
Db 916 AAGAAATGTGACATCAAAATGGAGTCCCTCGGAGAGAGGGTAAATGCTTCAAAATCTTC 975

QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 976 CAGACTCTGAGGACCAAGAGCTGACTTACACGTTGACAGCCAGACCCCTGTGAGCAAC 1035

QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 1036 AATTCTGACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCCT 1092

RESULT 14
ADL57104
ID ADL57104 standard; DNA; 1581 BP.
XX
XX AC ADL57104;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX Human NOV5b gene SEQ ID NO:49.
DE
DE ds; gene; human; antidiabetic; anorectic; cardiant; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipaemic; gene therapy;
KW fibroblast growth factor receptor 4; FGFR4;
KW complement factor 1 precursor; matrix metalloproteinase-15 precursor;
KW MDC3; T-lymphocyte surface antigen Ly-9 precursor;
KW fibroblast growth factor-21; FGF-21;
KW alpha-2 macroglobulin-like polypeptide variant;
KW antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
KW transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1. .1581
FT CDS /*tag= a
XX
XX WO2004022723-A2.
XX
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-US028141.
XX
XX 09-SEP-2002; 2002US-0409145P.
PR 10-SEP-2002; 2002US-0409544P.
PR 12-SEP-2002; 2002US-0410320P.
PR 16-SEP-2002; 2002US-0411060P.
PR 23-SEP-2002; 2002US-0412766P.
PR 23-SEP-2002; 2002US-0412825P.
PR 24-SEP-2002; 2002US-0412767P.
PR 25-SEP-2002; 2002US-0413342P.
PR 30-SEP-2002; 2002US-0414832P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK;
PI P-PSDB; ADL57105.
XX
XX WPI; 2004-315567/29.
DR
DR P-PSDB; ADL57105.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
XX Claim 17; SEQ ID NO 49; 214pp; English.
PS
XX
XX The invention relates to a novel isolated polypeptide (NOVX) comprising a
CC mature form of any of the 37 amino acid sequences fully defined in the
CC specification. A polypeptide of the invention has antidiabetic.
CC anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic,
CC virucide, antibacterial, fungicide, protozoacide, neurotropic,
CC neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
CC antiarthritic, antiinflammatory, dermatological, antiasthmatic, and
CC antilipaemic activity. A polynucleotide of the invention may have a use
CC in gene therapy. The polypeptides, nucleic acid molecules and antibodies

CC are useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, preferably a NOVX-associated disorder.
CC The nucleic acid molecules, polypeptides and antibodies are useful for
CC treating, preventing or diagnosing diseases such as metabolic disorders,
CC diabetes, obesity, infectious diseases (viral, bacterial, fungal,
CC helminthic, and protozoal), anorexia, cancer, cardiovascular diseases
CC (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's
CC disease, Parkinson's disease, epilepsy, immune disorders
CC (osteoarthritis), haematopoietic disorders, inflammatory skin disorders,
CC asthma, and various dyslipidaemias. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, haematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridisation probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. The NOVX
CC polypeptides of the invention show homology to certain known human
CC proteins: NOV1a-it show homology to fibroblast growth factor receptor 4
CC (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a
CC shows homology to matrix metalloproteinase-15 precursor; NOV4a shows
CC homology to MDC3; NOV5a-5c show homology to T-lymphocyte surface antigen
CC Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21
CC (FGF-21); NOV7a-7c show homology to alpha-2 macroglobulin-like
CC polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1
CC precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology
CC to nuclear hormone receptor NOR-1; NOV11a-11j show homology to
CC transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin
CC -dynorphin precursor. The present sequence encodes a NOVX polypeptide of
CC the invention.
XX
SQ Sequence 1581 BP; 422 A; 442 C; 397 G; 320 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,73e-29 Length: 1581
Score: 352.00 Matches: 77
Percent Similarity: 58.42% Conservatives: 41
Best Local Similarity: 38.12% Mismatches: 70
Query Match: 33.88% Indels: 14
DB: 12 Gaps: 5

US-09-882-171-483_COPY_22_220 (1-199) x ADL57104 (1-1581)
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 22 AAGGACTCAGCCCAACAGTGGTGCAGGGATCCTAGGGGGTTCGGTGACTCTCCCCCTA 81
QY 21 AsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSer---LysThrSerVal 39
DB 82 AACATCTCAGTACACACAGAGATTGAGACGTCATCTGGATTGGTCCCAAAATGCTCTT 141
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
DB 142 GCITTCGACGTCCTCCCAAGAAAT-----GTAACCATTTATGGTCAAAAGC 186
QY 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
DB 187 TACCTGGCGCGACTAGACATCACCAAGTGGAGTTACTCCCTGGCATCAGCAATCTGACT 246
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
DB 247 CTGAATGATGACGATCTCTACAAAGCCAGATAAACCAGGAATTTTGAAGTCACCACT 306
QY 100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProlysIleThr---Gln 118
DB 307 GAGGAGGAATATCCCTGTTCTGTATGACAGCTGCAGGAGCCCAAGTCACCATGAAG 366
QY 119 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 138
DB 367 TCTGTGAAGGTGCTGAGAACTTCTCTGTGAACATCACTATATGTGCTCCGTTGAGGGG 426
QY 139 GluGluLysAsnValThrTyrAsnTrpSerProLeu-----GlyGlu 152

Db 427 GCAGAGAAAGTGTCTGTACTAGCTGGACCCCAAGGAAACCCCATGCTTCTGAGTCCAAT 486
Qy 153 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
Db 487 GGAGGCTCCATTTCTTACCGTCTCCGAAACACCATGTGACCCAGCCTGCGCATACATCTGC 546
Qy 173 ThrAlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys 191
Db 547 ACAGCCAGAAACCCCGTCACCCAGAGAGAGTCCCTCCTGTCATGTTGGCAGTCTGT 606
Qy 192 AlaAsp 193
Db 607 ACAGAT 612
RESULT 15
ADK98595
ID ADK98595 standard; cDNA; 1723 BP.
XX
AC ADK98595;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human immune response associated protein IRAP-23 cDNA.
XX
KW immune response associated protein; IRAP; antiarteriosclerotic;
KW cytosolic; neuroprotective; antiparkinsonian; hepatotropic;
KW cerebroprotective; antiinflammatory; nootropic; vasotropic;
KW arteriosclerotic; cirrhosis; cancer; stroke; Alzheimer's disease;
KW Parkinson's; Crohn's; gene therapy; human; ss; gene.
XX
OS Homo sapiens.
XX
PN WO2004020593-A2.
XX
PD 11-MAR-2004.
XX
PF 26-AUG-2003; 2003WO-US026988.
XX
PR 30-AUG-2002; 2002US-0407561P.
PR 11-SEP-2002; 2002US-0410178P.
PR 13-SEP-2002; 2002US-0410571P.
PR 18-OCT-2002; 2002US-0419906P.
PR 25-OCT-2002; 2002US-0421445P.
XX
(INCY-) INCYTE CORP.
XX
PI Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;
PI Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;
XX
WPI: 2004-239178/22.
DR N-PSDB; ADK98560.
XX
New isolated immune response associated proteins (IRAP) polypeptide and
PT polynucleotide, useful for diagnosing and/or treating disorders with
PT aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
PT and stroke.
XX
Claim 5; SEQ ID NO 58; 207pp; English.
XX
The invention relates to a novel isolated immune response associated
CC protein (IRAP) comprising any of 35 fully defined sequences given in the
CC specification. The polypeptide of the invention demonstrates
CC antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,
CC hepatotropic, cerebroprotective, antiinflammatory, nootropic and
CC vasotropic activities and may be useful for treating a disease or
CC condition associated with decreased expression or overexpression of
CC functional immune response associated proteins, while the antibody is
CC useful for diagnosing a condition or disease associated with the
CC expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke,
CC Alzheimer's disease, Parkinson's disease and Crohn's disease.
CC Furthermore, the molecules of the invention may be utilised during gene
CC therapy procedures. The current sequence is that of a human IRAP cDNA of
CC the invention.

```
XX
SQ Sequence 1723 BP; 456 A; 486 C; 427 G; 354 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      5,31e-29      Length:      1723
Score:          352.00      Matches:      77
Percent Similarity: 58.42%      Conservative: 41
Best Local Similarity: 38.12%      Mismatches: 70
Query Match:      33.88%      Indels:      14
DB:              12          Gaps:      5

US-09-882-171-483_copy_22_220 (1-199) x ADK98595 (1-1723)

QY      1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB      149 AAGGACTCAGCCCAACACAGTGGTTCAGGATCTCTAGGGGGTTCGGTGACTCTCCCCCTA 208
QY      21 AsnIleGlnGluProArgGlnValLysIleIleAlaTyrThrSer---LysThrSerVal 39
DB      209 AACATCTCAGTAGACACACAGAGATTGAGACGTCATCTGGATTGGTCCCAAAAATGCTCTT 268
QY      40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
DB      269 GCTTTCGACGTCCTCCAAAGAAAT-----GTAACCATTTATGGTCAAAAGC 313
QY      60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
DB      314 TACCTGGCGCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 373
QY      80 MetGluAsnAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
DB      374 CTGAATGATCCAGATCTCTACAAAGCCAGATTAACCAAGGAATTTTGAAGTCACCACT 433
QY      100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118
DB      434 GAGGAGCAATTCACCCCTGTTCTGTCATGACGAGCTGCAGGAGGCCCAAGTCACCATGAAG 493
QY      119 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 138
DB      494 TCTGTGAAGGTGCTCGAAGACTTCTCCTGTAAACATCACTCTAATGTGCTCCGTGAAGGGG 553
QY      139 GluGluLysAsnValThrTyrAsnTyrSerProLeu-----GlyGlu 152
DB      554 GCAGAGAAAGTGTCTGTACAGCTGGACCCCAAGGGAACCCCATGCTTCTGAGTCCAAT 613
QY      153 GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
DB      614 GGAGGCTCCATTCTTACCGTCTCCCGAAACCATGTGACCCAGACCTGCCCATACATCTGC 673
QY      173 ThrAlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys 191
DB      674 ACAGCCCAAGAACCCCGTCAGCCAGAGAAGCTCCCTCCCTGTCATGTGGGCAGTCTCTGT 733
QY      192 AlaAsp 193
DB      734 ACAGAT 739
```

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 5, 2005, 06:13:46 ; Search time 134.551 Seconds
(without alignments)
2420.040 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220
Perfect score: 1039
Sequence: 1 KDSFTFTVNGILGESVTFPV.....NNSDISARQLCADIAMGFR 199

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO spoil/US09882171/runat_04022005_114004_26047/app_query.fasta_1.910
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09882171 @CGN_1_1_93 @runat_04022005_114004_26047 -NCP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1039	100.0	3173	3	US-09-149-476-174
2	1039	100.0	3296	4	US-09-949-016-1456
3	1039	100.0	3299	4	US-09-949-016-557
4	571	55.0	37475	4	US-09-949-016-12299
5	571	55.0	37492	4	US-09-949-016-13198
6	302	29.1	1140	3	US-09-227-357-53
7	160	15.4	1020	1	US-08-348-792-5
8	160	15.4	1020	2	US-08-462-738-5
9	160	15.4	1020	3	US-09-199-955-5
10	160	15.4	1020	3	US-08-880-875-5
11	160	15.4	1079	1	US-08-348-792-7
12	160	15.4	1079	2	US-08-462-738-7

13	160	15.4	1079	3	US-09-199-955-7	Sequence 7, Appli
14	160	15.4	1079	3	US-08-880-875-7	Sequence 7, Appli
15	160	15.4	1716	1	US-08-348-792-1	Sequence 1, Appli
16	160	15.4	1716	2	US-08-462-738-1	Sequence 1, Appli
17	160	15.4	1716	3	US-09-199-955-1	Sequence 1, Appli
18	160	15.4	1716	3	US-08-880-875-1	Sequence 1, Appli
19	160	15.4	1789	4	US-09-023-655-1504	Sequence 1504, Ap
20	160	15.4	1852	1	US-08-348-792-3	Sequence 3, Appli
21	160	15.4	1852	2	US-08-462-738-3	Sequence 3, Appli
22	160	15.4	1852	3	US-09-199-955-3	Sequence 3, Appli
23	160	15.4	1852	3	US-08-880-875-3	Sequence 3, Appli
24	160	15.4	1852	4	US-09-148-545-258	Sequence 258, App
25	153	14.7	1140	1	US-08-348-792-11	Sequence 11, Appli
26	153	14.7	1140	2	US-08-462-738-11	Sequence 11, Appli
27	153	14.7	1140	3	US-09-199-955-11	Sequence 11, Appli
28	153	14.7	1140	3	US-08-880-875-11	Sequence 11, Appli
29	153	14.7	1200	1	US-08-348-792-9	Sequence 9, Appli
30	153	14.7	1200	2	US-08-462-738-9	Sequence 9, Appli
31	153	14.7	1200	3	US-09-199-955-9	Sequence 9, Appli
32	153	14.7	1200	3	US-08-880-875-9	Sequence 9, Appli
33	146	14.1	448	4	US-09-513-999C-276	Sequence 276, App
34	140.5	13.5	2839	3	US-08-468-856B-5	Sequence 5, Appli
35	140.5	13.5	2839	3	US-08-468-859A-5	Sequence 5, Appli
36	139.5	13.4	3220	4	US-09-369-248A-1	Sequence 1, Appli
37	138	13.3	2110	4	US-09-907-794A-319	Sequence 319, App
38	138	13.3	2110	4	US-09-905-125A-319	Sequence 319, App
39	138	13.3	2110	4	US-09-902-775A-319	Sequence 319, App
40	138	13.3	2110	4	US-09-906-700-319	Sequence 319, App
41	138	13.3	2110	4	US-09-903-603A-319	Sequence 319, App
42	138	13.3	2110	4	US-09-904-920A-319	Sequence 319, App
43	138	13.3	2110	4	US-09-909-064-319	Sequence 319, App
44	138	13.3	2110	4	US-09-905-381A-319	Sequence 319, App
45	138	13.3	2110	4	US-09-906-618-319	Sequence 319, App

ALIGNMENTS

RESULT 1
US-09-149-476-174
; Sequence 174, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23

[illegible]

EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.: 2,73e-122 Length: 3173
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-149-476-174 (1-3173)

QY 1 LysAspSerGluIlePheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 114 AAAGACTCGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCATCTTCCCTGTA 173
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 174 AATATCCAGAACCCAGGCAAGTTAAATCATTTGCTGGACTTCTAAACATCTGTGCT 233
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 234 TATGTAACACCCAGGAGACTCAGAAACAGCACCGCTAGTTACTGTGACCCACAGAAATAT 293
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 294 TATGTAACCGGATACATGCTTAGTCCGAATCAATCTGGTCAATAGCGATCTGAGGATG 353
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 354 GAAGACGCGAGGAGACTACAAAGCAGACATATAATACACAGGCTGATCCCTACACCCACC 413
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 414 AAGCGCTACAACTGCAAACTCTATCGTCGGCTTGGGAAACCAAAAAATTACACAGAGTTA 473
QY 121 MetAlaSerValAsnSerThrCysAsnValThrIleuThrCysSerValGluLysGluGlu 140
DB 474 ATGGCATCTGTGAACAGCACCTGTAATGTGCACACTGCATGCTCTGTAGAGAAGAGAA 533
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 534 AAGAAATGTGACATACAAATTTGAGTCCCTGGGAGAGAGGGTAAATGTCTTCAAAATCTTC 593
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 594 CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAGACCCCTGTGAGCAAC 653
QY 181 AsnSerAspSerIleSerAlaArgGlnIleuCysAlaAspIleAlaMetGlyPheArg 199
DB 654 AATTCTGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTCCCGT 710

RESULT 2
US-09-949-016-1456

Sequence 1456, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1456
LENGTH: 3296
TYPE: DNA
ORGANISM: Human
US-09-949-016-1456

Alignment Scores:
Pred. No.: 2,89e-122 Length: 3296
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-949-016-1456 (1-3296)

QY 1 LysAspSerGluIlePheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 106 AAAGACTCGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCATCTTCCCTGTA 155
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 166 AATATCCAGAACCCAGGCAAGTTAAATCATTTGCTGGACTTCTAAACATCTGTGCT 225
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 226 TATGTAACACCCAGGAGACTCAGAAACAGCACCGCTAGTTACTGTGACCCACAGAAATAT 285
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 286 TATGTAACCGGATACATGCTTAGTCCGAATCAATCTGGTCAATAGCGATCTGAGGATG 345
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 346 GAAGACGCGAGGAGACTACAAAGCAGACATATAATACACAGGCTGATCCCTACACCCACC 405
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 406 AAGCGCTACAACTGCAAACTCTATCGTCGGCTTGGGAAACCAAAAAATTACACAGAGTTA 465
QY 121 MetAlaSerValAsnSerThrCysAsnValThrIleuThrCysSerValGluLysGluGlu 140
DB 466 ATGGCATCTGTGAACAGCACCTGTAATGTGCACACTGCATGCTCTGTAGAGAAGAGAA 525
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 526 AAGAAATGTGACATACAAATTTGAGTCCCTGGGAGAGAGGGTAAATGTCTTCAAAATCTTC 585
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 586 CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAGACCCCTGTGAGCAAC 645
QY 181 AsnSerAspSerIleSerAlaArgGlnIleuCysAlaAspIleAlaMetGlyPheArg 199
DB 646 AATTCTGACTCCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTCCCGT 702

RESULT 3

US-09-949-016-557
; Sequence 557, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 557
; LENGTH: 3299
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-557

Alignment Scores:

Pred. No.: 2,9e-122 Length: 3299
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-949-016-557 (1-3299)

QY 1 LysAspSerGluIlePheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 108 AAGACTCAGAAATCTTCACAGTGAATGGATTCTGGAGAGTCAGTCATCTCCCTGTA 167
QY 21 AsnIleGlnGluProArgGlnValIysIleAlaIleAlaIleThrSerLysThrSerValAla 40
DB 168 AATATCCAGAACACCGGCAAGTAAATCATCTGGACTTCTAAACATCTCTTGTCT 227
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 228 TATGTAACACAGGAGAGCTCAGAAACAGACCCGTTAGTCTGTGACCCACAGAAATAT 287
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 288 TATGAACGGATACATGCCTTAGTCCGAACCTACATCTGGTCACTAGCGATCTGAGGATG 347
QY 81 GluAspAlaGlyAspTyrIysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 348 GAAGACGCGAGAGAGCTACAAAGCAGACATAAATACACAGGCTGATCCCTCACACCACC 407
QY 101 LysArgTyrAsnLeuGlnIleTyrArgGluGlyProLysProLysIleThrGlnSerLeu 120
DB 408 AAGCCCTTCAACCTCAATCTATCTCGCTTGGGAACCAAAATATACACAGATTGA 467
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
DB 468 ATGGCATCTGTGAACAGCACCTGTAAATGTGCACACTGACATGCTCTGTAGAGAAAGAA 527
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 528 AAGAATGTGCATACATAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAATCTTC 587
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 588 CAGATCTCTGAGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGAGCAAC 647
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199

DB 648 AATTCTGACTCATCTCTGCCCGCAGCTCTGTGCAGACATCGCAATGGGCTTCGGT 704

RESULT 4

US-09-949-016-12299
; Sequence 12299, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12299
; LENGTH: 37475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12299

Alignment Scores:
Pred. No.: 7,95e-61 Length: 37475
Score: 571.00 Matches: 109
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.00% Mismatches: 0
Query Match: 54.96% Indels: 0
DB: 4 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-949-016-12299 (1-37475)

QY 1 LysAspSerGluIlePheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 15752 AAGACTCAGAAATCTTCACAGTGAATGGGATCTGGAGAGTCAGTCATCTCCCTGTA 15811
QY 21 AsnIleGlnGluProArgGlnValIysIleAlaIleAlaIleThrSerLysThrSerValAla 40
DB 15812 AATATCCAGAACACCGGCAAGTAAATCATCTGGACTTCTAAACATCTCTTGTCT 15871
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 15872 TATGTAACACAGGAGAGCTCAGAAACAGACCCGTTAGTCTGTGACCCACAGAAATAT 15931
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 15932 TATGAACGGATACATGCCTTAGTCCGAACCTACATCTGGTCACTAGCGATCTGAGGATG 15991
QY 81 GluAspAlaGlyAspTyrIysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 15992 GAAGACGCGAGAGAGCTACAAAGCAGACATAAATACACAGGCTGATCCCTCACACCACC 16051
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArg 110
DB 16052 AAGCGCTACACCTGCAATCTATCTCGTAAG 16081

RESULT 5

US-09-949-016-13198
; Sequence 13198, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755


```
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13198
; LENGTH: 37492
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13198

Alignment Scores:
Pred. No.: 7,966-61 Length: 37492
Score: 571.00 Matches: 109
Percent Similarity: 100.00% Conservatave: 1
Best Local Similarity: 99.09% Mismatches: 0
Query Match: 54.96% Indels: 0
DB: 4 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-949-016-13198 (1-37492)

QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 15752 AAAGACTCAGAATCTTCACAGTGAATGGATTCTGGAGAGTCACTTCCCTGTA 15811

QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 15812 AATATCAAGAACCCAGCGCAAGTAAATCATTTGCTTGGACTTCTAAACATCTGTGCT 15871

QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 15872 TATGTAACACCGAGACTCAGAAACAGCACCGCTAGTACTGTGACCCACAGAAATTAT 15931

QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 15932 TATGAACGGATACATGCTTAGTTCGACTACAACTGGTCAATAGCATCTGAGATG 15991

QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 15992 GAAGACGACGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 16051

QY 101 LysArgTyrAsnLeuGlnIleTyrArgArg 110
DB 16052 AAGCGCTACAACTGCAAAATCTATCGTAAG 16081

RESULT 6
US-09-227-357-53
; Sequence 53, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-357-53

Alignment Scores:
Pred. No.: 1,07e-28 Length: 1140
Score: 302.00 Matches: 69
Percent Similarity: 56.83% Conservatave: 35
Best Local Similarity: 37.70% Mismatches: 71
Query Match: 29.07% Indels: 8
DB: 3 Gaps: 1

US-09-882-171-483_COPY_22_220 (1-199) x US-09-227-357-53 (1-1140)

QY 8 ValAsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGlnGluProArgGln 27
DB 171 GTGGTTGCGGCTCTCTCAGGAGTCCATCAGCTCCCTCGGAATATACCACCATGAGAG 230
QY 28 ValLysIleIleAlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSer 47
```

```
Db 231 GTTGAGACATATCTGGTCCTCTCAAAAGTCTTGCACATGTGTGCACGGAAAGAG 290
QY 48 GluThrAlaProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeu 67
Db 291 GGACATCCAGTACCATCATGTGTGACCAATCCACACTACCGGGCCAAAGTGAGCTTCCTG 350
QY 68 GlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrIlys 87
Db 351 GACCCCARCTATTCCTCGATATCAGCAATCTGAGCTGGGAGGATTCAGGGCTTTACCAA 410
QY 88 AlaAspIleAsnThrGlnAlaAspProTyrThrThrLysArgTyrAsnLeuGlnIle 107
Db 411 GTCAGTCAACTGAGACATCCAGATCTCTACCATCGACGATACATATGTGTGTC 470
QY 108 TyrArgArgLeuGlyLys-ProLysIleThrGlnSerLeuMetAlaSerValAsnSerTh 127
Db 471 TACCGATGGCTGTACAGAGDCCACATCACTGTGAACCTTGAGAGTTCTGGGGAAGGTGC 530
QY 127 rCysAsnValThrLeuThrCysSerValGlu-LysGluGluLysAsnValThrTyrAsnT 147
Db 531 CTGCAATATGTCCTGGTGTCTGTGTGGAGRAAGCGCATGATATGACCTACAGCT 590
QY 147 rpSerProLeuGlyGlu-----GluGlyAsnValLeuGlnIlePheG 161
Db 591 GGCTCTCCCGGGGATAGCACTTATACATTCATGAAGGCCCTGTCTCAGCACATCCT 650
QY 161 InThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsnA 181
Db 651 GGAGGCGGGGACAGTGCCCTCTCTACACCTGACAGACCAACCCCATCAGCAACG 710
QY 181 snSer 182
Db 711 TCAGT 715
```

RESULT 7

```
US-08-348-792-5
; Sequence 5, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1020 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..975
; US-08-348-792-5

Alignment Scores:
Pred. No.: 1,31e-10 Length: 1020
Score: 160.00 Matches: 50
Percent Similarity: 43.15% Conservative: 35
Best Local Similarity: 25.38% Mismatches: 78
Query Match: 15.40% Indels: 34
DB: 1 Gaps: 8

US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-5 (1-1020)

QY 12 LeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluProArg 26
Db 175 TTGGAGACAAAGTGTCTGCTCCCTGACATATGAAAGGATAAATAAGAGCATGAACAAA 234
QY 27 GlnValIleIleAlaTTrpThr-SerIysThr-----SerVal 39
Db 235 AGCATCCACATTTGCTGCACAAATGGCAAAATCCTGGAGAACAGTGTGCGAAACAAATA 294
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
Db 295 GTGTCTCTGTATCCATCCGAAGCAGGCGCTCCAGCTTATCTAGGAGATCGCTACAAGTTT 354
QY 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
Db 355 TATCTGGAG-----AATCTCACCTGGGGATACGGGAAGCAGG 393
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
Db 394 AAGGAGGATGAGGATGGTACTTATGACCCCTG-----GAGAAAAATGTTTCA 441
QY 100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
Db 442 GTTCAGGCGCTTTTGCCTGTCAGTTTATGAGGCTTATGAGCAGGTCTCCACTCCAGAAATAAA 501
QY 118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 137
Db 502 GTTTTAAACAGACCCAGGAGAACGGACCTGACCTTGATACITGGCTGCACAGTGGAG 561
QY 138 LysGluGluLysAsnValThrTyrAsnTrpSer-----ProLeu--- 150
Db 562 AAGGGGAGAC---CATGTGGCTTACAGCTGGAGTGAAGGCGGCGCACCCCACTGAAC 618
QY 151 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
Db 619 CCAGCCCAACAGCTCCACCTCTCTGCTCCCTCACCCTCGGCGCCCGACATGTGACAATATC 678
QY 170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
Db 679 TACATCTGCACCGTGAGCAACCCCTATCAGCAACAATTTCCCAAGACCTTCAGC 729

RESULT 8
US-08-462-738-5
; Sequence 5, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
```



```
; Sequence 7, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..1073
; US-08-348-792-7

Alignment Scores:
Pred. No.: 1.42e-10 Length: 1079
Score: 160.00 Matches: 50
Percent Similarity: 43.15% Conservative: 35
Best Local Similarity: 25.38% Mismatches: 78
Query Match: 15.40% Indels: 34
DB: 8 Gaps: 8

US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-7 (1-1079)

Qy 12 LeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluProArg 26
Db 183 TTGGGAAGCAAGTGTGCTGCCCTGCATATGAAGGATAATAAGAGCATGAACAA 242
Qy 27 GlnValLysIleAlaTTrSerLysThr-----SerVal 39
Db 243 AGCATCACATTGCTGCACATATGGCAAAATCATCGGAGACAGTGTGAGAACAAATA 302
Qy 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValHisArgAsn 59
Db 303 GTGCTCTTGATCCATCCGAAGCAGCGCCCTCCACGTTATCTAGGAGATCGTACAGTTT 362
Qy 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
Db 363 TATCTGGAG-----AATCTCACCTGGGGATACGGGAAGCAGG 401
Qy 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 99
; 402 AAGGAGGATGAGGGATGCTTATGACCCCTG-----GAGAAAAATGTTTCA 449
; 100 ThrLysArgTyrAsnLeuGln-----IleTyrArgAlaGLeuGlyLysProLysIleThr 117
; 450 GTTCAGCGCTTTTGCTGCTGAGCTTATGAGCAGGTCTCCACTCCAGAAATATAA 509
; 118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 137
; 510 GTTTTAAACAAGACCCAGGAGAACGGACCTGCACCTTGATACCTGGCTGCACAGTGAG 569
; 138 LysGluGluLysAsnValThrTyrAsnTrpSer-----ProLeu--- 150
; 570 AAGGGGGAC---CATGTGCTTACAGCTGGAGTGAAGAGCGGGGACCCACCACCTGAAC 626
; 151 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
; 627 CCAGCAACAGCTCCACCTCTCTGCTCCCTCACCTCGGCCCGCCAGCATCTGACAAATC 686
; 170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
; 687 TACATCTGCACCGTGCAGCAACCTTATCAGCAACAATTCAGACCTTTCAGC 737

RESULT 12
US-08-462-738-7
; Sequence 7, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..1073
; US-08-462-738-7

Alignment Scores:
```

```

Pred. No.: 1,42e-10 Length: 1079
Score: 160.00 Matches: 50
Percent Similarity: 43.15% Conservative: 35
Best Local Similarity: 25.38% Mismatches: 78
Query Match: 15.40% Indels: 34
DB: 2 Gaps: 8

US-09-882-171-483_COPY_22_220 (1-199) x US-08-462-738-7 (1-1079)

Qy 12 LeuGlyGluSerValThrPhePro-----ValAsnIleGlnGluProArg 26
Db 183 TTGGGAAGCAAGTGTCTGCTGCCCTGACATATGAAAGGATAAATAGAGCATGAACAAA 242
Qy 27 GlnValLysIleAlaThrSerLysThr-----SerVal 39
Db 243 AGCATCCACATTCGTCTGCAATGGCAAAATCTGGAGAACAGTGTGAGAACAAATA 302
Qy 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValHisArgAsn 59
Db 303 GTGTCTCTGTATCCATCCGAAGCAGGCCCTCCAGGTTATCTAGGAGATCGCTACAAGTTT 362
Qy 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
Db 363 TATCTGGAG-----AATCTCACCTCGGGATACGGGAAGCAGG 401
Qy 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
Db 402 AAGGAGATGAGGATGTACTTATGACCCCTG-----GAGAAATAATGTTTCA 449
Qy 100 ThrLysArgTyrAsnLeuGln-----IleTyrArgLeuGlyLysProLysIleThr 117
Db 450 GTTCAGCGCTTTTGCCTGCGATTTGAGGCTTTATGACAGGTCTCCACTCCAGAAATATA 509
Qy 118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 137
Db 510 GTTTTAAACAGACCAGAGAACGGGACCTGTCACCTCCCTGCGGCCCCAGCATGTGACAAATATC 569
Qy 138 LysGluGluLysAsnValThrTyrAsnTrpSer-----ProLeu--- 150
Db 570 AAGGGGAC---CATGTGGCTTACAGTGTGAGTGAAGAGGGGGGACCCACCATGTGAAC 626
Qy 151 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
Db 627 CCAGCCAAACAGTCTCCACCTCTGCTCCCTCCCTGCGGCCCCAGCATGTGACAAATATC 686
Qy 170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
Db 687 TACATCTGACCTGTAGCAACCTTATCAGCAACAATTCAGACCTTCCAGACCTTCCAGC 737

RESULT 13
US-09-199-955-7
; Sequence 7, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

QY 170 TTTTCTGACCGTGGAGCAACCTTATCAGCAACAATTCCAGACCTTTCAGC 186
DB 687 TATCTGACCGTGGAGCAACCTTATCAGCAACAATTCCAGACCTTTCAGC 737

RESULT 14
US-08-880-875-7
; Sequence 7, Application US/08880875
; Patent No. 6399065
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,777
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..1073
; US-08-880-875-7

Alignment Scores:
Pred. No.: 1.42e-10 Length: 1079
Score: 160.00 Matches: 50
Percent Similarity: 43.15% Conservative: 35
Best Local Similarity: 25.38% Mismatches: 78
Query Match: 15.40% Indels: 34
DB: 3 Gaps: 8

US-09-882-171-483_COPY_22_220 (1-199) x US-08-880-875-7 (1-1079)
QY 12 LeuGluSerValThrPhePro-----ValAsnIleGlnGluProArg 26
DB 183 TTGGGAAGCAAGTGTCTGCTGCCCTGCACATATGAAGAGGATAAAGAGCATGAACAAA 242
QY 27 GlnValIleIleAlaTrpThrSerLysThr-----SerVal 39

DB 243 AGCATCCACATTGTCGTACCAATGCAAAATCACTGGAGAACAGTGTGAGAACAAAATA 302
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
DB 303 GTGTCTCTTGATCCATCCGAGCAGCCCTCCACGTTATCTAGGAGATCGCTACAAGTTT 362
QY 60 TTTTCTGACCGTGGAGCAACCTTATCAGCAACAATTCCAGACCTTTCAGC 79
DB 363 TATCTGGAG-----AATCTCACCCCTGGGATACGGGAAGCAGG 401
QY 80 MetGluAspAlaGlyAspTyrIlysalasplleAsnThrGlnAlaaspProTyrThrThr 99
DB 402 AAGGAGGATGAGGATGCTTATGACCCCTG-----GAGAAAATGTTTCA 449
QY 100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
DB 450 GTTCAGCGCTTTTGCTGCGAGTTGAGGCTTATGAGCAGGCTCTCCACTCCAGAAATAAA 509
QY 118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 137
DB 510 GTTTTAAACAAGACCCAGGAGAACCGGACCTGCACCTTGATCTAGCTGGCTGCACAGTGGAG 569
QY 138 LysGluGluLysAsnValThrTyrAsnTrpSer-----ProLeu--- 150
DB 570 AAGGGGGAC---CATGTGGCTTACAGCTGGAGTGAAGGCGGGGACCCACCCACTGAAC 626
QY 151 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
DB 627 CCAGCCCAACAGCTCCACCTCTGTCCTCCCTCACCCTCGGCCCGCCGAGCATGTCACATATC 686
QY 170 TTTTCTGACCGTGGAGCAACCTTATCAGCAACAATTCCAGACCTTTCAGC 737
DB 687 TATCTGACCGTGGAGCAACCTTATCAGCAACAATTCCAGACCTTTCAGC 737

RESULT 15
US-08-348-792-1
; Sequence 1, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1716 base pairs
; TYPE: nucleic acid

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 5, 2005, 09:29:36 ; Search time 423.629 Seconds
(without alignments)
2703.765 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220
Perfect score: 1039
Sequence: 1 KDSFTFTVNGILGESVTFPV.....NNSDISARQLCADIAMGR 199

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114005_26092/app_query.fasta_1.910
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOPCLI=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09882171@cgn_1_582@runat_04022005_114005_26092
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US16_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039	100.0	1040	16	US-10-436-523-29
2	1039	100.0	1067	18	US-10-723-860-1885
3	1039	100.0	3173	10	US-09-809-391-174
4	1039	100.0	3173	10	US-09-882-171-174
5	1039	100.0	3173	17	US-10-164-861-174
6	1039	100.0	3326	18	US-10-723-860-6219
7	1039	100.0	3687	14	US-10-198-846-13255
8	352	33.9	1849	17	US-10-471-449-20
9	352	33.9	2286	10	US-09-860-836B-12
10	343.5	33.1	2448	18	US-10-310-612-1
11	343.5	33.1	2448	18	US-10-328-538-1
12	332	32.0	652	16	US-10-436-523-84
13	332	32.0	711	16	US-10-436-523-87
14	332	32.0	870	16	US-10-436-523-75
15	332	32.0	870	16	US-10-436-523-93
16	332	32.0	870	16	US-10-436-523-95
17	332	32.0	1139	16	US-10-436-523-74
18	332	32.0	1139	17	US-10-170-385-132
19	332	32.0	1423	15	US-10-220-946-17
20	331	31.9	870	16	US-10-436-523-92
21	329	31.7	870	16	US-10-436-523-94
22	320	30.8	1147	17	US-10-264-237-216
23	316.5	30.5	609	16	US-10-436-523-50
24	316.5	30.5	609	16	US-10-436-523-55
25	316.5	30.5	927	16	US-10-436-523-44
26	316.5	30.5	993	16	US-10-436-523-2
27	316.5	30.5	1041	17	US-10-257-174-9
28	316.5	30.5	1225	14	US-10-104-943-40
29	316.5	30.5	1463	17	US-10-471-449-17
30	316.5	30.5	1868	14	US-10-245-752-75
31	316.5	30.5	1868	14	US-10-245-859-75
32	316.5	30.5	1868	14	US-10-245-103-75
33	316.5	30.5	1868	14	US-10-245-107-75
34	316.5	30.5	1868	14	US-10-245-143-75
35	316.5	30.5	1868	14	US-10-245-771-75
36	316.5	30.5	1868	14	US-10-245-851-75
37	316.5	30.5	1868	14	US-10-245-883-75
38	316.5	30.5	1868	14	US-10-237-535-75
39	316.5	30.5	1868	14	US-10-238-183-75
40	316.5	30.5	1868	14	US-10-238-283-75
41	316.5	30.5	1868	14	US-10-238-370-75
42	316.5	30.5	1868	14	US-10-245-055-75
43	316.5	30.5	1868	14	US-10-245-147-75
44	316.5	30.5	1868	14	US-10-245-730-75
45	316.5	30.5	1868	14	US-10-245-739-75

ALIGNMENTS

RESULT 1
US-10-436-523-29
; Sequence 29, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraxel, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-436-523-29

Alignment Scores:

Pred. No.: 7,63e-125 Length: 1040
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-10-436-523-29 (1-1040)

QY 1 LysAspSerGluThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 105 AAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGAGAGTCAGTCATCTTCCTGTA 164
QY 21 AsnIleGlnProArgGlnValLysIleIleAlaThrThrSerLysThrSerValAla 40
DB 165 AATATCCAGAACCCAGGCAAGTTAAATCAATCTTGGACTTCTAAACATCTGTGCT 224
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 225 TATGTAAACACAGAGACTCAGAAACAGACCCGCTAGTTACTCTGACCCACAGAAATAT 284
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 285 TATGAACGGATACATGCTTAGTCCGAACCTACATCTGCTATTAGCGATCTGAGGATG 344
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 345 GAAGACGCGAGGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 404
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 405 AAGCGTACAACTGCAATCTATCTGCTGGGAAACCAAAATATACACAGATTTA 464
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
DB 465 ATGGCATCTGTGACAGCACCCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAA 524
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
DB 525 AAGAATGTGACATACATAATGGAGTCCCTGGGAGAAGAGGGTAATGTCTTCAAATCTTC 584
QY 161 GlnThrProGluAspGlnLeuThrTyrThrCysThrAlaAsnProValSerAsn 180
DB 585 CAGACTCCTGAGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAAC 644
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 645 AATTCGACTCCATCTCTGCGCGGAGCTCTGTGACAGATCGCAATGGGCTTCGCT 701

RESULT 2

US-10-723-860-1885
; Sequence 1885, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1885
; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-723-860-1885

Alignment Scores:

Pred. No.: 7,93e-125 Length: 1067
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-10-723-860-1885 (1-1067)

QY 1 LysAspSerGluThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
DB 133 AAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGAGAGTCACTCTTCCCTGTA 192
QY 21 AsnIleGlnProArgGlnValLysIleIleAlaThrThrSerLysThrSerValAla 40
DB 193 AATATCCAGAACCCAGGCAAGTTAAATCAATCTTGGACTTCTAAACATCTGTGCT 252
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 253 TATGTAAACACAGAGACTCAGAAACAGACCCGCTAGTTACTCTGACCCACAGAAATAT 312
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
DB 313 TATGAACGGATACATGCTTAGTCCGAACCTACAAATCTGCTCATTTAGCGATCTGAGGATG 372
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 373 GAAGACGCGAGGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 432
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 433 AAGCGTACAACTGCAATCTATCTGCTGGGAAACCAAAATATACACAGATTTA 492
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
DB 493 ATGGCATCTGTGAGACAGCACCCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAA 552
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
DB 553 AAGAATGTGACATACATAATGGAGTCCCTGGGAGAAGAGGGTAATGTCTTCAAATCTTC 612
QY 161 GlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 613 CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAAC 672
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 673 AATTCGACTCCATCTCTGCGCGGAGCTCTGTGACAGATCGCAATGGGCTTCGCT 729

RESULT 3

US-09-809-391-174
; Sequence 174, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 3173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3119)
; OTHER INFORMATION: n equals a.t.g. or c

```
; NAME/KEY: SITE
; LOCATION: (3121)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-174

Alignment Scores:
Pred. No.: 4,06e-124 Length: 3173
Matches: 199
Score: 1039.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
DB: 10 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-09-809-391-174 (1-3173)

Qy 1 LysAspSerGluLeuPheThrValAlaGlyLeuGlyCysValThrPheProVal 20
Db 114 MAAGACTCAGAAATCTTCAGTGAATGGGATTCGGAGAGTCACTCTTCCCTGTA 173
Qy 21 AsnIleGlnGluProArgGlnValLysIleAlaThrThrSerLysThrSerValAla 40
Db 174 AATATCAAGAACCCAGCGGAAGTTAAATCATTTGCTTGACATCTTAAACATCTGTGCT 233
Qy 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 234 TAATGTAACACAGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTA 293
Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValLysSerAspLeuArgMet 80
Db 294 TATGAACGGATACATGCTTAGTCCGAACACTACAATCTGGTCAATAGCGATCTGAGGATG 353
Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 354 GAAGACGACGAGACTACAAAGCAGACATATAATACACAGGCTGATCCCTACACACACC 413
Qy 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 414 AAGCGTACAACTGCAATCTATCTCGCTGGGAAACCAAAATTCACAGAGTTTA 473
Qy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 474 ATGGCTCTGTGAACAGCACCTGTAATGTGCACACTGCATGCTGTAGAGAAAGAGAA 533
Qy 141 LysAsnValThrTyrAsnThrProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
Db 534 AAGAATGTGATACATAATGAGTCCCTGGGAGAGAGGGTAATGCTTCAAAATCTTC 593
Qy 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 594 CAGACTCTGAGGACCAAGAGCTGACTTACCGTGTACGCCAGAACCCCTGTGAGCAAC 653
Qy 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
Db 654 AATTCTGACTCCATCTCTGCCGCGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT 710

RESULT 4
US-09-882-171-174
; Sequence 174, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
```

/	PRIOR APPLICATION NUMBER:	60/047,593
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/047,614
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/043,578
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/043,576
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/047,501
/	PRIOR FILING DATE:	1997-05-23
/	PRIOR APPLICATION NUMBER:	60/043,670
/	PRIOR FILING DATE:	1997-04-11
/	PRIOR APPLICATION NUMBER:	60/056,632
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,664
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,876
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,881
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,909
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,875
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,862
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,887
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/056,908
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/048,964
/	PRIOR FILING DATE:	1997-06-06
/	PRIOR APPLICATION NUMBER:	60/057,650
/	PRIOR FILING DATE:	1997-09-05
/	PRIOR APPLICATION NUMBER:	60/056,884
/	PRIOR FILING DATE:	1997-08-22
/	PRIOR APPLICATION NUMBER:	60/057,669
/	PRIOR FILING DATE:	1997-09-05
Alignment Scores:		
Pred. No.:	4,06e-124	Length: 3173
Score:	1039.00	Matches: 199
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	10	Gaps: 0
US-09-882-171-483_COPY_22_220 (1-199) x US-09-882-171-174 (1-3173)		
Qy	1	LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Dd	114	AAGACTCAGAATCTTCACAGTGAATGGATTCTGGAGAGTCAGTCACTTTCCCTGTA 173
Qy	21	AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
Dd	174	AATATCCAAGAACCGCAAGTTAAATCATTTGTGGACTTCTAAAAACATCTGTGTCT 233
Qy	41	TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Dd	234	TATGTAACACACAGGAGACTCAGAAAACAGCACCGGTAGTACTGTGACCACACAGAAATYAT 293
Qy	61	TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Dd	294	TATGAACGGATACATGCCTTAGGTCCGAACATAAATACACAGCTGATCCCTACACACCCACC 353
Qy	81	GluAspAlaGlyVasPTryLysAlaAspIleAsnThrGlnAlaaspProTyrThrThrThr 100
Dd	354	GAGACGCAGGAGACTACAAGCAGACATAAATACACAGCTGATCCCTACACACCCACC 413
Qy	101	LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
Dd	414	AAGCGCTACAACTGCATAATCTATCGTCGGCTTGGAACCAACCAAAATTTACACAGAGTTTA 473

121	MetAlaSerValAsnSerThrCysAsnValThrIleuThrCysSerValGluIysGluGlu	140
Qy		
474	ATGGCATCTGTGAACAGCACCATGTAATGTACACTGACATGCTCTGTAGAGAAAGAAGAA	533
Db		
141	LysAsnValThrTyrAsnTrpSerProIeuGlyCyluGluAsnValIleuGlnIlePhe	160
Qy		
534	AAGAATGTGACATACAATTTGGAGTCCCTGGGAGAAGAGGTAAATGTCTTTCAAATCTTTC	593
Db		
161	GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn	180
Qy		
594	CAGACTCTCTAGGACCAAGAGCTGACTTACAGTGTATACGCCAGAACCTCTGCACCAAC	653
Db		
181	AsnSerAspSerIleSerAlaArgGlnIleuCysAlaAspIleAlaMetGlyPheArg	199
Qy		
654	ATTCTGTACTCATCTCTTCTGCGCAGCTGTGTGCACATCGCAATGGGTTTCCTG	710
Db		

354	DB	GNAGAGCAGGAGACTCAAAGCAGACATAAATACACAGGCTGATCCCTACACCAACC	413
101	QY	LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysValThrGlnSerLeu	120
414	DB	AAGCCCTACAACCTGCAGAAATCTATGTCGGCTTGGGAACCAANAATTACACAGATTTA	473
121	QY	MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu	140
474	DB	ATGGCATCTGTGAACAGCACCTGTAAATGTCACACTGACATGCTGTAGAGAAAGAAGAA	533
141	QY	LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe	160
534	DB	AGAATGTGCATACAAATTGGAGTCCCTCGGAGAGAGGGTAATGTCTCTCAAACTCTC	593
161	QY	GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn	180
594	DB	CAGACTCTCTGGAGCAACAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTCAGCAAC	653
181	QY	AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg	199
654	DB	ATTATTGATCAATCTTSCCCGACGCTGTGCAGACATCGCAATGGGCTTCGT	710

Db 315 TATGAACGATACATCGCTTAGTCCGACCTACAACTCTGGTCAATCGATCGATCGAGATG 374
Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 375 GAAGACGAGAGAGACTACAAAGCAGACAGATAAATACACAGGCTGATCCCTACACCACC 434
Qy 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 435 AAGCGCTACAACTCGCAAACTATCGCTGGGTAACCAAAATACACAGAGTTTA 494
Qy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 495 ATGGCACTGTGACACAGACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAGAA 554
Qy 141 LysAsnValThrTyrAsnTyrSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
Db 555 AAGAAATGTGACATCAAAATGGAGTCCCTGGGAGAGAGGGTAATGCTTCAAACTTC 614
Qy 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 615 CAGACTCTGAGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTCAGCAAC 674
Qy 181 AsnSerAspSerIleSerAlaArgGlnLeuGlyAlaAspIleAlaMetGlyPheArg 199
Db 675 AATCTGACTCCATCTCTGCGCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCTG 731

RESULT 7

US-10-198-846-13255
; Sequence 13255, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13255
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2-3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677,
; LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13255

Alignment Scores:
Pred. No.: 5,09e-124 Length: 3687
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x US-10-198-846-13255 (1-3687)

Qy 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 496 AAAGACTCAGAATCTTACAGTGAATGGGATCTTGGGAGAGATCAGTCACTTTCCTGTA 555
Qy 21 AsnIleGlnProArgGlnValLysIleIleAlaThrSerLysThrSerValAla 40

Db 556 AATATCCAAGAACCCAGCGCAAGTTAAATCATTTGCTTGGACTTCTAAACCATCTCTGCT 615
Qy 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 616 TATGTAACACACAGGAGACTCAGAAACAGACACCCGCTAGTTACTGTGACCCACAGAAATTAT 675
Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 676 TATGAACGGATACATAGCTTAGTCCGAATACAACTCTGGTCAATAGCGATCTGAGGATG 735
Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 736 GAAGACGAGAGAGACTTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 795
Qy 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 796 AAGCGCTCAACCTCGCAAACTATCTGCTCGGCTTGGGAACCCAAAATATACACAGTTTA 855
Qy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluGluGlu 140
Db 856 ATGGCACTGTGAACAGACACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAGAA 915
Qy 141 LysAsnValThrTyrAsnTyrSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 916 AAGAAATGTGACATCAAAATGGAGTCCCTGGGAGAGAGGGTAATGTCCTTCAAACTTC 975
Qy 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 976 CAGACTCTGAGAGCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAAC 1035
Qy 181 AsnSerAspSerIleSerAlaArgGlnLeuGlyAlaAspIleAlaMetGlyPheArg 199
Db 1036 AATCTGACTCCATCTCTGCGCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCTG 1092

RESULT 8

US-10-471-449-20
; Sequence 20, Application US/10471449
; Publication No. US2004009771A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry; XU, Yuming;
; APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
; APPLICANT: TANG, Y. Tom; DUGGAN, Brendan M.;
; APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
; APPLICANT: HONCHELL, Cynthia D.; BUREFORD, Neil;
; APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
; APPLICANT: MASON, Patricia W.
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0925 USN
; CURRENT APPLICATION NUMBER: US/10/471,449
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US02/09052
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/275,249
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/316,810
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/323,977
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/348,447
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/343,880
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7500099CBI
US-10-471-449-20

Alignment Scores: 5.25e-35 Length: 1849
Pred. No.: 77
Score: 352.00 Matches: 77
Percent Similarity: 58.42% Conservative: 41
Best Local Similarity: 38.12% Mismatches: 70
Query Match: 33.88% Indels: 14
DB: 17 Gaps: 5

US-09-882-171-483_COPY_22_220 (1-199) x US-10-471-449-20 (1-1849)

QY 1 LysAspSerGluIlePheThrValAenGlyVileLeuGlyGluSerValThrPheProVal 20
DB 153 AAGGACTCAGCCCAACAGTGGTCTCAGGATCCTAGGGGTTCCGTGACTCTCCCCCTA 212
QY 21 AsnIleGlnProArgGlnValLysIleAlaThrPheSer---LysThrSerVal 39
DB 213 AACATCTCAGTACACAGAGATTGAGAAGCTCATCTGGATTGGTCCCAAAAATGCTCTT 272
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
DB 273 GCTTTTCGACGTCCTCCAAAGAAAT-----GTAAACCATTTATGGTCAAAAGC 317
QY 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
DB 318 TACCTGGCCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 377
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
DB 378 CTGAATGATCGAGGATCTTACAAAGCCAGATAAACCAAGGAATTTTGAAGTCACCACT 437
QY 100 ThrLysArgTyrAsnLeuGlnIleTyrArgGluGlyLysProLysIleThr---Gln 118
DB 438 GAGGAGAAATTCACCTGTTCTATGACGAGCTGCAGGAGCCCAAGTCACCATGAAG 497
QY 119 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 138
DB 498 TCTGTGAAGTGTCTGAGAACTTCTCTGTAAACATCACTCTAATGTGCTCCGTGAAGGG 557
QY 139 GluGluLysAsnValThrTyrAsnTrpSerProLeu-----GlyGlu 152
DB 558 GCAGAGAAAAGTGTCTGTACAGCTGAGCCCAAGGAGGAGCCCATGAGTCCAAT 617
QY 153 GluGluLysAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
DB 618 GGAGGCTCCATCTTACCGTCTCCGAAACACCATGTGACCCAGACCTGCCATACATCTGC 677
QY 173 ThrAlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys 191
DB 678 ACAGCCAGAACCCCGTCAGCAGAGAGGCTCCCTCCCTGTCATGTTGGCAGTTCTGT 737
QY 192 AlaAsp 193
DB 738 ACAGAT 743

RESULT 9
US-09-860-836B-12
; Sequence 12, Application US/09860836B
; Publication No. US20030054002A1
; GENERAL INFORMATION:
; APPLICANT: WAKELAND, WARD
; APPLICANT: WANDSTADT, AMY
; APPLICANT: MOREL, LAURENCE
; TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
; FILE REFERENCE: US/09/860,836B
; CURRENT APPLICATION NUMBER: 60/204,963
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 2286

TYPE: DNA
; ORGANISM: Homo sapien
US-09-860-836B-12

Alignment Scores: 7.22e-35 Length: 2286
Pred. No.: 77
Score: 352.00 Matches: 77
Percent Similarity: 58.42% Conservative: 41
Best Local Similarity: 38.12% Mismatches: 70
Query Match: 33.88% Indels: 14
DB: 10 Gaps: 5

US-09-882-171-483_COPY_22_220 (1-199) x US-09-860-836B-12 (1-2286)

QY 1 LysAspSerGluIlePheThrValAenGlyVileLeuGlyGluSerValThrPheProVal 20
DB 49 AAGGACTCAGCCCAACAGTGGTGTGACAGGATCCTAGGGGTTCCGTGACTCTCCCCCTA 108
QY 21 AsnIleGlnProArgGlnValLysIleAlaThrPheSer---LysThrSerVal 39
DB 109 AACATCTCAGTACACAGAGATTGAGAAGCTCATCTGGATTGGTCCCAAAAATGCTCTT 168
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
DB 169 GCTTTTCGACGTCCTCCAAAGAAAT-----GTAAACCATTTATGGTCAAAAGC 213
QY 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
DB 214 TACCTGGCCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 273
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
DB 274 CTGAATGATCGAGGATCTTACAAAGCCAGATAAACCAAGGAATTTTGAAGTCACCACT 333
QY 100 ThrLysArgTyrAsnLeuGlnIleTyrArgGluGlyLysProLysIleThr---Gln 118
DB 334 GAGGAGAAATTCACCTGTTCTATGACGAGCTGCAGGAGCCCAAGTCACCATGAAG 393
QY 119 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 138
DB 394 TCTGTGAAGTGTCTGAGAACTTCTCTGTAAACATCACTCTAATGTGCTCCGTGAAGGG 453
QY 139 GluGluLysAsnValThrTyrAsnTrpSerProLeu-----GlyGlu 152
DB 454 GCAGAGAAAAGTGTCTGTACAGCTGAGCCCAAGGAGGAGCCCATGAGTCCAAT 513
QY 153 GluGluLysAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
DB 514 GGAGGCTCCATCTTACCGTCTCCGAAACACCATGTGACCCAGACCTGCCATACATCTGC 573
QY 173 ThrAlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys 191
DB 574 ACAGCCAGAACCCCGTCAGCAGAGAGGCTCCCTCCCTGTCATGTTGGCAGTTCTGT 633
QY 192 AlaAsp 193
DB 634 ACAGAT 639

RESULT 10
US-10-310-612-1
; Sequence 1, Application US/10310612
; Publication No. US20040109862A1
; GENERAL INFORMATION:
; APPLICANT: Emage, Peter
; TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
; FILE REFERENCE: HYS-68
; CURRENT APPLICATION NUMBER: US/10/310,612
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2448


```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-612-1

Alignment Scores:
Pred. No.: 1,02e-33 Length: 2448
Score: 343.50 Matches: 74
Percent Similarity: 56.72% Conservative: 40
Best Local Similarity: 36.82% Mismatches: 74
Query Match: 33.06% Indels: 13
DB: 18 Gaps: 4

US-09-882-171-483_COPY_22_220 (1-199) x US-10-310-612-1 (1-2448)

QY 1 LysAspSerGluPheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
Db 172 AAGGACTCAGCCCAACAGTGTGTCAGGATCCTAGGGGTTCCGTGACTCTCCCCCTA 231
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaThrThrSer---LysThrSerVal 39
Db 232 AACATCTCAGTAGACACAGAGATTGAGAACGTCTATCGATTGGTCCCAAAATGCTCTT 291
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
Db 292 GCTTTCGCGCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 396
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
Db 397 CTGAATGATGAGGATCTTACAAAGCCAGATAAACCAAGGAATTTGGAAGTCCACT 456
QY 100 ThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSer 119
Db 457 GAGGAGGAATTCACCTGTTCTGTCATGAGAGCTGCAGGAGCCCAAGTCCACTGAAG 516
QY 120 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 139
Db 517 TCTGTGAAGGTGCTGAGAACTTCTGTAAACATCACTCTAATGTCTCGTGAAGGGGCA 576
QY 140 GluLysAsnValThrTyrAsnTrpSerProLeu-----GlyGluGlu 153
Db 577 GAGAAAGTGTCTGACAGCTGGACCCCAAGGAAACCCATGCTTCTGAGTCCATGA 636
QY 154 GlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCysThr 173
Db 637 GGCTCCATTCTTACCGTCTCCCGAACACCATGTGACCCAGACCTGCCATACATCTGCACA 696
QY 174 AlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCysAla 192
Db 697 GCCCAGAACCCGTCAGCAGAGAAAGTCCCTCCCTGTGTCATGTTGGGCGAGTCTGTACA 756
QY 193 Asp 193
Db 757 GAT 759

RESULT 11
US-10-328-538-1
; Sequence 1, Application US/10328538
; Publication No. US20040109863A1
; GENERAL INFORMATION:
; APPLICANT: Entage, Peter
; TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
; FILE REFERENCE: HYS-68CP
; CURRENT APPLICATION NUMBER: US/10/328,538
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 10/310,612
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1
; LENGTH: 2448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-328-538-1

Alignment Scores:
Pred. No.: 1,02e-33 Length: 2448
Score: 343.50 Matches: 74
Percent Similarity: 56.72% Conservative: 40
Best Local Similarity: 36.82% Mismatches: 74
Query Match: 33.06% Indels: 13
DB: 18 Gaps: 4

US-09-882-171-483_COPY_22_220 (1-199) x US-10-328-538-1 (1-2448)

QY 1 LysAspSerGluPheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
Db 172 AAGGACTCAGCCCAACAGTGTGTCAGGATCCTAGGGGTTCCGTGACTCTCCCCCTA 231
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaThrThrSer---LysThrSerVal 39
Db 232 AACATCTCAGTAGACACAGAGATTGAGAACGTCTATCGATTGGTCCCAAAATGCTCTT 291
QY 40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
Db 292 GCTTTCGCGCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 396
QY 60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79
Db 337 TACCTGGCGCGACTAGACATCACCAAGTGGAGTTACTCCCTGTGCATCAGCAATCTGACT 396
QY 80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
Db 397 CTGAATGATGAGGATCTTACAAAGCCAGATAAACCAAGGAATTTGGAAGTCCACT 456
QY 100 ThrLysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSer 119
Db 457 GAGGAGGAATTCACCTGTTCTGTCATGAGAGCTGCAGGAGCCCAAGTCCACTGAAG 516
QY 120 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 139
Db 517 TCTGTGAAGGTGCTGAGAACTTCTGTAAACATCACTCTAATGTCTCGTGAAGGGGCA 576
QY 140 GluLysAsnValThrTyrAsnTrpSerProLeu-----GlyGluGlu 153
Db 577 GAGAAAGTGTCTGACAGCTGGACCCCAAGGAAACCCATGCTTCTGAGTCCATGA 636
QY 154 GlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCysThr 173
Db 637 GGCTCCATTCTTACCGTCTCCCGAACACCATGTGACCCAGACCTGCCATACATCTGCACA 696
QY 174 AlaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCysAla 192
Db 697 GCCCAGAACCCGTCAGCAGAGAAAGTCCCTCCCTGTGTCATGTTGGGCGAGTCTGTACA 756
QY 193 Asp 193
Db 757 GAT 759

RESULT 12
US-10-436-523-84
; Sequence 84, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
```



```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-523-75

Alignment Scores:
Pred. No.: 6,83e-33 Length: 870
Score: 332.00 Matches: 69
Percent Similarity: 58.56% Conservatives: 37
Best Local Similarity: 38.12% Mismatches: 69
Query Match: 31.95% Indels: 6
DB: 16 Gaps: 1

US-09-882-171-483_COPY_22_220 (1-199) x US-10-436-523-75 (1-870)

QY 8 ValAsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGlnGluProArgGln 27
Db 88 GTGGTTGGCGTCTTCAGAGTCCATCAGCCTCCCTGGAAATACCACCATGAAGAG 147
QY 28 ValLysIleIleAlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSer 47
Db 148 GTTGAGAACATCATCTGGTCTCTCACAAGTCTTGCCACTGTGGTCCAGGAAAGAG 207
QY 48 GluThrAlaProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeu 67
Db 208 GGACATCCAGCTACCATCATGTGACCAATCCACACTACACGGGCCAAGTTCCTG 267
QY 68 GlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrLys 87
Db 268 GACCCAGCTATTCCCTGCATATCAGCAATCTGAGCTGGAGGATTCAGGGCTTTACCAA 327
QY 88 AlaAspIleAsnThrGlnAlaAspProTyrThrThrLysArgTyrAsnLeuGlnIle 107
Db 328 GCTCAAGTCAACCTGAGAACATCCAGATCTTACCATGACGACGATACATCTATGTGTC 387
QY 108 TyrArgArgLeuGlyLysProLysIleThrGlnSerLeuMetAlaSerValAsnSerThr 127
Db 388 TACCGATGCTGTACAGAGCCAGATCACTGTGAACCTTTGAGAGTTCTGGGAAGTGCC 447
QY 128 CysAsnValThrLeuThrCysSerValGluLysGluLysAsnValThrTyrAsnTrp 147
Db 448 TGCAGTATGCTGCTGTGCTCTGTGGAAGGAGGAGGATGATGATGATGATGATGATG 507
QY 148 SerProLeuGlyGlu-----GluGlyAsnValLeuGlnIlePheGln 161
Db 508 CTCCTCCGGGGGATAGCACTTATACATTCATGAGGCCCTGCTCCTACGACATCCTGG 567
QY 162 ThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsnAsn 181
Db 568 AGGCCGGGGGACAGTGCCTCTCTACACCTGACAGGAGGAGGAGGAGGAGGAGGAGG 627
QY 182 Ser 182
Db 628 AGT 630

Search completed: February 5, 2005, 14:07:58
Job time : 427.629 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2005, 03:27:31 ; Search time 2623.94 Seconds
(without alignments)
2886.805 Million cell updates/sec

Title: US-09-882-171-483_COPY_22_220

Perfect score: 1039
Sequence: 1 KDSFPTVNGILGVSPTPV.....NNSDSISARQLCADIAMGFR 199

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-O=/cgn2_1/USPTO.spool/US09882171/runat_04022005_114004_26033/app_query.fasta_1.910
-DB=EST -OPMT=fastap -SUFFIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cddi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09882171 @CNG 1.1 4385 @runat 04022005_114004_26033 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: EST:

1:	gb_est1.*
2:	gb_est2.*
3:	gb_hic.*
4:	gb_est3.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_gsa1.*
9:	gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1039	100.0	987	9 AY408981	AY408981 Homo sapi
2	1025	98.7	987	9 AY408982	AY408982 Pan trogl
3	950	91.4	608	7 CV023928	CV023928 1001 Full
4	930.5	89.6	1074	4 BG106937	BG106937 602291349
5	889	85.6	582	5 BP303350	BP303350 BP303350
6	731	70.4	535	2 BF754299	BF754299 FMO-CR054
7	727	70.0	739	6 CB467388	CB467388 733129 MA
8	697	67.1	582	5 BP303194	BP303194 BP303194
9	690	66.4	837	5 BP159730	BP159730 BP159730

c	10	683	65.7	402	2	AW013969	UI-H-B10-
	11	611.5	58.9	923	9	AY408983	Mus muscu
	12	610.5	58.8	671	6	BY748483	BY748483
	13	597.5	57.5	788	4	BI151764	BI151764
	14	596	57.4	466	5	BU927996	AGENCOURT
	15	562	54.1	677	9	AG090451	Pan trogl
	16	506	48.7	519	4	BM089070	BM089070
c	17	503	48.4	719	7	CK772231	CK772231
	18	501.5	48.3	651	6	BY724459	BY724459
	19	371	35.7	322	1	AL597403	AL597403
	20	352	33.9	759	4	BI907423	BI907423
	21	352	33.9	1133	5	BM922555	BM922555
	22	352	33.9	2030	3	CR590858	CR590858
	23	351	33.8	912	5	BX388160	BX388160
	24	350	33.7	1671	9	AY4113809	AY4113809
	25	349	33.6	1017	1	AL561509	AL561509
	26	347	33.4	2131	3	BC027920	BC027920
	27	346	33.3	1671	9	AY413808	AY413808
	28	340	32.7	951	1	AL561522	AL561522
	29	329	31.7	333	1	AA863565	AA863565
	30	329	31.7	616	6	BY749229	BY749229
	31	328.5	31.6	724	4	BI839154	BI839154
	32	323.5	31.1	1303	3	AK090041	AK090041
	33	321.5	30.9	1100	3	AK009505	AK009505
	34	321	30.9	1038	5	BX462597	BX462597
	35	302	29.1	733	6	BY709212	BY709212
	36	297.5	28.6	849	4	BG243220	BG243220
	37	296	28.5	874	5	BP158760	BP158760
	38	295	28.4	1642	3	AK042288	AK042288
	39	295	28.4	2158	3	AK087345	AK087345
	40	294.5	28.3	426	5	BY181022	BY181022
	41	294.5	28.3	953	4	BG173210	BG173210
	42	294	28.3	744	6	CD466225	CD466225
	43	294	28.3	2099	3	AK088815	AK088815
	44	293.5	28.2	599	2	BE449128	BE449128
	45	290.5	28.0	664	7	CN793369	CN793369

ALIGNMENTS

RESULT 1

AY408981

LOCUS

DEFINITION

Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,

AY408981

ACCESSION

AY408981

VERSION

AY408981.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 987)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL

PUBLISHED

14671302

REFERENCE

2 (bases 1 to 987)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1. .987

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>987
/gene="CD84"
/locus_tag="HCM3405"

ORIGIN

Alignment Scores:
Pred. No.: 1.47e-116 Length: 987
Score: 1039.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AY408981 (1-987)

QY 1 LysAspSerGluLeuPheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 64 AAAGACTCAGAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACITTCCTCGTA 123
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 124 AATATCCAGAACACCGCAAGCTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCT 183
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 184 TATGTAACACACGAGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 243
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 244 TATGAACGGATACATCGCTTGGTCCGAACACTCAATCTGGTCTTAGCGATCTGAGGATG 303
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 304 GAAGACGCGAGGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 423
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 364 AAGCGCTACAACTCGTTCGCTTGGGAAACCAAAATTTACACAGAGTTA 423
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
DB 424 ATGGCATCTGTGAACAGCACCTGTATGTACACTGACATGCTCTGTAGAGAAAGAGAA 483
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 484 AAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAAATGCTTCAATCTTC 543
QY 161 GlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 544 CAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAAC 603
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 604 AATCTGACTCCATCTCTGCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCGCT 660

RESULT 2
AY408982 987 bp DNA - linear GSS 15-DEC-2003
LOCUS Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408982
VERSION AY408982.1 GI:39764950
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 987)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..987
location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>987
/gene="CD84"
/locus_tag="HCM3405"

ORIGIN

Alignment Scores:
Pred. No.: 7.69e-115 Length: 987
Score: 1025.00 Matches: 196
Percent Similarity: 99.50% Conservative: 2
Best Local Similarity: 98.49% Mismatches: 1
Query Match: 98.65% Indels: 0
DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AY408982 (1-987)

QY 1 LysAspSerGluLeuPheThrValAsnGlyLeuGlyGluSerValThrPheProVal 20
DB 64 AAAGACTCAGAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACITTCCTCGTA 123
QY 21 AsnIleGlnGluProArgGlnValLysIleAlaTrpThrSerLysThrSerValAla 40
DB 124 AATATCCAGAACACCGCAAGCTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCT 183
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 184 TATGTAACACACGAGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 243
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 244 TATGAACGGATACATCGCTTGGTCCGAACACTCAATCTGGTCTTAGCGATCTGAGGATG 303
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
DB 304 GAAGACGCGAGGAGACTCAGAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATAT 423
QY 101 LysArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 364 AAGCGCTACAACTCGTTCGCTTGGGAAACCAAAATTTACACAGAGTTA 423
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu 140
DB 424 ATGGCATCTGTGAACAGCACCTGTATGTACACTGACATGCTCTGTAGAGAAAGAGAA 483
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
DB 484 AAGAATGTGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAAATGCTTCAATCTTC 543
QY 161 GlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
DB 544 CAGACTCTCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAAC 603
QY 181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
DB 604 AATCTGACTCCATCTCTGCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCGCT 660

RESULT 2
AY408982 987 bp DNA - linear GSS 15-DEC-2003
LOCUS Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408982
VERSION AY408982.1 GI:39764950
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 987)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..987
location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>987
/gene="CD84"
/locus_tag="HCM3405"

```

Db

604 AATCTGACTCCATCTCTGCGCGCAGCTCTGTGCAGACATGGCAATGGGCTCCCGT 660

RESULT 3

CV023928

LOCUS

DEFINITION

1001 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC020063, mRNA sequence.

CV023928

VERSION

CV023928.1 GI:51481736

KEYWORDS

SOURCE

EST.

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 608)

AUTHORS

Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., DiCot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingsmith,T.R., Hartley,J.L., Eposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,J., Guick,M.B., Albaladejo,J.S., Hill,D.E. and Vidal,M.

TITLE

Human ORFome Version 1.1: a Platform for Reverse Proteomics

JOURNAL

Genome Res. (2004) In press

COMMENT

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers

PCR Primers

FORWARD: ATGGCTCAGCACCACCTTA

BACKWARD: TAGATCAACAATTCATAGCTTGAAGT

Insert Length: 608 Std Error: 55.00

Plate: 11032 row: 11 column: E

Seq primer: ACTGCCGTCGTTTACACAGCTCGTACTGGGAAAC

High quality sequence start: 91

High quality sequence stop: 607

POLYA=No.

FEATURES

source

1..608

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="mixed"

/clone_lib="Full Length cDNA from the Mammalian Gene Collection"

/note="vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.:	6.3e-106	Length:	608
Score:	950.00	Matches:	181
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.43%	Indels:	0
DB:	7	Gaps:	0

US-09-882-171-483_COPY_22_220 (1-199) x CV023928 (1-608)

Qy

1 LysApSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20

Db

64 AAAGACTCAGAATCTTCACAGTGAATGGATCTTCGGAGAGTCAGTCACCTTCCTGTA 123

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 3,51e-103 Length: 1074
Score: 930.50 Matches: 186
Percent Similarity: 93.56% Conservative: 3
Best Local Similarity: 92.08% Mismatches: 10
Query Match: 89.56% Indels: 4
DB: 4 Gaps: 1

US-09-882-171-483_COPY_22_220 (1-199) x BG106937 (1-1074)

```
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGlySerValThrPheProVal 20
DB 114 AAAGACTCAGAAATCTTCACAGTGAATGGATTCTGGGAGAGTCAGTCACCTTCCTGTA 173

QY 21 AsnIleGlnGluProArgGlnValLysIleIleAlaThrSerLysThrSerValAla 40
DB 174 AATATCCAGAACCCAGCGCAATGTTGCTTGGACTTCTAAACATCTGTTGCT 233

QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
DB 234 TATGTAACACCCAGGAGACTCAGAAACAGCACCCGTTGTTACTGTGACCCACAGAAATAT 293

QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
DB 294 TATGAACGGATACATGCCTTAGTCCGAATACAAATCTGGTCATTAGCGATCTGAGGATG 353

QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
DB 354 CGACAGCGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTCACACACCACC 413

QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
DB 414 AAGCGCTACACTGCAATCTATCGTCGGCTTGGGAACCAAAATACACAGAGTTA 473

QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
DB 474 ATGGCATCTGTGAACAGCACCTGTAATGTACACTGCATGCTCTGTAGAGAAAGAA 533

QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLysGlnIlePhe 160
DB 534 AAGAATGTACATACAAATGGAGTCCCTGGGAGAGAGGGTAATGTCTTCACATCTTC 593

QY 161 GlnThrProGluAspGlnGluLeuThrTyr-ThrCysThrAlaGlnAsnProValSerAs 180
DB 594 CAGACTCCTGAGGACCAAGAGCTGACTTACCAGGTGACAGCCAGAGCCTGTGAGCAA 653

QY 180 nAen-----SerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPh 198
DB 654 CAATTTCTGAATCCATCATCTGCGCGGAAGGT-CTGGTGACAGACATCGCAATGGGCT 712

QY 198 eaq 199
DB 713 TCGG 716
```

RESULT 5
BP303350
LOCUS
DEFINITION
BP303350 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MFE08190, mRNA sequence.

ACCESSION
BP303350
VERSION
BP303350.1 GI:52232310

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)

REFERENCE

AUTHORS

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezukui@ims.u-tokyo.ac.jp.

Location/Qualifiers

source

1. 582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MFE08190"

/cell_type="macrophage"

/clone_lib="Sugano cDNA library, macrophage"

ORIGIN

Alignment Scores:
Pred. No.: 1.84e-98 Length: 582
Score: 889.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.56% Indels: 0
DB: 5 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x BP303350 (1-582)

```
QY 31 IleAlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSerGluThrAla 50
DB 1 ATTGCTTGGAATCTCTAAACATCTGTTGCTTATGTAACACCCAGGAGACTCAGAAACAGCA 60

QY 51 ProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeuGlyProAsn 70
DB 61 CCCGTAGTACTCTGTGACCCACAGAAATATTATTGAACGATACATGCTTAGGTCGGAAC 120

QY 71 TyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrLysAlaAspIle 90
DB 121 TACAATCTGGTCATTAGCGATCTGAGGATGGAAGACGAGAGACTACAAAGCAGACATA 180

QY 91 AsnThrGlnAlaAspProTyrThrThrThrLysArgTyrAsnLeuGlnIleTyrArgArg 110
DB 181 AATACACAGGCTGATCCCTACACCACCAAGCGCTACAACTGCAATCTATCGTCGG 240

QY 111 LeuGlyLysProLysIleThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnVal 130
DB 241 CTTGGGAACCAAAATTTACAGAGTTAATGGCACTCTGTGACAGCACCTGTAAATGTC 300

QY 131 ThrLeuThrCysSerValGluLysGluLysAsnValThrTyrAsnTrpSerProLeu 150
DB 301 ACACGTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAAATGGAGTCCCTG 360

QY 151 GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyr 170
DB 361 GGAGAAAGAGGGTAATGTCCTTCAAATCTTCAGACTCTCTGAGGACCAAGAGCTGACTTAC 420

QY 171 ThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGlnLeu 190
DB 421 ACGTGTACAGCCGAGAACCTGTGACGAACTTCTGACTCCATCTCTGCTCCCTCCCGGAGCTC 480

QY 191 CysAlaAspIleAlaMetGlyPheArg 199
DB 481 TGTGACAGACATCGCAATGGGCTTCGT 507
```

RESULT 6

BP754299

LOCUS

DEFINITION

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BP754299

VERSION

BP754299.1 GI:12081079

KEYWORDS

EST.

BP754299 535 bp mRNA linear EST 10-JAN-2001

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

BP754299

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

BP754299

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

BP754299

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

BP754299

PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 535)
 AUTHORS Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,
 Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
 Goldman G.H., Carvalho A.F., Matekuma A., Baia G.S., Simpson D.H.,
 Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
 O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
 Simpson A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=PM0-CT0547-091000-001-a04&t3=2000-10-09&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 533.

FEATURES

source

1..535

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CT0547"

/notes="Organ: colon; Vector: puc18; Site: 1: SmaI; Site 2:

SmaI; A mini-library was made by cloning products derived

from ORFESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 4,16e-79

Score: 731.00

Percent Similarity: 98.63%

Best Local Similarity: 98.63%

Query Match: 70.36%

DB: 2

Length: 535

Matches: 144

Conservative: 0

Mismatches: 1

Indels: 1

Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x BF754299 (1-535)

Qy 1 LysAspSerGluLeuPheThrVal-AenGlyLeuGlyGluSerValThrPheProVa 20

Db 98 AAAGACTCAGAAATCTTCACAGTGAATTCGATCCTGGGAGAGTCAGTCACTTCCCTGT 157

Qy 20 lAnlleGlnGluProArgGlnVallylleAlaTrpThrSerlysthrSerValAl 40

Db 158 AAATATCAAGAACCCAGCGAAGTAAATCATTTGCTGGACTTCTAAAACATCTGTTC 217

Qy 40 aTyrValThrProGlyAspSerGluThrAlaProValValThrHisArgAenTy 60

Db 218 TTATGTAAACACAGAGACTCAGAAACAGACCGCTAGTACTGTGACCCACAGAAATTA 277

Qy 60 rTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuVallyleSerAspLeuArgMe 80

Db 278 TTATGAACGGATACATCGCTTAGTCCGAACTACAAATCTGGTCATTAGCGATCTGAGAT 337

Qy 80 tGluAspAlaGlyAspTyrLysAlaAAspIleAsnThrGlnAlaAspProTyrThrThr 100
 Db 338 GGAAGCCGACGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCA 397
 Qy 100 rlyGArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProTyrIleThrGlnSerle 120
 Db 398 CAAGCGCTACAACTGCAAAATCTATCGCGCTTGGGAACCAAAATTTACACAGATTT 457
 Qy 120 uMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGl 140
 Db 458 AATGCATCTGTGAACAGCAGCACTGTAAATGTACACATGACATGCTCTGTAGAGAAAGA 517
 Qy 140 uLysAsnValThrTyr 145
 Db 518 AAAGAATGTGACATAC 533

RESULT 7

CB467388

LOCUS

DEFINITION

CB467388

ACCESSION

CB467388.1

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

REFERENCE

1 (bases 1 to 739)

Smith, T.P.L., Roberts, A.J., Ehternkamp, S.E., Chitko-McKown, C.G.,

Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

Unpublished (2003)

CONTACT: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross_match v0.990329.

Plate: LAMB010 row: M column: 23

Seq primer: GTAATACGACTCATATAGGG.

FEATURES

Location/Qualifiers

1..739

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 6BOV"

/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

ORIGIN

Alignment Scores:

Pred. No.: 2.04e-78

Score: 727.00

Percent Similarity: 83.08%

Best Local Similarity: 70.26%

Query Match: 69.97%

DB: 6

Length: 739

Matches: 137

Conservative: 25

Mismatches: 33

Indels: 0

Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x CB467388 (1-739)

Qy 2 AspSerGluPheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsn 21

Db 96 GACACAGACATCTTCATAGTGAATGGATCTCTGGGAGAGTCAGTCACTTCCCTTAAAT 155

Qy 22 IleGlnGluProArgGlnVallylleAlaTrpThrSerlysthrSerValAlaTyr 41


```

Db      156 ATCCACCATCAGAGAAAGTTACCATCTTCTGGCATTCAGAAACATCTGTTCTTC 215
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      42 ValThrProGlyAspSerGluThrAlaProValValThrValHisArgAsnTyrTyr 61
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      216 GTAAACACCAAGAACTTTGGAGAGAAACCATAGTTACCATAAACCCACCAAAATTTACCAT 275
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      62 GluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGlu 81
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      276 GAACGAAATAGTGTCTCAGGTGAGAACTATAAACCCTGGAGCTCAGAAATCTGAGAGTTGAA 335
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      82 AspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrLys 101
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      336 GACTCAGGATCTACAAACCCACATATAATGTAGAGACTCTAAAGTGACGACCAACAGG 395
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      102 ArgTyrAsnLeuGlnIleTyrArgLeuGlyLysProLysIleThrGlnSerLeuMet 121
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      396 TCCTACAACCTTCAAGTCTATCGTCTGTGAGAGCCCAAAATTTACTCAGAGTTTCGTG 455
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      122 AlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluLys 141
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      456 ACATCTGTGAACAGCACCTGTATGTACACTGATGCTCTGTGATAAGCAAGAAAG 515
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      142 AsnValThrTyrAsnTyrSerProLeuGlyGluGlyAsnValLeuGlnIlePheGln 161
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      516 ATGTGACATACAGTTGGAGTCCAGAGGGAAGAGGCAATGCTCTCAAAATCTTCAG 575
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      162 ThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 181
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      576 ACCCTGTGACAACCAAGAGAGAGACTTACACGTGTACAGCGTGAACCCCTGTGACAA 635
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      182 SerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMet 196
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      636 TCTGACTCCATCTCTGCCAGCAGCTGTGTGACAGACATCACAATG 680
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....

RESULT 8
BP303194
LOCUS      BP303194 Sugano cDNA library, macrophage Homo sapiens cDNA clone
DEFINITION
ACCESSION      BP303194.1 GI:52232154
VERSION
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
      Suzuki,Y., Yanashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
      Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE      Sequence comparison of human and mouse genes reveals a homologous
      block structure in the promoter regions
JOURNAL      Genome Res. 14 (9), 1711-1718 (2004)
COMMENT      Contact: Yutaka Suzuki
      Department of Virology
      Institute of Medical Science, University of Tokyo
      4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
      Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
      Location/Qualifiers
      1..582
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="WP07792"
      /cell_type="macrophage"
      /clone_lib="Sugano cDNA library, macrophage"

ORIGIN
Alignment Scores:      7.03e-75      Length:      582
Pred. No.:      697.00      Matches:      143
Score:      94.19%      Conservative:      3
Percent Similarity:      92.26%      Mismatches:      7
Best Local Similarity:

```

```

Query Match:      67.08%      Indels:      3
DB:      5      Gaps:      0

US-09-882-171-483_COPY_22_220 (1-199) x BP303194 (1-582)

Qy      1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      117 AAAGACTCAGAAATCTTCACAGTAGTAATGGGATCTGGAGAGAGTCAGTCACCTTCCCTGTA 176
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      21 AsnIleGlnGluProArgGlnValLysIleAlaIleAlaIleThrThrSerLysThrSerValAla 40
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      177 AATATCCAAGAACCAACGCGAAGTTAAATCATCTCTGGACTTCTAAACATCTGTTGCT 236
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      237 TATGTAAACACAGAGAGACTCAGAAACAGACCCCGTAGTCTACTGTGACCCACAGAAATTTAT 296
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      297 TATGAAGGATACATGCTTAGTCCGAACTACAAATCTGGTCATTAGGATCTGAGGATG 356
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      357 GAAGACGCGANGAGACTACATAGCAGACATAAATACACAGCGCTGATCCCTACACCAACC 416
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      417 AAGCGCTACACACCTGCAAAATCTATCGTCGGCTTGGGAAACCAAAATTT-ACACAGAGGTTA 475
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal-GluLysGluG1 140
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      476 ATGGCATCTGTGAACAGCAGCTGTAAATGTACACTGACATGCTCTGTAAAGAAAGAGA 535
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Qy      140 uLysAsnValThrTyrAsn-TripSerProLeuGlyGluGlu 153
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....
Db      536 AAGAATGTGACATACATCATTTGGAGGCCCTCGGCGAGAAAG 576
      ||||| ..... ||||| ..... ||||| ..... ||||| ..... ||||| .....

RESULT 9
BP159730
LOCUS      BP159730 837 bp mRNA linear EST 30-DEC-2003
DEFINITION      BP159730 full-length enriched swine cDNA library, adult thymus Sus
      scrofa cDNA clone THY010074A04 5', mRNA sequence.
ACCESSION      BP159730
VERSION
KEYWORDS      EST.
SOURCE      BP159730.1 GI:40409203
      Sus scrofa (pig)
ORGANISM      Sus scrofa
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
      Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
      Okumura,N., Hamasima,N. and Awata,T.
      1 (bases 1 to 837)
      PEDE (Pig EST Data Explorer): construction of a database for ESTs
      derived from porcine full-length cDNA libraries
      Nucleic Acids Res. 32 (1), D484-D488 (2004)
      Contact: Hirohide Uenishi
      Animal Genome Laboratory, Genome Research Department
      National Institute of Agrobiological Sciences
      2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
      Tel: +81-29-838-8627
      Fax: +81-29-838-8627
      Email: huenishi@affrc.go.jp
      EST project with full-length enriched cDNA libraries carried out in
      Animal Genome Research Program (Japan) by National Institute of
      Agrobiological Sciences and STAFF-Institute
      Single pass sequencing of clones derived from oligo-capped cDNA
      library
      Vector sequences were eliminated by RepeatMasker version 2002/07/13
      and crossmatch version 0.990319
      Low quality bases were trimmed based on the quality values.
FEATURES
      Location/Qualifiers
      1..837
      /organism="Sus scrofa"

```


TITLE		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL		Unpublished (1997)	
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html Seq primer: M13 Forward POLYA=Yes.	
FEATURES		Location/Qualifiers	
source		1..402	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:2709039"	
		/lab_host="DH10B (Life Technologies)"	
		/clone_lib="NCI CGAP Subi"	
		/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Sites: Not 1; Site 2: Eco RI; The NCI CGAP Subi library is a subtracted library derived from BI_ BI constitutes a mixture of 21 normalized or subtracted NCI CGAP libraries: NCI CGAP Co4, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Co10, NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12, NCI CGAP Kid3, NCI CGAP Kid11, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CUL1, NCI CGAP Lei2, NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24, NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones 132376-132391, 145608-145675, 150052-150285) NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 132392-132583, 1471368-1472903, 1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439) NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 - (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 - (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 530,000 recombinants. Subtraction was performed as previously described [Sondalio, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.	
		TAG TISSUE=colon	
		TAG_LIB=NCI CGAP_Co10	
		TAG_SEQ=AAACG	
ORIGIN		Alignment Scores:	
		Pred. No.: 2,18e-73 Length: 402	
		Score: 683.00 Matches: 131	
		Percent Similarity: 100.00% Conservatives: 2	
		Best Local Similarity: 98.50% Mismatches: 0	
		Query Match: 65.74% Indels: 0	
		DB: 2 Gaps: 0	
		US-09-882-171-483_COPY_22_220 (1-199) x AW013969 (1-402)	
Qy		9 AsnGlyLeuGlyGluSerValThrPheProValAsnIleGlnGluProArgGlnVal 28	
Db		402 AATGGGATTCGGGGAGTCAGTCACCTTCCCTGTAAATATCCAAGAACACCGCAAGTT 343	

```

QY 29 LysIleIleAlaTrpThrSerLysThrSerValAlaValThrProGlyAspSerGlu 48
Db 342 AAAATCATTGCTGGACTCTCTAAACATCTGTGCTTATGTATACACCGAGACTCAGAA 283
QY 49 ThrAlaProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeuGly 68
Db 282 ACAGACCCGCTAGTACTGTGACCCACAGAAATTTATGACGGATACATCGCTTAGGT 223
QY 69 ProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrLysAla 88
Db 222 CGGAATACAACTGCTGCTATTAGCGATCTGAGGATGGAAGACGCGAGACTTACAAGCA 163
QY 89 AspIleAsnThrGlnAlaAspProTyrThrThrLysArgTyrAsnLeuGlnIleTyr 108
Db 162 GACATAAATACACAGCTGATCCCTACACACCAAGCGCTCAACCTGCAATCTAT 103
QY 109 ArgArgLeuGlyLysProLysIleThrGlnSerLeuMetAlaSerValAsnSerThrCys 128
Db 102 CGTGGCTTGGAAACCAAAAATTTACACAGAGTTTAATGGCATCTGTGAACAGCCTGT 43
QY 129 AsnValThrLeuThrCysSerValGluLysGluGluLys 141
Db 42 AATGTCACACTGACATGCTCTCTGTAGAGAAAAA 4

RESULT 11
AY408983
LOCUS
DEFINITION
Mus musculus CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408983
VERSION
AY408983.1 GI:39764951
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 923)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 923)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..923
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>923
/gene="CD84"
/locus_tag="HCM3405"
ORIGIN
Alignment Scores:
Pred. No.: 4,29e-64 Length: 923
Score: 611.50 Matches: 119
Percent Similarity: 78.24% Conservative: 32
Best Local Similarity: 61.66% Mismatches: 39
Query Match: 58.83% Indels: 3
DB: . 9 Gaps: 2

```

```

US-09-882-171-483_COPY_22_220 (1-199) x AY408983 (1-923)
QY 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 18 AAAGATGCAGACCCGATGGTAATGAATGGGATTTCTTGGGGAGTCAGTTACTTCTCTTA 77
QY 21 AsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla 40
Db 78 AATATTCAAGAACCAAGAAATTTGACAACATTCCTGGACTTCTCAATCATCATCTGTGCT 137
QY 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 138 TTTATAAACACGAGAGTCAATAAAGCTGAA-----GTTACCAATAACCCAGGCACTTAT 191
QY 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 192 AAAGACCAATAGAAATCATAGATCAGAAATGATGACCTGGTCAATTAGAGACCTGAGGATG 251
QY 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 252 GAAGATGCAGGAACCTTCAAGACGACATCAATGAAGAGAATGAGGAA---ACCATCACC 308
QY 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db 309 AAGATCTACTACTCTCATATCTACCGTCGACTTAAACACCAAAAATTTACACAGATTG 368
QY 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db 369 ATATCATCTTTGAACAATACCTGTGAATATACACTGACATGCTCTGTGGAAGGAAGAA 428
QY 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db 429 AAGATGTCACATATAGCTGGAGTCCCTTTCGAGAGAAACCAATGTCTTCAATATCGTC 488
QY 161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
Db 489 CACTCCCCCATGGACCAAAAACCTGACCTACACATGTACAGCCAGAACCTGTGTCAGCAAC 548
QY 191 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAsp 193
Db 549 AGTTCTGACTCTGCTACTGTCCTCAGCAGCCATGTATGACAGAC 587

RESULT 12
BY748483
LOCUS
DEFINITION
BY748483 RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus cDNA clone F630108106 5', mRNA
sequence.
ACCESSION
BY748483
VERSION
BY748483.1 GI:27177315
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 671)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Reisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

```



```

/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5066478"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin."
/lab host="DH10B"
/clone_lib="NCI CGAP Lu29"
/organ="lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 1.8e-62 Length: 788
Score: 597.50 Matches: 119
Percent Similarity: 77.84% Conservative: 32
Best Local Similarity: 61.34% Mismatches: 39
Query Match: 57.51% Indels: 4
DB: 4 Gaps: 2

US-09-882-171-483_COPY_22_220 (1-199) x B1151764 (1-788)

Qy 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
57 AAAGATGACAGCCCGGTGGTAAATGATGGATCTTGGGGAGTCAGTTACTTCTCTTA 116
Qy 21 AsnIleGlnGluProArgGlnValLysIleLeuAlaIlePheThrSerLysThrValAla 40
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
117 AATATTCAGAACCAAGAAATTCACCAATTCGCTGCATCTTCATCATCTGTTGCT 176
Qy 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
177 TTTATAAACCCAGGAGTCAATAAGCTGAA-----GTTACCATTAACCCAGGCACTTAT 230
Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
231 AAAGACGAGATAGAAATCATAGATCAGAGTATGACCTGGTTCATTAGAGACTGAGGATG 290
Qy 81 GluAspAlaGlyAspTyrIleAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
291 GAAGATGCAGGAACCTACAAAGCAGACATCAATGAAGAAGATGAGGAA---ACCATCACC 347
Qy 101 LysArgTyrAsnLeuGluIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
348 AAGATCTACTACCTCATATCTACCGTCGACTTAAACACCAAAATTAACAGAGTTG 407
Qy 121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
408 ATATCATCTTTGAACAATACCTGTAATATATACACTGACATGCTCTGTGGAAAGGAAGAA 467
Qy 141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe 160
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
468 AAGATGTGCATATAGCTGGAGTCCCTTTGGAGAGAAAGCAATGTCTTCAATCGTC 527
Qy 161 GlnThrProGluAspGlnLeuThrTyrThrCysThrAlaGlnAsnPro-ValSerAs 180
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
528 CACTCCCCCATGGACAAAACTGACCTACATGATACAGCCAGCAACCCGGTGCAGCAA 587
Qy 180 nAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAsp 193
Db |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
588 CAGTCTGACTCTGTCACGTGCTCCAGCAGCCATGTACAGAC 627

RESULT 14
BU927996
LOCUS
DEFINITION
AGENCOURT_10434334 NIH_MGC_126 Homo sapiens cdna clone
IMAGE:6653558 5', mRNA sequence.
ACCESSION
BU927996
VERSION
BU927996.1 GI:24116726
KEYWORDS
EST.
Homo sapiens (human)

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
NIH-MGC http://mhc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2903 row: m column: 14
High quality sequence stop: 437.
FEATURES
Location/Qualifiers
1..466
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6653558"
/tissue_type="mixed (pool of 40 RNAs)"
/lab host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgcctggccc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGTGGCCATTCAGCCGGG-3' and
5'-ATTCTAGAGCGGAGCGGCGCATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

Alignment Scores:
Pred. No.: 1.31e-62 Length: 466
Score: 596.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.36% Indels: 0
DB: 5 Gaps: 0
US-09-882-171-483_COPY_22_220 (1-199) x BU927996 (1-466)
Qy 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 91 AAAGACTCAGAAATCTTCACAGTGAATGGGATTTGGGAGAGTCACTTCCTCTGTA 150
Qy 21 AsnIleGlnGluProArgGlnValLysIleLeuAlaIlePheThrSerLysThrSerValAla 40
Db 151 AATATCCAAAGAACCAAGTAAATCATCTTGTGGACTTCTTAAACATCTGTGCT 210
Qy 41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
Db 211 TATGTAAACACAGAGACTCAGAAACAGACCCCGTAGTACTGTGACCCAGAAATAT 270
Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 271 TATGAACGATACATGCTTAGTCCGACACTACAACTCTGGTCAATAGCATCTGAGGATG 330
Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

Db 331 GAAGACGAGGAGACTACAAACGACATATAACACAGGCTGATCCCTACACCAACC 390
Qy 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysPro 114
Db 391 AAGCGCTAACACCTGCAATCTATCGTCGGCTTGGGAACCN 432

RESULT 15
AG090451
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-090A06.F, genomic survey sequence.
ACCESSION AG090451
VERSION AG090451.1 GI:16642253
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170]

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .677
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-090A06.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES
source
1. .677
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-090A06.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Alignment Scores:
Pred. No.: 3.32e-58 Length: 677
Score: 562.00 Matches: 107
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 97.27% Mismatches: 1
Query Match: 54.09% Indels: 0
DB: 9 Gaps: 0

US-09-882-171-483_COPY_22_220 (1-199) x AG090451 (1-677)

Qy 1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 20
Db 216 AAGACTCAGAAATCTTCACAGTGAATGGGATTCGGGAGAGTCAGTCACCTTCCCTGTA 275
Qy 21 AsnIleGlnGluProArgGlnValLysIleIleAlaThrThrSerLysThrSerValAla 40
Db 276 AATATCCGAGAACCCAGCGCAAGTTAAATCATTCCTGGAGCTCTTAAACATCTGTGCT 335

Qy 41 TyrValThrProGlyAspSerGluThrAlaProValThrValThrHisArgAsnTyr 60
Db 336 TATGTAAACACGAGAGACTCAGAAACAGCAGCCCGCTAGTACTGTGACCCACAGAAATTAT 395

Qy 61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet 80
Db 396 TATGACCGATACATGCTTAGGTCGGAACATACTGGTCAATCTAGCGATCTGAGAATG 455
Qy 81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Db 456 GAAGACGCGAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCAACC 515
Qy 101 LysArgTyrAsnLeuGlnIleTyrArgArg 110
Db 516 AAGCGCTACAACCTGCACATCTATCGCAAG 545

Search completed: February 5, 2005, 11:25:39
Job time : 2627.94 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2005, 11:32:01 ; Search time 13391 Seconds
(without alignments)
11481.473 Million cell updates/sec

Title: US-09-882-171-174
Perfect score: 3173
Sequence: 1 tcgacccacagcgctcgtgc.....gcacacatctgtagtcctccag 3173

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3169.4	99.9	3173	6 BD191209	BD191209 186 human
2	3169.4	99.9	3173	6 AX924719	AX924719 Sequence
3	3161.8	99.6	3299	6 HSAJ3324	AJ223324 Homo sapi
4	3154.2	99.4	3296	6 CQ178714	CQ178714 Sequence
5	3142.2	99.0	3278	9 BC020063	BC020063 Homo sapi
6	2201.2	69.4	175386	9 AL138930	AL138930 Human DNA
7	2201.2	69.4	176698	2 AL355996	AL355996 Homo sapi
8	2201.2	69.4	179614	2 AC012471	AC012471 Homo sapi
9	2201.2	69.4	189057	2 AC027082	AC027082 Homo sapi
10	1034	32.6	1067	9 AF054815	AF054815 Homo sapi
11	1033.4	32.6	1040	6 AX474268	AX474268 Sequence
12	1033.4	32.6	1040	9 HSU82988	U82988 Human leuko
13	991	31.2	1100	9 HSLDACD84	Y12632 H.sapiens m
14	982.4	31.0	984	9 CR541847	CR541847 Homo sapi
15	973	30.7	1118	9 AF054816	AF054816 Homo sapi
16	826	26.0	967	9 AF054817	AF054817 Homo sapi
17	813	25.6	828	6 BD191331	BD191331 186 human
18	813	25.6	828	6 AX924841	AX924841 Sequence
19	796.4	25.1	1299	9 HSU96627	U96627 Homo sapien

20	676.2	21.3	858	9 AF054818	AF054818 Homo sapi
21	659.2	20.8	70557	2 AC090143	AC090143 Homo sapi
22	516.8	16.3	1132	10 AF043445	AF043445 Mus muscu
23	346.8	10.9	1088	9 HSLDA1	AF101030 Homo sapi
24	346.8	10.9	179614	2 AC012471	AC012471 Homo sapi
25	312.4	9.8	748	6 CQ431481	CQ431481 Sequence
26	271	8.5	296	6 BD247970	BD247970 5' ESTs f
27	271	8.5	296	6 CQ771933	CQ771933 Sequence
28	252.2	7.9	70557	2 AC090143	AC090143 Homo sapi
29	252	7.9	584	9 HSLDA2	AF101031 Homo sapi
30	236	7.4	301	6 BD247968	BD247968 5' ESTs f
31	236	7.4	301	6 CQ771931	CQ771931 Sequence
32	220	6.9	235509	10 AC091523	AC091523 Mus muscu
33	212.4	6.7	669	6 CQ422630	CQ422630 Sequence
34	180.2	5.7	220349	2 AC118856	AC118856 Rattus no
35	180.2	5.7	232373	2 AC134805	AC134805 Rattus no
36	180.2	5.7	237455	2 AC096815	AC096815 Rattus no
37	143.6	4.5	76052	2 AC023262	AC023262 Homo sapi
38	143.6	4.5	172525	9 AC008514	AC008514 Homo sapi
39	142.6	4.5	100951	9 H5184J9	AL031428 Human DNA
40	142.6	4.5	134814	2 AL831787	AL831787 Homo sapi
41	142.6	4.5	139203	2 AC068311	AC068311 Homo sapi
42	142	4.5	47506	2 AC106022	AC106022 Homo sapi
43	141.4	4.5	173275	9 AC092375	AC092375 Homo sapi
44	141.4	4.5	202004	9 HUAF001549	AF001549 Human Chr
45	141.2	4.5	101384	9 AL139014	AL139014 Human DNA

ALIGNMENTS

RESULT 1	BD191209	3173 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD191209	186 human secreted proteins.			
DEFINITION	BD191209				
ACCESSION	BD191209.1	GI:33000948			
VERSION	JP 2002510192-A/173.				
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 3173)				
AUTHORS	Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C., Bednarik,D.P., Endress,G.A., Yu,G.L., N.J., Feng,P., Young,P.E., Greene,J.M., Ferris,A.M., Duan,R., Hu,J.S., Florence,K.A., Olsen,H.S., Eber,R., Brewer,L.A., Moore,P.A., Shi,Y., Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.				
TITLE	186 human secreted proteins				
JOURNAL	Patent: JP 2002510192-A 173 02-APR-2002;				
COMMENT	HUMAN GENOME SCIENCES INC				
	PN JP 2002510192-A/173				
	PD 02-APR-2002				
	PF 06-MAR-1998	JP 1998538883			
	PR 07-MAR-1997	US 60/040162,07-MAR-1997	US 60/040333	PR	
	07-MAR-1997	US 60/038621,07-MAR-1997	US 60/040161	PR	
	07-MAR-1997	US 60/040626,07-MAR-1997	US 60/040334	PR	
	11-APR-1997	US 60/040336,07-MAR-1997	US 60/040163	PR	
	07-MAR-1997	US 60/043580,11-APR-1997	US 60/043568	PI	STEVEN
	M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET, PI				
	KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY				
	A ENDRESS,GUO LIANG				
	PI YU,JIAN NI,				
	PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN				
	M FERRIE,ROXANNE DUAN,				
	PI JING SHAN HU,KIMBERLY A FLORENCE,HENRIK				
	S OLSEN,REINHARD EBER,				
	PI LAURIE A BREWER,PAUL A MOORE,YANGU SHI,DAVID W LAFLEUR PI				
	YI LI,ZHIZHEN ZENG,				
	PI HLA KYAW				
	PC C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC				
	G01N33/50,				
	PC G01N33/53,G01N33/68,A61K38/17				
	CC Strandedness: Double;				

CC Topology: Linear;		Location/Qualifiers.	
PH	Key	Location/Qualifiers	
FEATURES		source	
		1..3173	
		/organism="unidentified"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:32644"	
ORIGIN			
Query Match		99.9%; Score 3169.4; DB 6; Length 3173;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 3173; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	TCGACCCCAAGCGTCCGTCGTTTTTCCACAGAGAGTTAGACCCCTGGAAGAGATGGCTCAGC	60
Db	1	TCGACCCCAAGCGTCCGTCGTTTTTCCACAGAGAGTTAGACCCCTGGAAGAGATGGCTCAGC	60
Qy	61	ACACCTATGGATCTTGCTCTCTTTGGCTGCAAACTGGCCGGAAGCAGCTGGAAGAAGACT	120
Db	61	ACCACTATGGATCTTGCTCTCTTTGGCTGCAAACTGGCCGGAAGCAGCTGGAAGAAGACT	120
Qy	121	CAGAAATCTTCAGTGAATGGATCTGGGAGATCAGTCACTTTCCCTGTAAATATCC	180
Db	121	CAGAAATCTTCAGTGAATGGGATCTGGGAGATCAGTCACTTTCCCTGTAAATATCC	180
Qy	181	AAGAAACCCGCAAGTAAATCATTTGCTTGGACTCTTAAACATCTGTGCTTATGTAA	240
Db	181	AAGAACCCGCAAGTAAATCATTTGCTTGGACTCTTAAACATCTGTGCTTATGTAA	240
Qy	241	CACAGGAGACTCAGAAACAGCACCGCTAGTTACTGTGACCCACAGAAATATATGAAC	300
Db	241	CACAGGAGACTCAGAAACAGCACCGCTAGTTACTGTGACCCACAGAAATATATGAAC	300
Qy	301	GGATACATGCTTAGGTCCGAATCAATCTGGTCAATAGCGATCTGAGGATGGAAGACG	360
Db	301	GGATACATGCTTAGGTCCGAATCAATCTGGTCAATAGCGATCTGAGGATGGAAGACG	360
Qy	361	CAGGAGACTTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACCAAGCGCT	420
Db	361	CAGGAGACTTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACCAAGCGCT	420
Qy	421	ACAACCTGCAATCTATCGTCCGCTTGGGAAACCAAAATATACACAGAGTTTAAATGGCAT	480
Db	421	ACAACCTGCAATCTATCGTCCGCTTGGGAAACCAAAATATACACAGAGTTTAAATGGCAT	480
Qy	481	CTGTGAACAGACCTGTAAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATG	540
Db	481	CTGTGAACAGACCTGTAAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATG	540
Qy	541	TGACATACAAATTTGGAGTCCCTGGGAGAGAGGTAATGTCCTTCAAATCTTCCAGACTC	600
Db	541	TGACATACAAATTTGGAGTCCCTGGGAGAGAGGTAATGTCCTTCAAATCTTCCAGACTC	600
Qy	601	CTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTACAGCAACATTTCTG	660
Db	601	CTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTACAGCAACATTTCTG	660
Qy	661	ACTCCATCTCTGCCCGCAGCTCTGTGAGACATCGCAATGGGCTTCCGTACTCAACCA	720
Db	661	ACTCCATCTCTGCCCGCAGCTCTGTGAGACATCGCAATGGGCTTCCGTACTCAACCA	720
Qy	721	CCGGTGTGCTGAGCGTGTGGCTATGTTCTTTCTGCTGTTCTCATTTCTCAGTGT	780
Db	721	CCGGTGTGCTGAGCGTGTGGCTATGTTCTTTCTGCTGTTCTCATTTCTCAGTGT	780
Qy	781	TTTTTGTTCGTTTTCAGAGAGAACAGATGCTGCCTCAAAGAAAACCATATACAT	840
Db	781	TTTTTGTTCGTTTTCAGAGAGAACAGATGCTGCCTCAAAGAAAACCATATACAT	840
Qy	841	ATATCATGGCTTCAAGGAACCCGACGAGTCCAGAAATCTATGATGAATCTCTGC	900
Db	841	ATATCATGGCTTCAAGGAACCCGACGAGTCCAGAAATCTATGATGAATCTCTGC	900

Qy	901	AGTCCAAGGTGCTTCCCTCCAAGAGAGCCAGTGAACACAGTTTATTTCCGAAGTGCAGT	960
Db	901	AGTCCAAGGTGCTTCCCTCCAAGAGAGCCAGTGAACACAGTTTATTTCCGAAGTGCAGT	960
Qy	961	TTGCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGGACTTCAAGCT	1020
Db	961	TTGCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGGACTTCAAGCT	1020
Qy	1021	ATGAAATTTGTGATCTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACCA	1080
Db	1021	ATGAAATTTGTGATCTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACCA	1080
Qy	1081	CCAATCTGCGAGAGTTCCCTGATCCAGATCTTCTGCCCCAACCTTACTTGGGAGATTG	1140
Db	1081	CCAATCTGCGAGAGTTCCCTGGATCCAGATCTTCTGCCCCAACCTTACTTGGGAGATTG	1140
Qy	1141	CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTTGT	1200
Db	1141	CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTTGT	1200
Qy	1201	GCCTAAATGGACAAATGGATGATACCTCTTCTGAAATGACTCCCTTCTGAATGATGAC	1260
Db	1201	GCCTAAATGGACAAATGGATGATACCTCTTCTGAAATGACTCCCTTCTGAATGATGAC	1260
Qy	1261	AAAGCAGGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAA	1320
Db	1261	AAAGCAGGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAA	1320
Qy	1321	TAATATTTTATGGCACACTGGGATAAACAAAGCAAGATTTGCTCACTTCTGGAAGCTGCAT	1380
Db	1321	TAATATTTTATGGCACACTGGGATAAACAAAGCAAGATTTGCTCACTTCTGGAAGCTGCAT	1380
Qy	1381	ATGACTAGAGCCTCTTGTGACTGGAGTAAACAACTGCCCCAGTAACCTGTGGGAGAGG	1440
Db	1381	ATGACTAGAGCCTCTTGTGACTGGAGTAAACAACTGCCCCAGTAACCTGTGGGAGAGG	1440
Qy	1441	GGATCAATTTTTCACACCTGTAATAGGCATAGGCATAGGCATAGGCATAGGCATAGGCAT	1500
Db	1441	GGATCAATTTTTCACACCTGTAATAGGCATAGGCATAGGCATAGGCATAGGCATAGGCAT	1500
Qy	1501	CAGTCAGTATGTGTAAGATCCCTGGTGGCTTCAACACGATCTTCTGAGCAAAATTA	1560
Db	1501	CAGTCAGTATGTGTAAGATCCCTGGTGGCTTCAACACGATCTTCTGAGCAAAATTA	1560
Qy	1561	GGAAATGTACCTTCCCTGAGGAGATGACGCTTCCCTCCGAGTGCATGGCTTGGAG	1620
Db	1561	GGAAATGTACCTTCCCTGAGGAGATGACGCTTCCCTCCGAGTGCATGGCTTGGAG	1620
Qy	1621	AGCAATGTGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTTGTGACAGG	1680
Db	1621	AGCAATGTGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTTGTGACAGG	1680
Qy	1681	GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTCAAG	1740
Db	1681	GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTCAAG	1740
Qy	1741	TTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTCT	1800
Db	1741	TTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTCT	1800
Qy	1801	GCAGGCTCAGAGACTGCTGGGACACTTTTCTGGAGTGTACTTCAAGAGCTTATAGG	1860
Db	1801	GCAGGCTCAGAGACTGCTGGGACACTTTTCTGGAGTGTACTTCAAGAGCTTATAGG	1860
Qy	1861	ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCCTCAGCAGAGAGC	1920
Db	1861	ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCCTCAGCAGAGAGC	1920
Qy	1921	AGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1980
Db	1921	AGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1980
Qy	1981	CTGGGAACTGGGTATTAATCCAACTCAAAATAGAGACCTTGTCAAGAGCAGAGTCAAT	2040

1981 CTGGGAACTGGGTATATCCAAACATCAAATAGAGACCTTGCAGAGACAGATCAT 2040
2041 TCTCAGAGGAACCTGGGAGATGATGGTGAGATGATGAACCTGGGTTTATCCAGTTC 2100
2041 TCTCAGAGGAACCTGGGAGATGATGGTGAGATGATGAACCTGGGTTTATCCAGTTC 2100
2101 CAAAGACTCAGAGAACTAGAGTTTAACTGAGCAGAGAGTGCAGAGTGCAGTGC 2160
2101 CAAAGACTCAGAGAACTAGAGTTTAACTGAGCAGAGAGTGCAGAGTGCAGTGC 2160
2161 ACAACACAGATCAACGACAGCTTACACAGGCAATTAACCTCTCAATGAGGAAGATCAT 2220
2161 ACAACACAGATCAACGACAGCTTACACAGGCAATTAACCTCTCAATGAGGAAGATCAT 2220
2221 TCACAACTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTAGC 2280
2221 TCACAACTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTAGC 2280
2281 AAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGC 2340
2281 AAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGC 2340
2341 TGCAAATTAGGCGAGATAAGACATCAGTCCAGTAATGAATCCATAGACTCATCTAGCAC 2400
2341 TGCAAATTAGGCGAGATAAGACATCAGTCCAGTAATGAATCCATAGACTCATCTAGCAC 2400
2401 CAACTACCAATAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTCATAT 2460
2401 CAACTACCAATAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTCATAT 2460
2461 GTCTGCTCTTGTTAGTACAGAGCAATTCAGACAGACACTACAGTTAAGCTGAAC 2520
2461 GTCTGCTCTTGTTAGTACAGAGCAATTCAGACAGACACTACAGTTAAGCTGAAC 2520
2521 TGCAGCTGCAAGTAATAGATGAACAGTCAAGAAAAATACCTTATGAGGGGCGAGGCTGA 2580
2521 TGCAGCTGCAAGTAATAGATGAACAGTCAAGAAAAATACCTTATGAGGGGCGAGGCTGA 2580
2581 AGCTGGGCTTGAAGATGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGCTCC 2640
2581 AGCTGGGCTTGAAGATGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGCTCC 2640
2641 AAGTGAGAGAGCATGAATAATGAGCGGCTGATCAGTGGGGTGTATTACAGAGCAC 2700
2641 AAGTGAGAGAGCATGAATAATGAGCGGCTGATCAGTGGGGTGTATTACAGAGCAC 2700
2701 CTCTCCAGATGCACCATGCTACAGTCCCTTGCCTATGTTGGCAGAGTGTCCAG 2760
2701 CTCTCCAGATGCACCATGCTACAGTCCCTTGCCTATGTTGGCAGAGTGTCCAG 2760
2761 CCAGATGTGTGCCCCCACCCTATGTCATTTAATGTCCTTCAATGCCACCTCAAAGG 2820
2761 CCAGATGTGTGCCCCCACCCTATGTCATTTAATGTCCTTCAATGCCACCTCAAAGG 2820
2821 TACCTCTTCTGAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2821 TACCTCTTCTGAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2881 CACTGCTGTTTTTCTCTTGTGCTTCTATCACTAAATCTCATCTCAGCCTTAC 2940
2881 CACTGCTGTTTTTCTCTTGTGCTTCTATCACTAAATCTCATCTCAGCCTTAC 2940
2941 AGCATAAATAATTTGTTTCTCTACTACTATGTAATGTAATGAGGAATTAAGATAAAG 3000
2941 AGCATAAATAATTTGTTTCTCTACTACTATGTAATGTAATGAGGAATTAAGATAAAG 3000
3001 GAAGCCKGCTGGGTGGTGGCTCAGCGCTGTATCCCAACACTTTGGGGGCCCAAGGCG 3060
3001 GAAGCCKGCTGGGTGGTGGCTCAGCGCTGTATCCCAACACTTTGGGGGCCCAAGGCG 3060
3061 GCGGATCACTGAGTCCAGGATTCGAGATTTARTCTGGCCAAATGTTGTAAGAAACCCCATNT 3120

Db 3061 GCGGATCACTGAGTCCAGGTCAGGATTTGAGATTTARTCTGGCCAAACATGGTGAACCCCATNT 3120
Qy 3121 NTACTTAAATAACGAAATTTAGCCAGGTGTGGTGACACATCTGTAGTCCAG 3173
Db 3121 NTACTTAAATAACGAAATTTAGCCAGGTGTGGTGACACATCTGTAGTCCAG 3173
RESULT 2
LOCUS AX924719 3173 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 174 from Patent EP1352962.
ACCESSION AX924719
VERSION AX924719.1 GI:40242664
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Olsen,H.S., Yu,G.L., Endress,G.A., Bednarik,D.P., Carter,K.C.,
Feng,P., Soppet,D.R., Young,P.E., Duan,D.R., Florence,K.A.,
Greene,J.M., Fischer,C.L., Hu,J.S., Ruben,S.M., Ebner,R.,
Brewer,L.A., Ferrie,A.M., Moore,P.A., Ni,J., Shi,Y., Lafleur,D.W.,
Li,Y., Zeng,Z., Kyaw,H. and Rosen,C.A.
186 human secreted proteins
Patent: EP 1352962-A 174 15-OCT-2003;
HUMAN GENOME SCIENCES, INC. (US)
FEATURES
source 1..3173
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 99.9%; Score 3169.4; DB 6; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGACCCCAAGCGTCCGTCCTTTCCACAGAGAGTTAGACCCCTGAAAGAGATGGCTCAGC 60
Db 1 TCGACCCCAAGCGTCCGTCCTTTCCACAGAGAGTTAGACCCCTGAAAGAGATGGCTCAGC 60
Qy 61 ACCACATATGATCTTGTCTCTTTGCTGCAAACTGGCCGGAAGCAGCTGGAAGAGACT 120
Db 61 ACCACATATGATCTTGTCTCTTTGCTGCAAACTGGCCGGAAGCAGCTGGAAGAGACT 120
Qy 121 CAGAAATCTTCAAGTGAATGGATTTCTGGAGAGTCACTCTTCCCTGTAATATTC 180
Db 121 CAGAAATCTTCAAGTGAATGGATTTCTGGAGAGTCACTCTTCCCTGTAATATTC 180
Qy 181 AAGAACCCGCAAGTTAAATCAATTTGGAATTTCTAAACATCTGTTGCTTATGTAA 240
Db 181 AAGAACCCGCAAGTTAAATCAATTTGGAATTTCTAAACATCTGTTGCTTATGTAA 240
Qy 241 CACAGGAGACTCAGAAACAGACACCGGTAGTTACTGTGACCCACAGAAATTTATGTAAC 300
Db 241 CACAGGAGACTCAGAAACAGACACCGGTAGTTACTGTGACCCACAGAAATTTATGTAAC 300
Qy 301 GGNATACGCTTAGTCCGAACTACAATCTGTCTATTAGCGATCTGAGATGGAAGACG 360
Db 301 GGNATACGCTTAGTCCGAACTACAATCTGTCTATTAGCGATCTGAGATGGAAGACG 360
Qy 361 CAGGAGACTCAAAAGCAGACATAAATACACAGCTGATCCCTACACCAACCAAGCGCT 420
Db 361 CAGGAGACTCAAAAGCAGACATAAATACACAGCTGATCCCTACACCAACCAAGCGCT 420
Qy 421 ACAACCTGCAAAATCTATCTGTCGGCTTGGGAAACCAAAAATTTACACAGATTTTATGGCAT 480
Db 421 ACAACCTGCAAAATCTATCTGTCGGCTTGGGAAACCAAAAATTTACACAGATTTTATGGCAT 480
Qy 481 CTGTGACAGCAGCTCTTAATGTACACACTGACATGCTCTGTAGAGAAAGAAAGAAAGATG 540
Db 481 CTGTGACAGCAGCTCTTAATGTACACACTGACATGCTCTGTAGAGAAAGAAAGAAAGATG 540

Qy	541	TGACATACAAATTGGAGTCCCTGGGAGAAGAGGGTAATGTCTTTCAAATCTTCAGACTC	600
Db	541	TGACATACAAATTGGAGTCCCTGGGAGAAGAGGGTAATGTCTTTCAAATCTTCAGACTC	600
Qy	601	CTGAGGACCAAGAGCTGACTTTACAGCTGTACAGCCCGAGAAACCTGTGCAGCAACAATCTG	660
Db	601	CTGAGGACCAAGAGCTGACTTTACAGCTGTACAGCCCGAGAAACCTGTGCAGCAACAATCTG	660
Qy	661	ACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCGGTACTCACCACA	720
Db	661	ACTCCATCTCTGCCCGGAGCTCTGTGCAGACATCGCAATGGGCTTCGGTACTCACCACA	720
Qy	721	CCGGTGTCTCAGCGGTGCTGCTATGTTCTTTCTGCTTGTCTCATTTCTGTCTTCAGTGT	780
Db	721	CCGGTGTCTCAGCGGTGCTGCTATGTTCTTTCTGCTTGTCTCATTTCTGTCTTCAGTGT	780
Qy	781	TTTTGTTCCGTTTGTTCGAAGAGAAGACAAGATGTGCTCAAGAAACCATATACACAT	840
Db	781	TTTTGTTCCGTTTGTTCGAAGAGAAGACAAGATGTGCTCAAGAAACCATATACACAT	840
Qy	841	ATATCATGGCTTCAAGNAACCCAGCCAGCAGAGTCCAGAACTATATGATGAATCTCTGC	900
Db	841	ATATCATGGCTTCAAGNAACCCAGCCAGCAGAGTCCAGAACTATATGATGAATCTCTGC	900
Qy	901	AGTCCAAGGTCTTCCCTCCAAGGAAGACCGACAGTGAACACAGTTTATTTCCGAAGTGCAGT	960
Db	901	AGTCCAAGGTCTTCCCTCCAAGGAAGACCGACAGTGAACACAGTTTATTTCCGAAGTGCAGT	960
Qy	961	TTGCTGATAGATGGGGAAGCCAGACACAGGACAGTAAACCTCTCGGACATTCAGACT	1020
Db	961	TTGCTGATAGATGGGGAAGCCAGACACAGGACAGTAAACCTCTCGGACATTCAGACT	1020
Qy	1021	ATGAAATTTGTATCTAGCTCTCGGCTGAATTCCTCCTCTGGAAACTGTACTCGGAGATTG	1080
Db	1021	ATGAAATTTGTATCTAGCTCTCGGCTGAATTCCTCCTCTGGAAACTGTACTCGGAGATTG	1080
Qy	1081	CCAATACTGGCAGTTCCCTGGATCCAGATCTTCTCTGCCAACTCTTACTCGGAGATTG	1140
Db	1081	CCAATACTGGCAGTTCCCTGGATCCAGATCTTCTCTGCCAACTCTTACTCGGAGATTG	1140
Qy	1141	CAAACTGCCACATCTCAGCTGTAAAGCAAGCAGGAACCTTCTGCTGGCAGTAGCTGT	1200
Db	1141	CAAACTGCCACATCTCAGCTGTAAAGCAAGCAGGAACCTTCTGCTGGCAGTAGCTGT	1200
Qy	1201	GCCTAAATGGACAAATGGATGCATACCTCTCTGAAATGACTCCCTTCTGAATGAATGAC	1260
Db	1201	GCCTAAATGGACAAATGGATGCATACCTCTCTGAAATGACTCCCTTCTGAATGAATGAC	1260
Qy	1261	AAAGCAGTTTACCTAGTATAGTTTCCCAACTCTTCCCATCATAGCACATGTAGAAA	1320
Db	1261	AAAGCAGTTTACCTAGTATAGTTTCCCAACTCTTCCCATCATAGCACATGTAGAAA	1320
Qy	1321	TAATATTTTATGGCACACTGGGATAAACAGCAAGATTGCTCACTTCTCGAAGCTGCAT	1380
Db	1321	TAATATTTTATGGCACACTGGGATAAACAGCAAGATTGCTCACTTCTCGAAGCTGCAT	1380
Qy	1381	ATGCTAGAGGCTCTTGTGACTGGAGGTAAACCTCTGCCAGTAACTGTGGGAGAAAG	1440
Db	1381	ATGCTAGAGGCTCTTGTGACTGGAGGTAAACCTCTGCCAGTAACTGTGGGAGAAAG	1440
Qy	1441	GGATCAATATTTTGCACACTGTAAATAGGCCATGGCACACGACCAAGATGCTCTGCTCA	1500
Db	1441	GGATCAATATTTTGCACACTGTAAATAGGCCATGGCACACGACCAAGATGCTCTGCTCA	1500
Qy	1501	CAGTCAGTATGTGGAAGATCCCTGGTGGTGGCTTACCACGCACTTTTGAGCAAAATTA	1560
Db	1501	CAGTCAGTATGTGGAAGATCCCTGGTGGTGGCTTACCACGCACTTTTGAGCAAAATTA	1560
Qy	1561	GGAAATGTACCTTCCCTTGAAGCAGTCCGCTTCCCGAGTGCATGCTTGGAG	1620
Db	1561	GGAAATGTACCTTCCCTTGAAGCAGTCCGCTTCCCGAGTGCATGCTTGGAG	1620
Qy	1621	AGCAGAAATGGGCTGCATATAGCACACTCATCCCTTTGTCTGGGAATCTTTTGTGCAGG	1680

Db	1621	AGCAGAAATGTGGGCTGCATATAAGCACACATCACTCCCTTTGTCTGGGAATCTTTGTGCAGG	1680
Qy	1681	GCATAACAGCGCTAGTAAGTCCAAAACACAGATCACAGTCTGTGTGGGTCTGTCTCAGAG	1740
Db	1681	GCATAACAGCGCTAGTAAGTCCAAAACACAGATCACAGTCTGTGTGGGTCTGTCTCAGAG	1740
Qy	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTTCT	1800
Db	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTTCT	1800
Qy	1801	GCAGGCTTAGAGACTGCTGGGACATTTTCTTTGGAGTGTCTCTCAGAAGCCTTATAGG	1860
Db	1801	GCAGGCTTAGAGACTGCTGGGACATTTTCTTTGGAGTGTCTCTCAGAAGCCTTATAGG	1860
Qy	1861	ATTTTCTTTCTGGCCAAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAC	1920
Db	1861	ATTTTCTTTCTGGCCAAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAC	1920
Qy	1921	AGCCATGCCCAGTATTCCTCACTCTCCAAAAGGAATGACAGCTTATATTTCTCACATTT	1980
Db	1921	AGCCATGCCCAGTATTCCTCACTCTCCAAAAGGAATGACAGCTTATATTTCTCACATTT	1980
Qy	1981	CTGGGAACTGGGTATAATCCAAACCACTAAAATAGAAAGACCTTGCAAGAAAGCAGAGTCAT	2040
Db	1981	CTGGGAACTGGGTATAATCCAAACCACTAAAATAGAAAGACCTTGCAAGAAAGCAGAGTCAT	2040
Qy	2041	TCTCCAGAAGAACTTTGGGAGATGATGGTGCAGATGATGAATCTGGGTTTCATCCCAGTTTC	2100
Db	2041	TCTCCAGAAGAACTTTGGGAGATGATGGTGCAGATGATGAATCTGGGTTTCATCCCAGTTTC	2100
Qy	2101	CAAGACTCAGAGAACTAGAGTTTAAGCTTGAGCGCAGTGC CGCACCTGCGATGCC	2160
Db	2101	CAAGACTCAGAGAACTAGAGTTTAAGCTTGAGCGCAGTGC CGCACCTGCGATGCC	2160
Qy	2161	ACAAACAGATCACAGCCAGCTTACACAGGCATTAACCTCTCTCAATGAGGAAGAAATCAT	2220
Db	2161	ACAAACAGATCACAGCCAGCTTACACAGGCATTAACCTCTCTCAATGAGGAAGAAATCAT	2220
Qy	2221	TCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGC	2280
Db	2221	TCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGC	2280
Qy	2281	AAGTATAAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGC	2340
Db	2281	AAGTATAAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGC	2340
Qy	2341	TGCAATTAGGCAGATAAGACATCAGTCCCGATTAATGAATCCATAGACTCATCTAGCAC	2400
Db	2341	TGCAATTAGGCAGATAAGACATCAGTCCCGATTAATGAATCCATAGACTCATCTAGCAC	2400
Qy	2401	CAACTACCAATTAGCATATGTTAGGAGCTGCAAGGCCCAAAAGTAAAGATGTGCATAAT	2460
Db	2401	CAACTACCAATTAGCATATGTTAGGAGCTGCAAGGCCCAAAAGTAAAGATGTGCATAAT	2460
Qy	2461	GTCTGTCTTGTGTAGCTCAGGAGCAATTCAGACACACTACAGTTAACTGTGAAAC	2520
Db	2461	GTCTGTCTTGTGTAGCTCAGGAGCAATTCAGACACACTACAGTTAACTGTGAAAC	2520
Qy	2521	TGCAGCTGCAAGTAATAGCATGAACAGTTCAGAAAATACTTATCAGGGGCGCAGGCTGA	2580
Db	2521	TGCAGCTGCAAGTAATAGCATGAACAGTTCAGAAAATACTTATCAGGGGCGCAGGCTGA	2580
Qy	2581	AGCTGGGCTTGAAGGATGGAATTTGGATAGAGAAATGAGGAAGACAGAGGSCCTCC	2640
Db	2581	AGCTGGGCTTGAAGGATGGAATTTGGATAGAGAAATGAGGAAGACAGAGGSCCTCC	2640
Qy	2641	AAGTGAGAGAACTGAAAATTCAGACGGGCTCGATCAGTGGGTTGATTCAGAGCAC	2700
Db	2641	AAGTGAGAGAACTGAAAATTCAGACGGGCTCGATCAGTGGGTTGATTCAGAGCAC	2700
Qy	2701	CTCTCAGATGCACCATGCATCTCACAGTCCCTTTGCCTATGTGTGGCAGAGTGTCCAG	2760

Db 2701 CTCTCCAGATGCACATGCTCATGCTCAGATCCCTTGTGTCCTTATGTGTGGCAGAGTGTCCCG 2760
Qy 2761 CCAGATGTGTGCCCCCACCACCCATGTCCTTACATGTCCTTCAATGCCACCTCAAAAGG 2820
Db 2761 CCAGATGTGTGCCCCCACCACCCATGTCCTTACATGTCCTTCAATGCCACCTCAAAAGG 2820
Qy 2821 TACCTCTCTGTAAAGCTTTTCCCTGTGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
Db 2821 TACCTCTCTGTAAAGCTTTTCCCTGTGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
Qy 2881 CACTGCTGTTTTTCTCTTTTGTGCTCTTATCACTAAACTCATCTCATCAGCCTTAC 2940
Db 2881 CACTGCTGTTTTTCTCTTTTGTGCTCTTATCACTAAACTCATCTCATCAGCCTTAC 2940
Qy 2941 AGCATAACTAAATTAATTTGTTTCTCTCACTACATGTTACATGTTGGGAATTAACAGATAACG 3000
Db 2941 AGCATAACTAAATTAATTTGTTTCTCTCACTACATGTTACATGTTGGGAATTAACAGATAACG 3000
Qy 3001 GAAGCCGCTGGGGTGTGGCTCAAGCTGTATCCCAACACTTTGGGAGGCCAAGCCAG 3060
Db 3001 GAAGCCGCTGGGGTGTGGCTCAAGCTGTATCCCAACACTTTGGGAGGCCAAGCCAG 3060
Qy 3061 GCGGATCAGCTGAGGTGAGGARTTCGAGATTAATCTGGCCAACTGTTGAAACCCCATNT 3120
Db 3061 GCGGATCAGCTGAGGTGAGGARTTCGAGATTAATCTGGCCAACTGTTGAAACCCCATNT 3120
Qy 3121 NTACTAAATAAGAAATAGCAGGTGTGGTGCGCACATCTGTAGTCCAG 3173
Db 3121 NTACTAAATAAGAAATAGCAGGTGTGGTGCGCACATCTGTAGTCCAG 3173

RESULT 3
HSAJ3324 3299 bp mRNA linear PRI 07-APR-2000
LOCUS Homo sapiens mRNA for MAX.3 cell surface antigen.
DEFINITION AJ223324
ACCESSION AJ223324.1 GI:3392916
VERSION cell surface antigen; glycoprotein; MAX.3 antigen.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Krause, S.W., Rehli, M., Heinz, S., Ebner, R. and Andreessen, R.
TITLE Characterization of MAX.3 antigen, a glycoprotein expressed on human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens
JOURNAL Blood 67 (5), 1257-1264 (1986)
MEDLINE 86188202
PUBMED 3008886
REFERENCE 2
AUTHORS Krause, S.W., Rehli, M., Heinz, S., Ebner, R. and Andreessen, R.
TITLE Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with CD84
JOURNAL Biochem. J. 346 Pt 3, 729-736 (2000)
MEDLINE 20164057
PUBMED 10698700
REFERENCE 3
AUTHORS Krause, S.W.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1998) Krause S.W., Hematology, University of Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042, GERMANY
FEATURES
source Location/Qualifiers
1. .3299
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HDPFF19"
/cell_type="dendrite"
45. .1031
/codon_start=1
CDS

/evidence=experimental
/product="MAX.3 cell surface antigen"
/protein_id="CAA11264.1"
/db_xref="GI:3392917"
/db_xref="GOA:O15430"
/db_xref="UniProt/TREMBL:O15430"
/translation="MAQHLLWLLLCQTPWPAAGKDSIFVINGILGESVTFPNVNIQ
EPROVKIATWTSKTSVAVTTPGDSAPVTVTHRYVYERHALGNPNLVLSDEKME
DAGDYKADINTQADPYTTTKRYNLQIYRLGKPKITQSLMASVNSTCNVLTCSVEKE
EKVYTNWSPIGSEGNVLIQIQTPEDOELTYCTAONPVSNNSDSISAROLCADIAMG
FRHTYGLGSLVLAFFLLVLLSSVFLFKRQDAAASKTIIYIIMASRNTQPAES
RIYDILQSKVLPSKEPNTVYSEVQFADKMGKASTQDSPPGTSSTFEIV"
45. .107
108. .1028
/product="MAX.3 cell surface antigen"
sig_peptide
mat_peptide
ORIGIN
Query Match 99.6%; Score 3161.8; DB 9; Length 3299;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3160; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CCASGGTCCGTGCTTTTCCACAGAGGTTAGACCTGAAAGAGATGGCTCAGCACCC 66
Db 1 CCACGCTCCGTGCTTTTCCACAGAGGTTAGACCTGAAAGAGATGGCTCAGCACCC 60
Qy 67 TATGATCTTGTCTCTTTCCTGCAAACTGCGCGGAGCAGCTGGAAGAGACTCAGAAA 126
Db 61 TATGATCTTGTCTCTTTCCTGCAAACTGCGCGGAGCAGCTGGAAGAGACTCAGAAA 120
Qy 127 TCTTCACTGTAATGGGATTTCTGGAGAGTCACTTCTTCCCTGTAATATATCAAGAAC 186
Db 121 TCTTCACTGTAATGGGATTTCTGGAGAGTCACTTCTTCCCTGTAATATATCAAGAAC 180
Qy 187 CAGGCAAGTTAAATCATTTGCTTGGACTTCTTAAACACTCTCTGCTATGTAACACCCAG 246
Db 181 CAGGCAAGTTAAATCATTTGCTTGGACTTCTTAAACACTCTCTGCTATGTAACACCCAG 240
Qy 247 GAGACTCAGAAAACAGCACCCGTAGTACTGTGTCGCCACCAAGAAATATTATGAACGGATAC 306
Db 241 GAGACTCAGAAAACAGCACCCGTAGTACTGTGTCGCCACCAAGAAATATTATGAACGGATAC 300
Qy 307 ATGCTTATGCTCCGAATACAAATCTGGTCACTTATGAGATCTGAGGATGGAAGACGAGGAG 366
Db 301 ATGCTTATGCTCCGAATACAAATCTGGTCACTTATGAGATCTGAGGATGGAAGACGAGGAG 360
Qy 367 ACTCAAGCAGACATAAATACACAGGCTGATCCCTTACACCCACCAAGCCGCTCAACACC 426
Db 361 ACTCAAGCAGACATAAATACACAGGCTGATCCCTTACACCCACCAAGCCGCTCAACACC 420
Qy 427 TGCAAATCTATCGTCCGCTTGGGAACCAAAATTAACACAGAGTTTAAATGGCATCTGTGA 486
Db 421 TGCAAATCTATCGTCCGCTTGGGAACCAAAATTAACACAGAGTTTAAATGGCATCTGTGA 480
Qy 487 ACAGCACCTGTAATGTGACATGACATGCTGTGTAGAGAAAGAAAGAAATGTGACAT 546
Db 481 ACAGCACCTGTAATGTGACATGACATGCTGTGTAGAGAAAGAAAGAAATGTGACAT 540
Qy 547 ACAATTTGGAGTCCCTTGGGAGAGAGGTAATGCTCTTCAAAATCTTCCAGACTCTCTGAGG 606
Db 541 ACAATTTGGAGTCCCTTGGGAGAGAGGTAATGCTCTTCAAAATCTTCCAGACTCTCTGAGG 600
Qy 607 ACCAAGAGCTGACTTACACGTGTACAGCCACAGAACCTGTGACAGCAAAATTTCTGACTCCA 666
Db 601 ACCAAGAGCTGACTTACACGTGTACAGCCACAGAACCTGTGACAGCAAAATTTCTGACTCCA 660
Qy 667 TCTCTCCCGGAGCTCTGTGACAGCATCGCAATGGGCTTCCGTACTCACCACACCGGGT 726
Db 661 TCTCTCCCGGAGCTCTGTGACAGCATCGCAATGGGCTTCCGTACTCACCACACCGGGT 720
Qy 727 TGCTGAGCGTGTGGCTATGTTCTTCTGCTTGTCTTCTCATCTGCTTCTGAGTCTTTTGT 786
Db 721 TGCTGAGCGTGTGGCTATGTTCTTCTGCTTGTCTTCTCATCTGCTTCTGAGTCTTTTGT 780

QY	787	TCCGTTTGTTC	TAAGAGACAAAGATGCTGCCTCAAGAAACCATATACACATATATCA	846
DB	781	TCCGTTTGTTC	TAAGAGACAAAGATGCTGCCTCAAGAAACCATATACACATATATCA	840
QY	847	TGGCTTCAAGGAA	CACCAGCCAGCAGAGTCCAGAACTATATGATCAAACTCTGCAGTCCA	906
DB	841	TGGCTTCAAGGAA	CACCAGCCAGCAGAGTCCAGAACTATATGATCAAACTCTGCAGTCCA	900
QY	907	AGTGCTTCCCT	CCAAAGAGAGCCAGTGAAACAGTTTTATTCGAAAGTGCAGTTTGTCTG	966
DB	901	AGTGCTTCCCT	CCAAAGAGAGCCAGTGAAACAGTTTTATTCGAAAGTGCAGTTTGTCTG	960
QY	967	ATAAGATGGGAAA	CCAGCACACAGGACAGTAAACCTCTCGGACACTTCAAGCTATGAAA	1026
DB	961	ATAAGATGGGAAA	CCAGCACACAGGACAGTAAACCTCTCGGACACTTCAAGCTATGAAA	1020
QY	1027	TTGTGATCTAG	CGCTGCTGGGCTGAAATCTCCCTCTGGAAACTGAGTTTACAACCAACAATA	1086
DB	1021	TTGTGATCTAG	CGCTGCTGGGCTGAAATCTCCCTCTGGAAACTGAGTTTACAACCAACAATA	1080
QY	1087	CTGGCAGTTC	CCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTGCAAACT	1146
DB	1081	CTGGCAGTTC	CCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTGCAAACT	1140
QY	1147	GCCACATCTCA	GCCTGTAAAGCAAGCAGGAAACCTCTCTGGGCATAGCTTGTGCCTAA	1206
DB	1141	GCCACATCTCA	GCCTGTAAAGCAAGCAGGAAACCTCTCTGGGCATAGCTTGTGCCTAA	1200
QY	1207	ATGACAAATGG	ATGATGATCCCTTCTGAAATGACTCCCTCTGAAATGAAATGAAAGCA	1266
DB	1201	ATGACAAATGG	ATGATGATCCCTTCTGAAATGACTCCCTCTGAAATGAAATGAAAGCA	1260
QY	1267	GGTTACCTAG	TATAGTTTTCCTTCCCAACTCTTCCCATCATAGCACATCTGAGAAATATAT	1326
DB	1261	GGTTACCTAG	TATAGTTTTCCTTCCCAACTCTTCCCATCATAGCACATCTGAGAAATATAT	1320
QY	1327	TTTTATGGCA	CACTGGGATTAACCAAGCAAGATTGCTCACTCTTGGAGCTGCATATGACT	1386
DB	1321	TTTTATGGCA	CACTGGGATTAACCAAGCAAGATTGCTCACTCTTGGAGCTGCATATGACT	1380
QY	1387	AGAGCCTCTTG	TCACCTGGAGTTAAACAACTGCCAGTAACCTGTGGGAGAGGGGATCA	1446
DB	1381	AGAGCCTCTTG	TCACCTGGAGTTAAACAACTGCCAGTAACCTGTGGGAGAGGGGATCA	1440
QY	1447	ATATTTTGC	ACACTGTAATAGGCCATGGCACACCAAGAGTCTCTGCTCACAGTCA	1506
DB	1441	ATATTTTGC	ACACTGTAATAGGCCATGGCACACCAAGAGTCTCTGCTCACAGTCA	1500
QY	1507	GTATGTGAG	ATCCCTGCTGGCTTCAACCAAGATCTTGGAGCAATTTAGGAAA	1566
DB	1501	GTATGTGAG	ATCCCTGCTGGCTTCAACCAAGATCTTGGAGCAATTTAGGAAA	1560
QY	1567	TGTACCCCTTG	AGGCAAGTGCAGCCCTTCCCGGAGTGCATGGCTTGGAGACAGA	1626
DB	1561	TGTACCCCTTG	AGGCAAGTGCAGCCCTTCCCGGAGTGCATGGCTTGGAGACAGA	1620
QY	1627	ATGTGGCTG	CATATAGCACATCATCCCTTGTCTGGGAATCTTTGTGCGAGGGCATAA	1686
DB	1621	ATGTGGCTG	CATATAGCACATCATCCCTTGTCTGGGAATCTTTGTGCGAGGGCATAA	1680
QY	1687	CAGGCTTAG	TAACTCCAAAACACAGATGACAGTCTGTGTGGGTCTCTGTGAGATTGTGG	1746
DB	1681	CAGGCTTAG	TAACTCCAAAACACAGATGACAGTCTGTGTGGGTCTCTGTGAGATTGTGG	1740
QY	1747	CTCTCAG	CCATGATGACACTCTCCAAATGGAGTGTGGAAAATGTCTTTCTGCGAGG	1806
DB	1741	CTCTCAG	CCATGATGACACTCTCCAAATGGAGTGTGGAAAATGTCTTTCTGCGAGG	1800
QY	1807	TCTAGAG	ACTGTGGGACATTTTCTTTGGAGTGTACTTTCAGAGCCTTATAGGATTTTC	1866
DB	1801	TCTAGAG	ACTGTGGGACATTTTCTTTGGAGTGTACTTTCAGAGCCTTATAGGATTTTC	1860
QY	1867	TTTCTGG	CAAGATTCTTCTGTGATCACTCCAAGCAGCCTCAGCAGAGAGACGCCAT	1926

[illegible]

2941	ACTAAATTATTTGTTTCCTCACTACATTTGTATACATGTGGGAAATTACAGATATAACCGAAGCC	3000
3007	KGCTGGGGTGGGCTCAGCGCTGTAAATCCCAACACATTTGGGAGGCCAAGCGAGCGGAT	3066
3001	GGCTGGGGTGGGCTCAGCGCTGTAAATCCCAACACATTTGGGAGGCCAAGCGAGCGGAT	3060
3067	CACCTGAGGTCAAGARTTCGAGATTAATCTGGCCAAACATGTTGAAACCCCATTTACTTA	3126
3061	CACCTGAGGTCAAGARTTCGAGATTAATCTGGCCAAACATGTTGAAACCCCATTTACTTA	3120
3127	AAAATACGAAATTAGCCAGGTGTGGTGGCCACACATCTGTAGTCCCG	3173
3121	AAAATACGAAATTAGCCAGGTGTGGTGGCCACACATCTGTAGTCCCG	3167
RESULT 4		
LOCUS	CQ718714	3296 bp DNA linear PAT 03-FEB-2004
DEFINITION	Sequence 4648 from Patent WO02068579.	
ACCESSION	CQ718714	
VERSION	CQ718714.1	GI:42279571
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W.	
JOURNAL	Kits, such as nucleic acid arrays, comprising a majority of	
FEATURES	humanexons or transcripts, for detecting expression and other uses	
source	thereof	
ORIGIN	Patent: WO 02068579-A 4648 06-SEP-2002;	
Query Match	PE Corporation (NY) (US)	
Best Local Similarity	Location/Qualifiers	
Matches 3153; Conservative	1. .3296	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
	99.4%; Score 3154.2; DB 6; Length 3296;	
	99.8%; Pred. No. 0;	
	Matches 3153; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Qy	15	CCGTGCTTTTCCACAGAGGTTAGACCTCGTAAAGAGATGGCTCAGCACCACTATGGATC 74
Db	7	CCGTGCTTTTCCACAGAGGTTAGACCTCGTAAAGAGATGGCTCAGCACCACTATGGATC 66
Qy	75	TTGCTCTTTGCTGCTCAAACTCTGGCGGAGCAGCTGGGAAAGACTCAGAAATCTTCACA 134
Db	67	TTGCTCTTTGCTGCTCAAACTCTGGCGGAGCAGCTGGGAAAGACTCAGAAATCTTCACA 126
Qy	135	GTGAATGGGATTTCTGGGAGGTCAGTCACTTTCCCTGTAAATATCCAGAGACCAAGCA 194
Db	127	GTGAATGGGATTTCTGGGAGGTCAGTCACTTTCCCTGTAAATATCCAGAGACCAAGCA 186
Qy	195	GTAAAAATCAATCTGTTGGACTTCTAAAAATCTGTTGCTTATGTATAACACCAAGGACTCA 254
Db	187	GTAAAAATCAATCTGTTGGACTTCTAAAAATCTGTTGCTTATGTATAACACCAAGGACTCA 246
Qy	255	GAACACGACCCGTATGTTACTGTGACCCACAGAAATTAATATGAAACGGATCATGCCCTTA 314
Db	247	GAACACGACCCGTATGTTACTGTGACCCACAGAAATTAATATGAAACGGATCATGCCCTTA 306
Qy	315	GGTCCGAACTTACAACTGTTGATAGCGATCTGAGGATGGAGAGCGAGGAGACTACAAA 374
Db	307	GGTCCGAACTTACAACTGTTGATAGCGATCTGAGGATGGAGAGCGAGGAGACTACAAA 366
Qy	375	GCAGACATAAATACAGAGGCTGATCCCTACACCAACCAAGCGCTACAACTGCAATC 434
Db	367	GCAGACATAAATACAGAGGCTGATCCCTACACCAACCAAGCGCTACAACTGCAATC 426
Qy	435	TATCGTCGGCTTGGGAAACCAAAAATTAACAGAGTTTAATGGCATCTGTGAAACAGCAC 494

1507 GAAGATCCCTGGTGGCTGGCCCTTACCACGATCTTGACCAAAATTAGGAAAATGTACCCCT 1566
1575 TGCCTTGAGGAGATGAGCGCCCTTCCCGAGTGCATGGCTTGGAGAGCAGAAATGTGGGC 1634
1567 TCGCTTGAGGAGATGAGCGCCCTTCCCGAGTGCATGGCTTGGAGAGCAGAAATGTGGGC 1626
1635 TGCATATAGCACACTCATCTCCCTTGTCTGGGAATCTTTGTGCAGGGCATACAGGCTTA 1694
1627 TGCATATAGCACACTCATCTCCCTTGTCTGGGAATCTTTGTGCAGGGCATACAGGCTTA 1686
1695 GTAAGTCCAAACACACAGATGACAGTGTCTGGGTCTCTGTGCAGAGTGTGGCTCTCAGC 1754
1687 GTAAGTCCAAACACACAGATGACAGTGTCTGGGTCTCTGTGCAGAGTGTGGCTCTCAGC 1746
1755 CATGTAGACACACTCTCCAAATGGAGTGTGGAAATCTTTCTGCAAGGCTCTAGAGA 1814
1747 CATGTAGACACACTCTCCAAATGGAGTGTGGAAATCTTTCTGCAAGGCTCTAGAGA 1806
1815 CTGCTGGGACACTTTCTTGGAGTGTCTCTCAGAGCCTTATAGGATTTCTTTCTGGC 1874
1807 CTGCTGGGACACTTTCTTGGAGTGTCTCTCAGAGCCTTATAGGATTTCTTTCTGGC 1866
1875 CAAGATTTCTCTGTATCACTCCAAGCAGCCTCAGCAGAAAGCAGCCATGCCAGTA 1934
1867 CAAGATTTCTCTGTATCACTCCAAGCAGCCTCAGCAGAAAGCAGCCATGCCAGTA 1926
1935 TTCCCACTCTCCAAAGGAACCTGACAGCTTATATTTCTCACCTTCTGGGAACTGGGT 1994
1927 TTCCCACTCTCCAAAGGAACCTGACAGCTTATATTTCTCACCTTCTGGGAACTGGGT 1986
1995 ATAATCCCAACCAATCAAAATAGAGACCTTGCAGAGCAGTCACTTCCAGAGGAAAC 2054
1987 ATAATCCCAACCAATCAAAATAGAGACCTTGCAGAGCAGTCACTTCCAGAGGAAAC 2046
2055 TTGGGAGATGATGGTGAGATGATGAACCTGGGTTTATCCCAAGTCTCAGAGA 2114
2047 TTGGGAGATGATGGTGAGATGATGAACCTGGGTTTATCCCAAGTCTCAGAGA 2106
2115 ACTAGATTTAGCTGAGGACAGTGCAGCCACCTTGGCATGCCGACCAACAGATCACC 2174
2107 ACTAGATTTAGCTGAGGACAGTGCAGCCACCTTGGCATGCCGACCAACAGATCACC 2166
2175 AGCCAGCTTACAGAGCACTTAATCTCTCAATGAGGAGAAATCAATCACAACTCAGCAA 2234
2167 AGCCAGCTTACAGAGCACTTAATCTCTCAATGAGGAGAAATCAATCACAACTCAGCAA 2226
2235 GACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTATAATCGGCT 2294
2227 GACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTATAATCGGCT 2286
2295 AACTCCTAAATCCCAATGATAGTCTTAGGCTGGACAGCAATGGGCTGCAATTAGGCGA 2354
2287 AACTCCTAAATCCCAATGATAGTCTTAGGCTGGACAGCAATGGGCTGCAATTAGGCGA 2346
2355 TAAAGACATCAGTCCAGTAAATGAATCCATAGATCATCTAGCAGCAACTACCAATTAGC 2414
2347 TAAAGACATCAGTCCAGTAAATGAATCCATAGATCATCTAGCAGCAACTACCAATTAGC 2406
2415 ACTATGTTAGGAGCTGCAAGGCCCAAAAGTAGAAGATGTCATAATGTCTGTCTTGTGT 2474
2407 ACTATGTTAGGAGCTGCAAGGCCCAAAAGTAGAAGATGTCATAATGTCTGTCTTGTGT 2466
2475 AGCTCAGGAGCAATTCAGACACACACTACAGTTAAGCTGAAGTGAAGTGAAGTGAAGTGA 2534
2467 AGCTCAGGAGCAATTCAGACACACACTACAGTTAAGCTGAAGTGAAGTGAAGTGAAGTGA 2526
2535 ATAGCATGAACAGTCCAGAAAAATACCTTATAGGGGGGAGGCTGAAAGTGGGCTTCAA 2594
2527 ATAGCATGAACAGTCCAGAAAAATACCTTATAGGGGGGAGGCTGAAAGTGGGCTTCAA 2586
2595 GGATGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTTCAAGTGAAGAGCA 2654
2587 GGATGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTTCAAGTGAAGAGCA 2646

QY 2655 TGAATAATGACAGGGGCTCGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGAC 2714
DB 2647 TGAATAATGACAGGGGCTCGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGAC 2706
QY 2715 CATGATGCTCACAGTCCCTTGCCTATGTGGGAGAGTGTCCAGGAGATGTGTGCC 2774
DB 2707 CATGATGCTCACAGTCCCTTGCCTATGTGGGAGAGTGTCCAGGAGATGTGTGCC 2766
QY 2775 CCACCCATGTCCATTTTACATGTCTTCAATGCCACCTCAAAAGGTACCTCTTCTGTAA 2834
DB 2767 CCACCCATGTCCATTTTACATGTCTTCAATGCCACCTCAAAAGGTACCTCTTCTGTAA 2826
QY 2835 AGCTTTCCCTCGTATCAGGAATCAAAATTAATCAGGAGTCTTTTCACACTGCTGTTTTT 2894
DB 2827 AGCTTTCCCTCGTATCAGGAATCAAAATTAATCAGGAGTCTTTTCACACTGCTGTTTTT 2886
QY 2895 CCTCTTGGTCTCTTATCACTAAACCTCATCTCAATCAGCTTACAGCACTAACTAATTA 2954
DB 2887 CCTCTTGGTCTCTTATCACTAAACCTCATCTCAATCAGCTTACAGCACTAACTAATTA 2946
QY 2955 TTTGTTTTCTCCTACATTTTACATGTGGGAATTCAGATAAAACGGAAGCKGTGGGG 3014
DB 2947 TTTGTTTTCTCCTACATTTTACATGTGGGAATTCAGATAAAACGGAAGCKGTGGGG 3006
QY 3015 TGGTGGCTCAGCCTGTAAATCCCAACACTTTGGGAGGCAAGGAGCGGATACCTGAG 3074
DB 3007 TGGTGGCTCAGCCTGTAAATCCCAACACTTTGGGAGGCAAGGAGCGGATACCTGAG 3066
QY 3075 GTGAGGATTCGAGATTAATCTGGCAACATGTGTGAACCCCATNTTACTTAAATAACG 3134
DB 3067 GTGAGGATTCGAGATTAATCTGGCAACATGTGTGAACCCCATNTTACTTAAATAACG 3126
QY 3135 AAATTAGCCAGTGTGGGACACATCTGTAGTCCCGAG 3173
DB 3127 AAATTAGCCAGTGTGGGACACATCTGTAGTCCCGAG 3165

RESULT 5

BC020063
LOCUS Homo sapiens CD84 antigen (leukocyte antigen), mRNA (cDNA clone
MG:21324 IMAGE:4385965), complete cds.

ACCESSION

BC020063
VERSION BC020063.1 GI:18043042

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (Bases 1 to 3278)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shavchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Burkhead, Y.S., Krzywicki, M.I., Skalek, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

AUTHORS

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED

12477932

REFERENCE 2 (bases 1 to 3278)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleaged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 26 Row: 0 Column: 19
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686.
 Location/Qualifiers
 1..3278
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:21324 IMAGE:4385965"
 /issue_type="Lymph, lymphoma"
 /clone_lib="NIH MGC 85"
 /lab_host="DH10B"
 /notes="Vector: pCMV-SPORT6"
 1..3278
 /gene="CD84"
 /notes="synonyms: SLAMP5, hCD84, mCD84, LY9B"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 25..1011
 /gene="CD84"
 /codon_start=1
 /product="CD84 antigen (leukocyte antigen)"
 /protein_id="AAH20063.1"
 /db_xref="GI:18043043"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 /translations="MAQHHLWLLLCLOTWPEAAGKDSIFTVNGILGESVTPVNIQ
 EPQVKLIATSKTSVAYTPGSETPAVVTVTHRYNYYRIHALGNYNLIVSLRME
 DAGDYKADINTQADPYTTTKRNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
 EKNVTYNWSPLEGVLAQI FOTPEDELTCTCAQNPVNSNDSISARQLCADAMG
 FRTHHTGLLSVLAFFLLVLLSSVFLFRKRODAASKTIYTYIMASRNTQPAES
 RYDEILQSKVLPSKEPNTVYSEVQFADKMGKASTQDSKPPGTSSYBIVT"

gene
 1..3278
 /gene="CD84"
 /notes="synonyms: SLAMP5, hCD84, mCD84, LY9B"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 25..1011
 /gene="CD84"
 /codon_start=1
 /product="CD84 antigen (leukocyte antigen)"
 /protein_id="AAH20063.1"
 /db_xref="GI:18043043"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 /translations="MAQHHLWLLLCLOTWPEAAGKDSIFTVNGILGESVTPVNIQ
 EPQVKLIATSKTSVAYTPGSETPAVVTVTHRYNYYRIHALGNYNLIVSLRME
 DAGDYKADINTQADPYTTTKRNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
 EKNVTYNWSPLEGVLAQI FOTPEDELTCTCAQNPVNSNDSISARQLCADAMG
 FRTHHTGLLSVLAFFLLVLLSSVFLFRKRODAASKTIYTYIMASRNTQPAES
 RYDEILQSKVLPSKEPNTVYSEVQFADKMGKASTQDSKPPGTSSYBIVT"

CDS
 1..3278
 /product="CD84 antigen (leukocyte antigen)"
 /protein_id="AAH20063.1"
 /db_xref="GI:18043043"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"
 25..1011
 /product="CD84 antigen (leukocyte antigen)"
 /protein_id="AAH20063.1"
 /db_xref="GI:18043043"
 /db_xref="LocusID:8832"
 /db_xref="MIM:604513"

ORIGIN
 Query Match 99.0%; Score 3142.2; DB 9; Length 3278;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3141; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 27 ACAGAAGTTAGACCTGAAGAGATGGCTCAGCACCACCTATGGATCTTGCTCCCTTGC 86
 1 ACAGAAGTTAGACCTGAAGAGATGGCTCAGCACCACCTATGGATCTTGCTCCCTTGC 60
 87 CTCGAAACCTGGCGGAGCAGCTGGAAAAGACTCAGAAAATCTTCACAGTGAATGGGATT 146
 61 CTGCAAACTGGCGGAGCAGCTGGAAAAGACTCAGAAAATCTTCACAGTGAATGGGATT 120
 147 CTGGGAGAGTCAGTCACCTTTCCCTGTAAATATCCAGAACCCAGCGCAAGTTAAATCAT 206
 121 CTGGGAGAGTCAGTCACCTTTCCCTGTAAATATCCAGAACCCAGCGCAAGTTAAATCAT 180

QY 207 GCTTGGACTTCTAAAAACATCTGTGTTGTTATGTAACACAGGAGACTCAGAAACAGCACCC 266
 DB 181 GCTTGGACTTCTAAAAACATCTGTGTTGTTATGTAACACAGGAGACTCAGAAACAGCACCC 240
 QY 267 GTAGTTACTGTGACCCACAGAAAATTTATGAAACGGATACATGCTTAGTCCGAACTAC 326
 DB 241 GTAGTTACTGTGACCCACAGAAAATTTATGAAACGGATACATGCTTAGTCCGAACTAC 300
 QY 327 AATCTGGTCATTAGCGATCTGAGGATGGAAGACGAGGAGACTCAAAAGCAGACATAAAT 386
 DB 301 AATCTGGTCATTAGCGATCTGAGGATGGAAGACGAGGAGACTCAAAAGCAGACATAAAT 360
 QY 387 ACACAGGCTGATCCCTACACACCAACCAAGCGCTACAACTGCAAAATCTATGTCGGTT 446
 DB 361 ACACAGGCTGATCCCTACACACCAACCAAGCGCTACAACTGCAAAATCTATGTCGGTT 420
 QY 447 GGGAAACCAAAAATTTACACAGATTTAATGGCATCTGTGAACAGCACCTGTAACTCACA 506
 DB 421 GGGAAACCAAAAATTTACACAGATTTAATGGCATCTGTGAACAGCACCTGTAACTCACA 480
 QY 507 CTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAAATTGGAGTCCCTCGGA 566
 DB 481 CTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAAATTGGAGTCCCTCGGA 540
 QY 567 GAAGAGGGTAAATGTCCTTCAAATCTTCCAGACTCTCTGAGGACCAAGAGCTGACTTAC 626
 DB 541 GAAGAGGGTAAATGTCCTTCAAATCTTCCAGACTCTCTGAGGACCAAGAGCTGACTTAC 600
 QY 627 TGTAAGCCCGAGAACCTGTGAGCAACAAATTTCTGACTCCATCTCTGCCCGGAGCTCTGT 586
 DB 601 TGTAAGCCCGAGAACCTGTGAGCAACAAATTTCTGACTCCATCTCTGCCCGGAGCTCTGT 660
 QY 687 CGACATCGCAATCGGCTTCGCTACTCACCACACCGGTTCTGAGCGTGTGCTGCTATG 746
 DB 661 CGACATCGCAATCGGCTTCGCTACTCACCACACCGGTTCTGAGCGTGTGCTGCTATG 720
 QY 747 TTCTTTCTGCTTGTCTCATCTCTTCACTTCTGCTTCACTTCTGCTTCAAGAGAAGA 806
 DB 721 TTCTTTCTGCTTGTCTCATCTCTTCACTTCTGCTTCACTTCTGCTTCAAGAGAAGA 780
 QY 807 CAAGATGCTGCTCAAGAAACCATATACATATATCATGCTTCAAGAGAACCCAG 866
 DB 781 CAAGATGCTGCTCAAGAAACCATATACATATATCATGCTTCAAGAGAACCCAG 840
 QY 867 CCAGCAGAGTCCAGAAATCTATGATGAAATCTGCAAGTCCCAAGTGTCTCCCTCCAGGAA 926
 DB 841 CCAGCAGAGTCCAGAAATCTATGATGAAATCTGCAAGTCCCAAGTGTCTCCCTCCAGGAA 900
 QY 927 GAGCCAGTGAAACACAGTTTATTTCCGAAGTGCAATTTGCTGATAAGATGGGAAAGCCAG 986
 DB 901 GAGCCAGTGAAACACAGTTTATTTCCGAAGTGCAATTTGCTGATAAGATGGGAAAGCCAG 960
 QY 987 ACACAGGACAGTAAACCTCTCGGAGCTTCAAGCTATGAAATTTGATCTTAGCTGCTGGG 1046
 DB 961 ACACAGGACAGTAAACCTCTCGGAGCTTCAAGCTATGAAATTTGATCTTAGCTGCTGGG 1020
 QY 1047 CTGAATTTCTCTGGAACCTGAGTTTACAAACCACTACTGCGAGGTTCCCTGATATCC 1106
 DB 1021 CTGAATTTCTCTGGAACCTGAGTTTACAAACCACTACTGCGAGGTTCCCTGATATCC 1080
 QY 1107 AGATCTTCTCTGCCCAACTCTTACTGGGAGATTTGCAAACTGCCACATCTCAGCTGTAA 1166
 DB 1081 AGATCTTCTCTGCCCAACTCTTACTGGGAGATTTGCAAACTGCCACATCTCAGCTGTAA 1140
 QY 1167 CAAAGCAGAAACCTTCTGCTGGGATAGCTTGTGCTTAATGGAATGGATGGATGATAC 1226
 DB 1141 CAAAGCAGAAACCTTCTGCTGGGATAGCTTGTGCTTAATGGAATGGATGGATGATAC 1200
 QY 1227 CCTTCTCTGAATGACTCCCTTCTGATGAATGATGAAGCAGAGGTTACTAGTAGTATTTTC 1286
 DB 1201 CCTTCTCTGAATGACTCCCTTCTGATGAATGATGAAGCAGAGGTTACTAGTAGTATTTTC 1260

1287 CCAAGCTTCTCCCATCATAGACATGTAGAAAATAATATATTTTATGGCACACTGGGATA 1346
1261 CCAAGCTTCTCCCATCATAGACATGTAGAAAATAATATATTTTATGGCACACTGGGATA 1320
1347 AACAGCAAGATGTCTCACTCTTGGAACTGCATATGACTAGAGGCTCTTGTGACTGGA 1406
1321 AACAGCAAGATGTCTCACTCTTGGAACTGCATATGACTAGAGGCTCTTGTGACTGGA 1380
1407 GGTAAACAACCTGCCAGTAACTGTGGGAGAAAGGGATCAATATATTTTGCACACCTGTAT 1466
1381 GGTAAACAACCTGCCAGTAACTGTGGGAGAAAGGGATCAATATATTTTGCACACCTGTAT 1440
1467 AGGCGATGGACACACAGCCCAAGATGCTCTGCTCACAGTCAGTATGTGTGAAGATCCCTGG 1526
1441 AGGCCATGGACACACAGCCCAAGATGCTCTGCTCACAGTCAGTATGTGTGAAGATCCCTGG 1500
1527 TGGCTGGCTTCAACACGCGATCTTGAGCAAAATAGGAAAATGTACCCCTTCGCTTGAGGCA 1586
1501 TGGCTGGCTTCAACACGCGATCTTGAGCAAAATAGGAAAATGTACCCCTTCGCTTGAGGCA 1560
1587 GATGAGCCCTTCCCCGAGTGCATGCTTGGAGAGCAAGATGTGGGCTGCATATAAGCA 1646
1561 GATGAGCCCTTCCCCGAGTGCATGCTTGGAGAGCAAGATGTGGGCTGCATATAAGCA 1620
1647 CACTCATCCCTTGTCTGGGAATCTTTGTCAGGGCATAAACAGGCTTAGTAGTCCAAAC 1706
1621 CACTCATCCCTTGTCTGGGAATCTTTGTCAGGGCATAAACAGGCTTAGTAGTCCAAAC 1680
1707 ACAGATGACAGTGTCTGTGGGTCTCTGTACAGATTTGTGGCTCTCAGGCCATGTAGACACA 1766
1681 ACAGATGACAGTGTCTGTGGGTCTCTGTACAGATTTGTGGCTCTCAGGCCATGTAGACACA 1740
1767 CTCTCCAAATGAGTGTGGAAAATGTTCTTCTGAGGGTCTAGAGACTGCTGGGACAC 1826
1741 CTCTCCAAATGAGTGTGGAAAATGTTCTTCTGAGGGTCTAGAGACTGCTGGGACAC 1800
1827 TTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTCTTCTGGCCAGATTTCTTT 1886
1801 TTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTCTTCTGGCCAGATTTCTTT 1860
1887 CTGTATCACTCAAGAGCCTCAGCAGAAAGAGAGCCATGCCAGTATTCCTCACTCTCC 1946
1861 CTGTATCACTCAAGAGCCTCAGCAGAAAGAGAGCCATGCCAGTATTCCTCACTCTCC 1920
1947 AAAAGAACTGACAGCTATATTTCTACACTCTCTGGGAGTGGGTATTAATCCAACCA 2006
1921 AAAAGAACTGACAGCTATATTTCTACACTCTCTGGGAGTGGGTATTAATCCAACCA 1980
2007 TCAAAATAGAGACCTTGCAAGAGCAGAGTCAATCTCCAGAAGAACTTGGGAGATGAT 2066
1981 TCAAAATAGAGACCTTGCAAGAGCAGAGTCAATCTCCAGAAGAACTTGGGAGATGAT 2040
2067 GTGCGAGATGATGAACCTGGGTTCATCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAA 2126
2041 GTGCGAGATGATGAACCTGGGTTCATCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAA 2100
2127 GCTGAGGAGAGTGGCCGACCTGGCATGGCATGCCCAACACAGATCACCAGCCAGCTTACA 2186
2101 GCTGAGGAGAGTGGCCGACCTGGCATGGCATGCCCAACACAGATCACCAGCCAGCTTACA 2160
2187 CAGGCAATTAATCTCTCCTCAATGAGGAAGATCAATTCACAACTGAGCAAGACATTCATATG 2246
2161 CAGGCAATTAATCTCTCCTCAATGAGGAAGATCAATTCACAACTGAGCAAGACATTCATATG 2220
2247 ATCAATTAAGGAGTGTTCCTTATGTGTAGCAAGTATTAATCGGCTAACTCCTAAATC 2306
2221 ATCAATTAAGGAGTGTTCCTTATGTGTAGCAAGTATTAATCGGCTAACTCCTAAATC 2280
2307 CCAATGAATAGTCTCCTAGGCTGGACAGCAATGGCTGCAATTAAGGAGCAATAAGACATCAG 2366
2281 CCAATGAATAGTCTCCTAGGCTGGACAGCAATGGCTGCAATTAAGGAGCAATAAGACATCAG 2340
2367 TCCAGTAAATGAATCCATAGACTCATAGACCAACTACATTAAGCACTATGTAGGA 2426

2341 TCCAGTAAATGAATCCATAGACTCATCTAGCAACCACTACCATTAGCACTATGTAGGA 2400
2427 GCTGCAAGGCCCCCAAGTAGAAGATGTGCAATAATGTCTGCTCTGTTGTAGCTCAGGAGAC 2486
2401 GCTGCAAGGCCCCCAAGTAGAAGATGTGCAATAATGTCTGCTCTGTTGTAGCTCAGGAGAC 2460
2487 AATTCCAGCAGACACACTACAGTTTAAACGCTGAACTGCAAGCTGCAAGTAAATAGCATGAACA 2546
2461 AATTCCAGCAGACACACTACAGTTTAAACGCTGAACTGCAAGTAAATAGCATGAACA 2520
2547 GTCAGAAAATACCTTATAGGGGGCAGGGCTGAAGCTGGCCCTTGAAGATGATGAATA 2606
2521 GTCAGAAAATACCTTATAGGGGGCAGGGCTGAAGCTGGCCCTTGAAGATGATGAATA 2580
2607 TTTGGATAGAAATGAGGAAGACAGAGAGGCTCCAAAGTGAGAGAGCATGAAAATAGAGC 2666
2581 TTTGGATAGAAATGAGGAAGACAGAGAGGCTCCAAAGTGAGAGAGCATGAAAATAGAGC 2640
2667 AGGGCTTGGATCAGTGGGGTGTATTAGAGACACTCTCCAGATGCAACCATGCAATGCTCA 2726
2641 AGGGCTTGGATCAGTGGGGTGTATTAGAGACACTCTCCAGATGCAACCATGCAATGCTCA 2700
2727 CAGTCCCTTGCCTATGTGTGCGCAGAGTCCAGCAGAGTGTGCCCCCAGCCCATGCTC 2786
2701 CAGTCCCTTGCCTATGTGTGCGCAGAGTGTCCAGCCAGATGTGTGCCCCCAGCCCATGCTC 2760
2787 CATTTACATGCTCTTCAATGCCACCTCAAAAGGTAGCTCTTCTGTAAAGCTTTCCCTGG 2846
2761 CATTTACATGCTCTTCAATGCCACCTCAAAAGGTAGCTCTTCTGTAAAGCTTTCCCTGG 2820
2847 TATCAGGAATCAAAATTAATCAGGGATCTTTTCACTGCTGTTTTTCTCTTTGGTCC 2906
2821 TATCAGGAATCAAAATTAATCAGGGATCTTTTCACTGCTGTTTTTCTCTTTGGTCC 2880
2907 TTCTATCACTAAACTCATCTCATTAGCCTTACAGCATAAATAATTTGTTTCTCCTC 2966
2881 TTCTATCACTAAACTCATCTCATTAGCCTTACAGCATAAATAATTTGTTTCTCCTC 2940
2967 ACTACATGTACATGTGGAAATACAGATAAAGAAAGCGTGGGGTGGTGGCTCAGC 3026
2941 ACTACATGTACATGTGGAAATACAGATAAAGAAAGCGTGGGGTGGTGGCTCAGC 3000
3027 CCTGTATCCACACACTTTGGAGGCCAAGCGAGGATCACTGAGGTGAGGATTCG 3086
3001 CCTGTATCCACACACTTTGGAGGCCAAGCGAGGATCACTGAGGTGAGGATTCG 3060
3087 AGATTATCTGGCCAAACATGTGAAACCCCATNTNTACTAAAAATACGAAATAGCCAGG 3146
3061 AGATTATCTGGCCAAACATGTGAAACCCCATCTCTACTAAAAATACGAAATAGCCAGG 3120
3147 TGTGCTGGCACACATCTGTAGTCCAG 3173
3121 TGTGCTGGCACACATCTGTAGTCCAG 3147

RESULT 6

AL138930/c
LOCUS Human DNA sequence from clone RP11-52861 on chromosome 1, complete
DEFINITION
ACCESSION AL138930
VERSION AL138930.15 GI:15546076
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 175386)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk
 On Sep 10, 2001 this sequence version replaced gi:15021284.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em., EMBL; Sw.,
 SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
 RP11-528G1 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-528G1. It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true left end of clone RP11-528G1 is at 1 in this sequence. The
 true left end of clone RP11-404F10 is at 17387 in this sequence.
 The true right end of clone RP11-517F10 is at 82222 in this
 sequence.

FEATURES
 Source
 1. .175386
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP11-528G1"
 /clone_lib="RP11-11.2"
 misc_feature
 31056..31193
 /note="Sequence from overlapping clone RP11-517F10
 (AL445230). Assembly confirmed by restriction digest."
 36248..36487
 /note="Sequence from overlapping clone RP11-517F10
 (AL445230). Assembly confirmed by restriction digest."
 misc_feature
 80985..80991
 /note="Sequence from overlapping clone RP11-517F10
 (AL445230). Assembly confirmed by restriction digest."
 ORIGIN
 Query Match 69.4%; Score 2201.2; DB 9; Length 175386;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2203; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 960 TTTGCTGATAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGC 1019
 DB 108996 TCTCCTGCACAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGC 108937
 QY 1020 TATGAATTTGATAGGCTGCTGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAC 1079
 DB 108936 TATGAATTTGATAGGCTGCTGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAC 108877
 QY 1080 ACCAATCTGCGAGTTCCCTGGATCCAGATCTTCTGCCCCAATCTTACTGGAGATT 1139
 DB 108876 ACCAATCTGCGAGTTCCCTGGATCCAGATCTTCTGCCCCAATCTTACTGGAGATT 108817
 QY 1140 GCAAACTGCCACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTG 1199
 DB 108816 GCAAACTGCCACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTG 108757

QY	1200	TGCCTAAATGGAACAAATGGATGCATACCCCTTCTGAAATGACTCCCTTCTTGAATGAATGA 1259
DB	108756	TGCCTAAATGGAACAAATGGATGCATACCCCTTCTGAAATGACTCCCTTCTTGAATGAATGA 108697
QY	1260	CAAGCAGGTTACCTAGTATAGTTTCCCAAACTTCTCCCATCATAGCACATGTAGAAA 1319
DB	108696	CAAGCAGGTTACCTAGTATAGTTTCCCAAACTTCTCCCATCATAGCACATGTAGAAA 108637
QY	1320	ATAATATTTTATGACACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA 1379
DB	108636	ATAATATTTTATGACACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA 108577
QY	1380	TATGACTAGAGGCTCTTGTGACTGGAGTAACAAACCTGCCCAGTAATCTGTGGGAGAAG 1439
DB	108576	TATGACTAGAGGCTCTTGTGACTGGAGTAACAAACCTGCCCAGTAATCTGTGGGAGAAG 108517
QY	1440	GGGATCAATATTTTGCACACCTGTATAGGCCATGGCACACCAAGCATCTTGTGCTC 1499
DB	108516	GGGATCAATATTTTGCACACCTGTATAGGCCATGGCACACCAAGCATCTTGTGCTC 108457
QY	1500	ACAGTCAGTATGTGTGAAGATCCCTGGTGGGCTTCCACCAAGCATCTTGTGCAAAAT 1559
DB	108456	ACAGTCAGTATGTGTGAAGATCCCTGGTGGGCTTCCACCAAGCATCTTGTGCAAAAT 108397
QY	1560	AGGAAATGTATACCTTTCGCTTGAGGCAGATGACAGCCCTTCCCGAGTGCATGGCTTGA 1619
DB	108396	AGGAAATGTATACCTTTCGCTTGAGGCAGATGACAGCCCTTCCCGAGTGCATGGCTTGA 108337
QY	1620	GAGCAGATGTGGGCTGCATATAGCAACATCATCCCTTGTCTGGGAATCTTGTGCGAG 1679
DB	108336	GAGCAGATGTGGGCTGCATATAGCAACATCATCCCTTGTCTGGGAATCTTGTGCGAG 108277
QY	1680	GCATTAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGA 1739
DB	108276	GCATTAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGA 108217
QY	1740	GTGTGGCTCTCAGCCATGTAGACACATCTTCCAAATGAGATGTTGGGAAATGTTCTTTC 1799
DB	108216	GTGTGGCTCTCAGCCATGTAGACACATCTTCCAAATGAGATGTTGGGAAATGTTCTTTC 108157
QY	1800	TGAGGCTCTAGAGACTGCTGGGACATCTTCTTGGAGTGCTACTTCCAGAGCCTTATAG 1859
DB	108156	TGAGGCTCTAGAGACTGCTGGGACATCTTCTTGGAGTGCTACTTCCAGAGCCTTATAG 108097
QY	1860	GATTTCTTCTGGCCCAAGATTTCTTCTGTATCACTCCAAAGCAGCTCTCAGCAGAGAAG 1919
DB	108096	GATTTCTTCTGGCCCAAGATTTCTTCTGTATCACTCCAAAGCAGCTCTCAGCAGAGAAG 108037
QY	1920	CAGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACCAAGCTTATATTTCTCACACT 1979
DB	108036	CAGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACCAAGCTTATATTTCTCACACT 107977
QY	1980	TCTGGGAACTGGGTATATCCAACTCAAAATAGAAAGCTTGCAGAGAGAGTCA 2039
DB	107976	TCTGGGAACTGGGTATATCCAACTCAAAATAGAAAGCTTGCAGAGAGAGTCA 107917
QY	2040	TTCTCCAGAGGAACTTGGGAGATGATGTGAGATGATGATAAAGCTGGGTTCATCCCAAGT 2099
DB	107916	TTCTCCAGAGGAACTTGGGAGATGATGTGAGATGATGATAAAGCTGGGTTCATCCCAAGT 107857
QY	2100	CCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGGCCCACTCCCTGGCATGCC 2159
DB	107856	CCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGGCCCACTCCCTGGCATGCC 107797
QY	2160	CACAAACAGATCACAGCAGCTTACAGGCAATTAATCTCTCAATGAGGAGATCA 2219
DB	107796	CACAAACAGATCACAGCAGCTTACAGGCAATTAATCTCTCAATGAGGAGATCA 107737
QY	2220	TTCAAACTGAGCAAGACATTCATATGATGATTTAAGGAGTGTTCCTCTTATGTGTAG 2279
DB	107736	TTCAAACTGAGCAAGACATTCATATGATGATTTAAGGAGTGTTCCTCTTATGTGTAG 107677

```
QY 2280 CAAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGG 2339
Db 107676 CAAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGG 107617
QY 2340 CTGCAATTAAGGCGAGATAAAGACATCATAGTCCCAAGTAATGAATCCATAGACTCATCTAGCA 2399
Db 107616 CTGCAATTAAGGCGAGATAAAGACATCATAGTCCCAAGTAATGAATCCATAGACTCATCTAGCA 107557
QY 2400 CCAACTACCATTAAGCACTATGTTAGGAGCTGCAAGGCCCCCAAGTAAGATGTGCATAA 2459
Db 107556 CCAACTACCATTAAGCACTATGTTAGGAGCTGCAAGGCCCCCAAGTAAGATGTGCATAA 107497
QY 2460 TGTCTGCTCTTGTGTAGCTCAGGAGACAATTCAGACACAGACATACAGTTAAACGCTGAA 2519
Db 107496 TGTCTGCTCTTGTGTAGCTCAGGAGACAATTCAGACACAGACATACAGTTAAACGCTGAA 107437
QY 2520 CTGACGCTCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGGCTG 2579
Db 107436 CTGACGCTCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGGCTG 107377
QY 2580 AAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGCGCTC 2639
Db 107376 AAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGCGCTC 107317
QY 2640 CAAAGTGAGAGAAAGCATGAAAAATGAGCAGGGGCGCTGATCAGTGGGGTGTATTTCAGAGCA 2699
Db 107316 CAAAGTGAGAGAAAGCATGAAAAATGAGCAGGGGCGCTGATCAGTGGGGTGTATTTCAGAGCA 107257
QY 2700 CTTCTCAGATGACATCATGCTCAGAGTCCCTTGTGCTATGTTGGCAGAGTGTCCCA 2759
Db 107256 CTTCTCAGATGACATCATGCTCAGAGTCCCTTGTGCTATGTTGGCAGAGTGTCCCA 107197
QY 2760 GCAGATGTGTCGCCCCACCCCATGTCATTTACATGTCCTTCAATGCCACCTCAAAAG 2819
Db 107196 GCAGATGTGTCGCCCCACCCCATGTCATTTACATGTCCTTCAATGCCACCTCAAAAG 107137
QY 2820 GTACCTCTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC 2879
Db 107136 GTACCTCTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC 107077
QY 2880 AACTGCTCTTTTCTCTTCTTCTTCTTCTATCATCAATAAATCATCTCATCTCAGCCTTA 2939
Db 107076 AACTGCTCTTTTCTCTTCTTCTTCTTCTATCATCAATAAATCATCTCATCTCAGCCTTA 107017
QY 2940 CAGCATAACTAATTAATTTCTTCTCTCTACTACATGTCATGTCGGAATTTACAGATAAAC 2999
Db 107016 CAGCATAACTAATTAATTTCTTCTCTCTACTACATGTCATGTCGGAATTTACAGATAAAC 106957
QY 3000 GGAAGCCKGCTGGGTGGTGGCTCAGCCTGTAATCCCAACACTTTGGAGGCCAAGGCA 3059
Db 106956 GGAAGCCKGCTGGGTGGTGGCTCAGCCTGTAATCCCAACACTTTGGAGGCCAAGGCA 106897
QY 3060 GCGGATCACTGAGTCAAGGATTCGAGATTAATCTGCGCAACATGTTGAACCCCATN 3119
Db 106896 GCGGATCACTGAGTCAAGGATTCGAGATTAATCTGCGCAACATGTTGAACCCCATN 106837
QY 3120 TTTACTAAAAATACGAAATTAAGCAGGTGTGGTGGCACACATCTGTAGTCCAG 3173
Db 106836 TTTACTAAAAATACGAAATTAAGCAGGTGTGGTGGCACACATCTGTAGTCCAG 106783
```

```
RESULT 7
AL355996/c
LOCUS Homo sapiens chromosome 1 clone RP11-77110 map q21.3-23.1, 11
DEFINITION Homo sapiens chromosome 1 clone RP11-77110 map q21.3-23.1, 11
unordered pieces.
ACCESSION AL355996
VERSION AL355996.3 GI:9926602
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE
AUTHORS
JOURNAL

COMMENT

```
1 Plumb,B.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9231058.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba77110
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 57% of reads
Chemistry: Dye-terminator ET-amersham; 42% of reads Consensus
quality: 170939 bases at least Q40
Consensus quality: 172842 bases at least Q30
Consensus quality: 173980 bases at least Q20
Insert size: 175698; sum-of-contigs
Insert size: 182579; 24.9% error; agarose-fp
Quality coverage: 5.06x in Q20 bases; sum-of-contigs Quality
coverage: 4.96x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 8004: contig of 8004 bp in length
* 8005 8104: gap of 100 bp
* 8105 11636: contig of 3532 bp in length
* 11637 11736: gap of 100 bp
* 11737 14534: contig of 2798 bp in length
* 14535 14634: gap of 100 bp
* 14635 94898: contig of 80264 bp in length
* 94899 94999: gap of 100 bp
* 94999 103152: contig of 8154 bp in length
* 103153 103252: gap of 100 bp
* 103253 121408: contig of 18156 bp in length
* 121409 121508: gap of 100 bp
* 121509 123702: contig of 2194 bp in length
* 123703 123802: gap of 100 bp
* 123803 127869: contig of 4067 bp in length
* 127870 127969: gap of 100 bp
* 127970 130403: contig of 2434 bp in length
* 130404 130503: gap of 100 bp
* 130504 13199: contig of 2696 bp in length
* 13200 13299: gap of 100 bp
* 13300 176698: contig of 43399 bp in length.
*
* Location/Qualifiers
* 1. 176698
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="1"
* /map="q21.3-23.1"
* /clone="RP11-77110"
* /clone_lib="RPCI-11.1"
* 1. .8004
* /note="assembly_fragment:00215
* fragment_chain:1
* clone_end:SP6
* vector_side:left"
* 8105. _11636
* /note="assembly_fragment:01702
* fragment_chain:1"
```

misc_feature 11737..14534
/note="assembly_fragment:01924
fragment_chain:2"
misc_feature 14635..94898
/note="assembly_fragment:00986
fragment_chain:2"
misc_feature 94999..103152
/note="assembly_fragment:01527
fragment_chain:2"
misc_feature 103253..121408
/note="assembly_fragment:02181
fragment_chain:2"
misc_feature 121509..123702
/note="assembly_fragment:01265
fragment_chain:3"
misc_feature 123803..127869
/note="assembly_fragment:02405
fragment_chain:3"
misc_feature 127970..130403
/note="assembly_fragment:01769
fragment_chain:3"
misc_feature 130504..133199
/note="assembly_fragment:01021"
133300..176698
/note="assembly_fragment:02197"

ORIGIN

Query Match 69.4%; Score 2201.2; DB 2; Length 176698;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2203; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 960 TTTCCTGATGATGAGGATGGGAAAGCAGCAGACAGGACAGTAAACCTCTGGGACTTCAAGC 1019
DB 78961 TTTCCTGATGATGAGGATGGGAAAGCAGCAGACAGGATTAACCTCTGGGACTTCAAGC 78902
QY 1020 TATGAAATTTGATCTAGGCTGTGGCTGGAATTTCTCCCTCTGGAACCTGAGTTACAAC 1079
DB 78901 TATGAAATTTGATCTAGGCTGTGGCTGGAATTTCTCCCTCTGGAACCTGAGTTACAAC 78842
QY 1080 ACCAATCTGGGAGGTTCCCTGATCGAGATCTTCTCTGCCCCAATCTTACTGGGAGATT 1139
DB 78841 ACCAATCTGGGAGGTTCCCTGATCGAGATCTTCTCTGCCCCAATCTTACTGGGAGATT 78782
QY 1140 GCAAACTGCCACATCTCAGCTCTGAGCAAGCAGGAAACCTTCTGCTGGGCTAGCTTG 1199
DB 78781 GCAAACTGCCACATCTCAGCTCTGAGCAAGCAGGAAACCTTCTGCTGGGCTAGCTTG 78722
QY 1200 TGCTAAATGGCAAAATGGATGCATACCTTCTCTGAAATGACTCCCTTCTGAAATGAATGA 1259
DB 78721 TGCTAAATGGCAAAATGGATGCATACCTTCTCTGAAATGACTCCCTTCTGAAATGAATGA 78662
QY 1260 CAAAGCAGGTTACTAGTATAGTTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAA 1319
DB 78661 CAAAGCAGGTTACTAGTATAGTTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAA 78602
QY 1320 ATATATATTTATGGCACATGGGATAAACAGCAGATGCTCACTTCTGGAAGCTGCA 1379
DB 78601 ATATATATTTATGGCACATGGGATAAACAGCAGATGCTCACTTCTGGAAGCTGCA 78542
QY 1380 TATGACTAGAGGCTCTTTGACTGAGGATTAACAAACCTCCCGAGTAACTGTGGGAGAAG 1439
DB 78541 TATGACTAGAGGCTCTTTGACTGAGGATTAACAAACCTCCCGAGTAACTGTGGGAGAAG 78482
QY 1440 GGGATCAATATTTTGGCACATCTGTAATAGGCGATGGCACACGAGGATGCTCTGCTC 1499
DB 78481 GGGATCAATATTTTGGCACATCTGTAATAGGCGATGGCACACGAGGATGCTCTGCTC 78422
QY 1500 ACAGTCAGTATGTGAGATCCCTGCTGGTGGCTTCCAGCGCATCTTGAGCAATT 1559
DB 78421 ACAGTCAGTATGTGAGATCCCTGCTGGTGGCTTCCAGCGCATCTTGAGCAATT 78362
QY 1560 AGGAAATGTACCTTCTGCTTGGGAGATGCGAGCCCTTCCCGAGTGCATGGCTTGGGA 1619
DB

DB 78361 AGGAAATGTACCTTCTGCTTGGGAGATGCGAGCCCTTCCCGAGTGCATGGCTTGA 78302
QY 1620 GAGCAGAAATGTGGCTGCATATAAGCACACATCATCTTGTCTGGGAATCTTTGTGCGAG 1679
DB 78301 GAGCAGAAATGTGGCTGCATATAAGCACACATCATCTTGTCTGGGAATCTTTGTGCGAG 78242
QY 1680 GGCATAACAGGCTTGTAGTAAAGTCCAAACACAGATGACAGTGTCTGTGGTCTCTGTGCA 1739
DB 78241 GGCATAACAGGCTTGTAGTAAAGTCCAAACACAGATGACAGTGTCTGTGGTCTCTGTGCA 78182
QY 1740 GTTGTGGCTCTCAGCCATGTAGACACATCTCCAAATGAGTGTGGGAAATGTTCTTTC 1799
DB 78181 GTTGTGGCTCTCAGCCATGTAGACACATCTCCAAATGAGTGTGGGAAATGTTCTTTC 78122
QY 1800 TGCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTACTTTCAGAACCTTATAG 1859
DB 78121 TGCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTACTTTCAGAACCTTATAG 78062
QY 1860 GATTTCTTTCTGGGCAAGATTTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAG 1919
DB 78061 GATTTCTTTCTGGGCAAGATTTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAGAG 78002
QY 1920 CAGCCATGCCAGTATTTCCACTCTCCAAAGGAACTGACAGCTTATATTTCTCACACT 1979
DB 78001 CAGCCATGCCAGTATTTCCACTCTCCAAAGGAACTGACAGCTTATATTTCTCACACT 77942
QY 1980 TCTGGGAACTGGGTATATCAACCATCAAAATAGAACCTTTCAGAACGAGAGTCA 2039
DB 77941 TCTGGGAACTGGGTATATCAACCATCAAAATAGAACCTTTCAGAACGAGAGTCA 77882
QY 2040 TTCTCCAGAGAACTTTGGGAGATGATGTGCAGATGATGAAACTGGGTTTATCCAGATT 2099
DB 77881 TTCTCCAGAGAACTTTGGGAGATGATGTGCAGATGATGAAACTGGGTTTATCCAGATT 77822
QY 2100 CCAAGACTCAGAGACTAGCTTTAAGCTGAGGAGAGTGCAGCCACCTGCGCATGCCCC 2159
DB 77821 CCAAGACTCAGAGACTAGCTTTAAGCTGAGGAGAGTGCAGCCACCTGCGCATGCCCC 77762
QY 2160 CCAAAACAGATCAACAGCAGCTTACACAGGATTAACCTCTCTCAATAGGAGAGATCA 2219
DB 77761 CCAAAACAGATCAACAGCAGCTTACACAGGATTAACCTCTCTCAATAGGAGAGATCA 77702
QY 2220 TTCAAACTGAGCAAGACATTCATATGATCATTTAAGGAGTGTTCCTTATGTGTAG 2279
DB 77701 TTCAAACTGAGCAAGACATTCATATGATCATTTAAGGAGTGTTCCTTATGTGTAG 77642
QY 2280 CAAATATATCGCTTAACCTTAAATCCCAATAGTCTAGGCTGGACAGCAATGGG 2339
DB 77641 CAAATATATCGCTTAACCTTAAATCCCAATAGTCTAGGCTGGACAGCAATGGG 77582
QY 2340 CTGCAATTAGGCAAGATTAAGACATCACTCCAGTAAATGAATCCATAGACTCATAGCA 2399
DB 77581 CTGCAATTAGGCAAGATTAAGACATCACTCCAGTAAATGAATCCATAGACTCATAGCA 77522
QY 2400 CCAACTACCATTAGCACTATGTTAGGAGTGCAGGCCCCCAAGATGAGATGTGCATAA 2459
DB 77521 CCAACTACCATTAGCACTATGTTAGGAGTGCAGGCCCCCAAGATGAGATGTGCATAA 77462
QY 2460 TGTCTCTCTTGTGTAGCTCAGGAGCAATTTCCAGCACAGACTCAGTTAAAGCTGAA 2519
DB 77461 TGTCTCTCTTGTGTAGCTCAGGAGCAATTTCCAGCACAGACTCAGTTAAAGCTGAA 77402
QY 2520 CTCAGCTGCAAGTATAGCATGAACAGTCCAGAAAAATACCTTATGAGGGGGCAGGGCTG 2579
DB 77401 CTCAGCTGCAAGTATAGCATGAACAGTCCAGAAAAATACCTTATGAGGGGGCAGGGCTG 77342
QY 2580 AAGCTGGGCTTCAAGGATGGATGAAATTTGGATAGAGATGAGAGACAGAGGGGCTC 2639
DB 77341 AAGCTGGGCTTCAAGGATGGATGAAATTTGGATAGAGATGAGAGACAGAGGGGCTC 77282
QY 2640 CAAAGTGAAGAACATGAAAAATGAGCAGGGGCTTGGATCAGTGGGTTATTCAGAGCA 2699
DB 77281 CAAAGTGAAGAACATGAAAAATGAGCAGGGGCTTGGATCAGTGGGTTATTCAGAGCA 77222

QY	1080	ACCAATACCTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCAACTCTTACTTGGGAGATT	1139	QY	2160	CACAAACAGATCACCCAGCCAGCTTTACACAGGCAATTAATCTCTCTCAATGAGGAAATCA	2219
DB	173435	ACCAATACCTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCACTCTTACTTGGGAGATT	173376	DB	172355	CACAAACAGATCACCCAGCCAGCTTTACACAGGCAATTAATCTCTCTCAATGAGGAAATCA	172296
QY	1140	GCAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTG	1199	QY	2220	TTCAAACTGAGCAAGACATTCATATGATCATTTAAGGAGCTTTTCCCTTATGTGTAG	2279
DB	173375	GCAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTG	173316	DB	172295	TTCAAACTGAGCAAGACATTCATATGATCATTTAAGGAGCTTTTCCCTTATGTGTAG	172236
QY	1200	TGCCTAAATGGCAAAATGATGCATACCCCTTCTGAAATGACTCCCTTCTGAAATGAATGA	1259	QY	2280	CAAGTATTAATCGGCTTAACCTCTTAATCCCAATGAATAGTCTCTAGGCTGGACAGCAATGG	2339
DB	173315	TGCCTAAATGGCAAAATGATGCATACCCCTTCTGAAATGACTCCCTTCTGAAATGAATGA	173256	DB	172235	CAAGTATTAATCGGCTTAACCTCTTAATCCCAATGAATAGTCTCTAGGCTGGACAGCAATGG	172176
QY	1260	CAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTCCCAATCATAGACACATGTAGAA	1319	QY	2340	CTGCAATTAGGCAGATAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCA	2399
DB	173255	CAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTCCCAATCATAGACACATGTAGAA	173196	DB	172175	CTGCAATTAGGCAGATAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCA	172116
QY	1320	ATAATATTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA	1379	QY	2400	CCAACTACATTAGCAGACTATGTTAGGAGCTGCAAGGCCCAAGTAGAGATGTCATAA	2459
DB	173195	ATAATATTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA	173136	DB	172115	CCAACTACATTAGCAGACTATGTTAGGAGCTGCAAGGCCCAAGTAGAGATGTCATAA	172056
QY	1380	TATGACTAGAGCCCTTCTGTGACTGGAGGTAAACAACCTTGGCCAGTAACCTGTGGGAGAG	1439	QY	2460	TGCTGCTCTTGTGTAGCTCAGGAGACAAATTCACGACACAGACATACACAGTTAAACGCTGAA	2519
DB	173135	TATGACTAGAGCCCTTCTGTGACTGGAGGTAAACAACCTTGGCCAGTAACCTGTGGGAGAG	173076	DB	172055	TGCTGCTCTTGTGTAGCTCAGGAGACAAATTCACGACACAGACATACACAGTTAAACGCTGAA	171996
QY	1440	GGGATCAATATTTTGCACACCTGTAAATAGGCCATGCGCACACAGCCAGATCTCTGCTC	1499	QY	2520	CTGCACTGCAAGTAAATAGCATGAAACAGTCAGAAAAATACTTATGAGGGGGCAGGGCTG	2579
DB	173075	GGGATCAATATTTTGCACACCTGTAAATAGGCCATGCGCACACAGCCAGATCTCTGCTC	173016	DB	171995	CTGCACTGCAAGTAAATAGCATGAAACAGTCAGAAAAATACTTATGAGGGGGCAGGGCTG	171936
QY	1500	ACAGTCAGTATGTGAAGATCCCTGGTGGCTTCCACCAAGCATCTTGAGCAAAAT	1559	QY	2580	AAGCTGGGCTTGAAGGATGGATGAATTTTGATAGAGATAGAGATAGAGAGACAGAGGCCCTC	2639
DB	173015	ACAGTCAGTATGTGAAGATCCCTGGTGGCTTCCACCAAGCATCTTGAGCAAAAT	172956	DB	171935	AAGCTGGGCTTGAAGGATGGATGAATTTTGATAGAGATAGAGATAGAGAGACAGAGGCCCTC	171876
QY	1560	AGGAAATGTACCCCTTGTGAGGAGATGAGCCCTTCCCCCGAGTGCATGGCTTGA	1619	QY	2640	CAAGTGAGAGAGATGAAAAATGAGCAGGGCCCTGGATCATGAGGGGTGTATTTCAGAGCA	2699
DB	172955	AGGAAATGTACCCCTTGTGAGGAGATGAGCCCTTCCCCCGAGTGCATGGCTTGA	172896	DB	171875	CAAGTGAGAGAGATGAAAAATGAGCAGGGCCCTGGATCATGAGGGGTGTATTTCAGAGCA	171816
QY	1620	GAGCAGATGGGCTGCATATAGCACATCATCCCTTGTCTGGGAATCTTTGTGCAG	1679	QY	2700	CCTCTCCAGATCACCATGCTCATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCCA	2759
DB	172895	GAGCAGATGGGCTGCATATAGCACATCATCCCTTGTCTGGGAATCTTTGTGCAG	172836	DB	171815	CCTCTCCAGATCACCATGCTCATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCCA	171756
QY	1680	GGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGA	1739	QY	2760	GCCAGATGTGGCCGCCACCCCATGCTCAATTTACATGTCTTCAATGCTTCAATGCTTCAATG	2819
DB	172835	GGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGA	172776	DB	171755	GCCAGATGTGGCCGCCACCCCATGCTCAATTTACATGTCTTCAATGCTTCAATGCTTCAATG	171696
QY	1740	GTTGTGGCTCTAGCCATGTAGACACACTCTCCAAATGGAGTGTGGGAAATGTTCTTTC	1779	QY	2820	GTACCTCTTCTGTAAAGCTTTCCTCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC	2879
DB	172775	GTTGTGGCTCTAGCCATGTAGACACACTCTCCAAATGGAGTGTGGGAAATGTTCTTTC	172716	DB	171695	GTACCTCTTCTGTAAAGCTTTCCTCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC	171636
QY	1800	TGCAGGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTACTTTCAGAGCCCTTATAG	1859	QY	2880	ACACTGCTGTTTTTCTCTTGGTCTTCTATCATCTATAAACTCATCTCATTCAGGCTTA	2939
DB	172715	TGCAGGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTACTTTCAGAGCCCTTATAG	172656	DB	171635	ACACTGCTGTTTTTCTCTTGGTCTTCTATCATCTATAAACTCATCTCATTCAGGCTTA	171576
QY	1860	GATTTTCTTCTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAAG	1919	QY	2940	CAGCATACTAATATTGTTTTTCTCTCATCTACATTTGTATGTGGGAATTCAGAGATAAAC	2999
DB	172655	GATTTTCTTCTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAAG	172596	DB	171575	CAGCATACTAATATTGTTTTTCTCTCATCTACATTTGTATGTGGGAATTCAGAGATAAAC	171516
QY	1920	CAGCCATGCCCAGTATTTCCACTCTCCAAAGAACTGACACAGCTTATTTCTCACACT	1979	QY	3000	GGAGCCGCTGGGGTGGTGGCTCAGCCTGTAAATCCCAACACTTTTGGGAGGCCAAGGCA	3059
DB	172595	CAGCCATGCCCAGTATTTCCACTCTCCAAAGAACTGACACAGCTTATTTCTCACACT	172536	DB	171515	GGAGCCGCTGGGGTGGTGGCTCAGCCTGTAAATCCCAACACTTTTGGGAGGCCAAGGCA	171456
QY	1980	CTCTGGGAACTGGGTATATCAACCATCAAAATAGAGACCTTGCAGAGCAGAGTCA	2039	QY	3060	GGCGGATCACCTGAGGTGAGGATTCAGATTAATCTGCGCCAAACATGTTGGAACCCCATN	3119
DB	172535	CTCTGGGAACTGGGTATATCAACCATCAAAATAGAGACCTTGCAGAGCAGAGTCA	172476	DB	171455	GGCGGATCACCTGAGGTGAGGATTCAGATTAATCTGCGCCAAACATGTTGGAACCCCATN	171396
QY	2040	TTCTCCAGAGGAACCTGGGAGATGATGGTGCAGATGATGAACTGGGTTTATCCCGAGTT	2099	QY	3120	TNTACTAAAAATACGAAATTAGCCAGGTGTGGGACACATCTGTAGTCCCGAG	3173
DB	172475	TTCTCCAGAGGAACCTGGGAGATGATGGTGCAGATGATGAACTGGGTTTATCCCGAGTT	172416	DB	171395	TCTACTAAAAATACGAAATTAGCCAGGTGTGGGACACATCTGTAGTCCCGAG	171342
QY	2100	CCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCCACCTGGCATGCC	2159				
DB	172415	CCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCCACCTGGCATGCC	172356				

RESULT 9
AC027082/c
LOCUS
DEFINITION

AC027082 189057 bp DNA linear HTG 24-AUG-2002
Homo sapiens chromosome 1 clone RP11-575N16 map 1, WORKING DRAFT

```

SEQUENCE, 27 unordered pieces.
AC027082.3 GI:10047876
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campomaiore,A., Castle,A., Choepel,Y., Collangelo,M., Collins,S.,
Collimore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Melarim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 189057)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campomaiore,A., Castle,A.,
Choepel,Y., Collangelo,M., Collins,S., Collimore,A., Cooke,P.,
DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neil,D., Oliver,J., Norman,C.H., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 10, 2000 this sequence version replaced gi:7596905.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: U8310
Center clone name: 575_N_16

```

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174880 bases at least Q40
Consensus quality: 182350 bases at least Q30
Consensus quality: 185136 bases at least Q20
Insert size: 176000; agarose-fp
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

575: contig of 575 bp in length	1
675: gap of 100 bp	576
2037: contig of 1362 bp in length	676
2137: gap of 100 bp	2038
3255: contig of 1118 bp in length	2138
3355: gap of 100 bp	3256
4509: contig of 1154 bp in length	3356
4609: gap of 100 bp	4510
5977: contig of 1368 bp in length	4610
6077: gap of 100 bp	5978
7093: contig of 1016 bp in length	6078
7193: gap of 100 bp	7094
8797: contig of 1604 bp in length	7194
8897: gap of 100 bp	8798
10577: contig of 1680 bp in length	8898
10677: gap of 100 bp	10578
11943: contig of 1266 bp in length	10678
12043: gap of 100 bp	11944
13982: contig of 1939 bp in length	12044
14082: gap of 100 bp	13983
15236: contig of 1154 bp in length	14083
15336: gap of 100 bp	15237
17412: contig of 2076 bp in length	15337
17512: gap of 100 bp	17413
19334: contig of 1822 bp in length	17513
19434: gap of 100 bp	19335
20682: contig of 1248 bp in length	19435
20782: gap of 100 bp	20683
22493: contig of 1711 bp in length	20783
22593: gap of 100 bp	22494
24397: contig of 1804 bp in length	22594
24497: gap of 100 bp	24398
27225: contig of 2728 bp in length	24498
27325: gap of 100 bp	27226
32481: contig of 5156 bp in length	27326
32581: gap of 100 bp	32482
38286: contig of 5705 bp in length	32582
38386: gap of 100 bp	38287
45665: contig of 7279 bp in length	38387
45765: gap of 100 bp	45666
56169: contig of 10404 bp in length	45766
56269: gap of 100 bp	56170
75705: contig of 19436 bp in length	56270
75805: gap of 100 bp	75706
94365: contig of 18560 bp in length	75806
94465: gap of 100 bp	94366
111724: contig of 17259 bp in length	94466
111824: gap of 100 bp	111725
131993: contig of 20169 bp in length	111825
132093: gap of 100 bp	131994
164072: contig of 31979 bp in length	132094
164172: gap of 100 bp	164073
189057: contig of 24885 bp in length.	164173

FEATURES
Source

Location/Qualifiers

1. 189057
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1"
/clone="RP11-575N16"
/clone_lib="RP11-11 Human Male BAC"
1. .575
/note="assembly_fragment
clone end:SP6
vector side:left"
676. .2037
/note="assembly_fragment"
2138. .3255
/note="assembly_fragment"
3356. .4509
/note="assembly_fragment"
4610. .5977
/note="assembly_fragment"
6078. .7093
/note="assembly_fragment"
7194. .8797
/note="assembly_fragment"
8998. .10577
/note="assembly_fragment"
10678. .11943
/note="assembly_fragment"
12044. .13982
/note="assembly_fragment"
14083. .15236
/note="assembly_fragment"
15337. .17412
/note="assembly_fragment"
17513. .19334
/note="assembly_fragment"
19435. .20682
/note="assembly_fragment"
20783. .22493
/note="assembly_fragment"
22594. .24397
/note="assembly_fragment"
24498. .27225
/note="assembly_fragment"
27326. .32481
/note="assembly_fragment"
32582. .38286
/note="assembly_fragment"
38387. .45665
/note="assembly_fragment"
45766. .56169

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

Query Match 69.4%; Score 2201.2; DB 2; Length 189057;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2203; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 960 TTGCTGATAGATGGGAAAGCCAGCACACAGACAGTAAACCTCTGGGACTTCAAGC 1019

DB 100126 TCTCTGCACAGATGGGAAAGCCAGCACACAGACAGTAAACCTCTGGGACTTCAAGC 100067

QY 1020 TATGAAATTTGATCTAGGCTGGCTGAATTCCTCTGGAACAGTTCACAAAC 1079

DB 100066 TATGAAATTTGATCTAGGCTGGCTGAATTCCTCTGGAACAGTTCACAAAC 100007

QY 1080 ACCAATCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCAACTCTTACTGGGAGATT 1139

DB 100006 ACCAATCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCAACTCTTACTGGGAGATT 99947

QY 1140 GCAAACTGCCACATCTCAGCCTGTAGCAAGAGGAAACCTTCTGCTGGGCATAGCTTG 1199

DB 99946 GCAAACTGCCACATCTCAGCCTGTAGCAAGAGGAAACCTTCTGCTGGGCATAGCTTG 99887

QY 1200 TGCCTAAATGGACAAATGATGATACCCCTTCTGAAATGACTCCCTTCTGAATGAATCA 1259
DB 99886 TGCCTAAATGGACAAATGATGATACCCCTTCTGAAATGACTCCCTTCTGAATGAATCA 99827
QY 1260 CAAACAGGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAA 1319
DB 99826 CAAACAGGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAA 99767
QY 1320 ATAATATTTTATGGCACACTGGGATAAACAAAGCAAGATTGTCTCACTTCTGGAAGCTGCA 1379
DB 99766 ATAATATTTTATGGCACACTGGGATAAACAAAGCAAGATTGTCTCACTTCTGGAAGCTGCA 99707
QY 1380 TATGACTAGAGCCCTTCTGTGACTGGAGGTAAACACCCCTGCCAGTAACTGTGGGAGAAG 1439
DB 99706 TATGACTAGAGCCCTTCTGTGACTGGAGGTAAACACCCCTGCCAGTAACTGTGGGAGAAG 99647
QY 1440 GGGATCAATATTTTGCACACCTGTAAATAGGCCATGGCACACAGCAAGATGCTCTGCTC 1499
DB 99646 GGGATCAATATTTTGCACACCTGTAAATAGGCCATGGCACACAGCAAGATGCTCTGCTC 99587
QY 1500 ACAGTCAGTATGTGTGAAGATCCCTGGTGGCTGGCCCTTCCACACGATCTTGAGCAAAAT 1559
DB 99586 ACAGTCAGTATGTGTGAAGATCCCTGGTGGCTGGCCCTTCCACACGATCTTGAGCAAAAT 99527
QY 1560 AGGAAATGTACCTTGGCTTGAGGCAGATGAGCCCTTCCCCAGTGCATGGCTTGA 1619
DB 99526 AGGAAATGTACCTTGGCTTGAGGCAGATGAGCCCTTCCCCAGTGCATGGCTTGA 99467
QY 1620 GAGCAGATGGGGTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGCGAG 1679
DB 99466 GAGCAGATGGGGTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGCGAG 99407
QY 1680 GGCATAACAGGCTTGTAGTCCAAACACAGATGACAGTGTCTGTGGGTCTCTGTGAGA 1739
DB 99406 GGCATAACAGGCTTGTAGTCCAAACACAGATGACAGTGTCTGTGGGTCTCTGTGAGA 99347
QY 1740 GTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGAGTGTGGGAAATCTTCTTTC 1799
DB 99346 GTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGAGTGTGGGAAATCTTCTTTC 99287
QY 1800 TGCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTCTTTCAGAGCCTTATAG 1859
DB 99286 TGCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTCTTTCAGAGCCTTATAG 99227
QY 1860 GATTTTCTTCTGGCCAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAAG 1919
DB 99226 GATTTTCTTCTGGCCAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAAG 99167
QY 1920 CAGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACCCAGCTTATATTTCTCACACT 1979
DB 99166 CAGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACCCAGCTTATATTTCTCACACT 99107
QY 1980 TCTGGGAACTGGGTATATCCAACTCAAAATAGAGACCTTGCAGAGCAGAGTCA 2039
DB 99106 TCTGGGAACTGGGTATATCCAACTCAAAATAGAGACCTTGCAGAGCAGAGTCA 99047
QY 2040 TTCTCCAGAGGAACCTTGGAGATGATGTGCAGATGATGAACTGGGTTTATCTCCAGCT 2099
DB 99046 TTCTCCAGAGGAACCTTGGAGATGATGTGCAGATGATGAACTGGGTTTATCTCCAGCT 99987
QY 2100 CCAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCCACCTGCGATGCCCC 2159
DB 99986 CCAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCCACCTGCGATGCCCC 98927
QY 2160 CACAAACAGATCAGCAGCAGCTTACACAGGCAATTAATCTCTCTCAATGAGGAGATCA 2219
DB 98926 CACAAACAGATCAGCAGCAGCTTACACAGGCAATTAATCTCTCTCAATGAGGAGATCA 98867
QY 2220 TTCCAACTGAGCAAGACATTCATATGATCATTTAAAGGAGTGTCTTCCCTTATGTGTAG 2279
DB 98866 TTCCAACTGAGCAAGACATTCATATGATCATTTAAAGGAGTGTCTTCCCTTATGTGTAG 98807
QY 2280 CAAGTATATCGGCTAACTCTCTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGG 2339

Qy	675	CGGCAGCTCTGTGACAGATCGCAATGGGCTTCCGTACTCACCAACCGGGTTGCTGAGC	734
Dd	694	CGGCAGCTCTGTGACAGATCGCAATGGGCTTCCGTACTCACCAACCGGGTTGCTGAGC	753
Qy	735	GTGCTGGTAATGTCCTTTCTGCTTGTTCTCATTTCTGTCTTCAGTGTGTTTTGTTCCGGTTG	794
Dd	754	GTGCTGGCTATGTTCTTTCTGCTTGTTCTCATTTCTGTCTTCAGTGTGTTTTGTTCCGGTTG	813
Qy	795	TTCACAGAGAACAAGATGCTGCTCAAAGAAAACCATATACACATATATCATGGGCTTCA	854
Dd	814	TTCACAGAGAACAAGATGCTGCTCAAAGAAAACCATATACACATATATCATGGGCTTCA	873
Qy	855	AGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGAATCTCTGCAAGTCCAAGGTGCTT	914
Dd	874	AGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGAATCTCTGCAAGTCCAAGGTGCTT	933
Qy	915	CCCTCCAAAGAACAGCCAGTGAACACAGTTTATTCCGAAGTCAGTTGCTGTGATAAGATG	974
Dd	934	CCCTCCAAAGAACAGCCAGTGAACACAGTTTATTCCGAAGTCAGTTGCTGTGATAAGATG	993
Qy	975	GGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC	1034
Dd	994	GGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC	1053
Qy	1035	TAGGCTGCTGGCT 1048	
Dd	1054	TAGGCTGCTGGCT 1067	
<hr/>			
RESULT 11			
AX474268			
LOCUS			
DEFINITION Sequence 29 from Patent EP1223218.			
ACCESSION AX474268			
VERSION AX474268.1 GI:22213881			
KEYWORDS			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE 1			
AUTHORS Fraser, C.C.			
TITLE CG2000 and cd2001 molecules and uses thereof			
JOURNAL Patent: EP 1223218-A 29 17-JUL-2002;			
Millennium Pharmaceuticals, Inc. (US)			
FEATURES			
Source Location/Qualifiers			
1..1040			
/organism="Homo sapiens"			
/mol_type="unassigned DNA"			
/dd_xref="taxon:9606"			
<hr/>			
ORIGIN			
Query Match 32.6%; Score 1033.4; DB 6; Length 1040;			
Best Local Similarity 99.9%; Pred. No. 6.9e-295;			
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	15	CCGTGCTTTTCCACAGAAGTTTAGACCCTGAAAGNAGTGGCTCAGCACACCTATGGATC	74
Dd	6	CGGTGCTTTTCCACAGAAGTTTAGACCCTGAAAGNAGTGGCTCAGCACACCTATGGATC	65
Qy	75	TTGCTCTTTTGGCTGCAAACTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA	134
Dd	66	TTGCTCTTTTGGCTGCAAACTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA	125
Qy	135	GTGAATGGGAATCTCGGAGAGTCACTTTCCCTGTAATATATCAAGAACCCAGGCAAA	194
Dd	126	GTGAATGGGAATCTCGGAGAGTCACTTTCCCTGTAATATATCAAGAACCCAGGCAAA	185
Qy	195	GTTAAATCATGTCTTGACTTCTAAAACTCTGTTGCTTATGTAACACCCAGGACTCA	254
Dd	186	GTTAAATCATGTCTTGACTTCTAAAACTCTGTTGCTTATGTAACACCCAGGACTCA	245

```
9310491
PUBMED
REFERENCE 2 (bases 1 to 1040)
AUTHORS de la Fuente,M.A., Pizcueta,P. and Engel,P.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1996) Hepatology, Fundacio Clinic, Villarroel
170, Barcelona 08036, Spain
FEATURES
Location/Qualifiers
1..1040
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1Q24"
/cell_line="Raji; B cell line"
42..1028
/Note="member of immunoglobulin superfamily"
CDS
/codon_start=1
/product="leukocyte antigen CD84"
/protein_id="AAB84364.1"
/db_xref="GI:2618740"
/translation="WAQHLLWLLLCLOTWPEAAKDSIEFTVNGILGESVTFPVNIO
EPQVKLIANTSKTSVAIVTGDSETAPVVTTHRYNYYERIHALGPNVNLISDLRME
DAGDYKADINTQADPYTTTKRYNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
EKVNTYNSPLGEEGNVLIQIFQPEDQLTYTCTAQNPNNSDSISARQLCADIAMG
FRHTHTGLSLVLAFFLLVILSSVFLFRKFRQDAASKKTIYTIYIMASRNTOPAES
RIYDEILQSKVLPSEKPEPNTVYSEVQFADKMGKASTQDSKPPGTSSEIYI"
ORIGIN
Query Match 32.6%; Score 1033.4; DB 9; Length 1040;
Best Local Similarity 99.9%; Pred. No. 6.9e-295;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CGTGCTTTTCCACAGAGTTAGACCTGGAAGAGATGGCTCAGCACACACCTATGGATC 74
DB 6 CGTGCTTTTCCACAGAGTTAGACCTGGAAGAGATGGCTCAGCACACACCTATGGATC 65
QY 75 TTGCTCCTTTGCTGCAACCTGGCCGGAAGCAGCTGGAAGAGACTCAGAAATCTTCACA 134
DB 66 TTGCTCCTTTGCTGCAACCTGGCCGGAAGCAGCTGGAAGAGACTCAGAAATCTTCACA 125
QY 135 GTGAATGGGATCTGGAGAGTCAGTCACCTTCCTCGTAAATATATCAAGAACACGGCAA 194
DB 126 GTGAATGGGATCTGGAGAGTCAGTCACCTTCCTCGTAAATATATCAAGAACACGGCAA 185
QY 195 GTTAAATCATTTGGACTTCTAAACATCTGTTGCTTATGTAACACACGAGACTCA 254
DB 186 GTTAAATCATTTGGACTTCTAAACATCTGTTGCTTATGTAACACACGAGACTCA 245
QY 255 GAAACAGACCCGTAGTTACTGTGACCCACAGAAATTAATTAACCGGATACATGCCTTA 314
DB 246 GAAACAGACCCGTAGTTACTGTGACCCACAGAAATTAATTAACCGGATACATGCCTTA 305
QY 315 GTTCCGAATACAATCTGTGATTTAGCGATCTGAGATGGAAGAGACGAGGACTACAAA 374
DB 306 GTTCCGAATACAATCTGTGATTTAGCGATCTGAGATGGAAGAGACGAGGACTACAAA 365
QY 375 GCAGACATAAATACACAGGCTCATCCTACACACACCAACGCGTCAACCTCGAAATC 434
DB 366 GCAGACATAAATACACAGGCTCATCCTACACACCAACGCGTCAACCTCGAAATC 425
QY 435 TATCGTCGGCTTTGGGAAACCAAAAATTAACAGAGTTTAATGGCATCTGTGAACGACCC 494
DB 426 TATCGTCGGCTTTGGGAAACCAAAAATTAACAGAGTTTAATGGCATCTGTGAACGACCC 485
QY 495 TGTAAATGTCACATGACATGCTCTGTAGAGAAAGAGAAAGAAATGTGCATACAAATGG 554
DB 486 TGTAAATGTCACATGACATGCTCTGTAGAGAAAGAGAAAGAAATGTGCATACAAATGG 545
QY 555 AGTCCCTCGGAGAGAGAGGTTAATGTCCTTCAAAATCTTCCAGACTCCTGAGGACCAAGAG 614
DB 546 AGTCCCTCGGAGAGAGAGGTTAATGTCCTTCAAAATCTTCCAGACTCCTGAGGACCAAGAG 605
QY 615 CTGACTTACGTGTACAGCCAGAACCCCTGTGACGAAACATTTCTGACTCCATCTCTGCC 674
```

```
Db 606 CTGACTTACAGTGTACAGCCAGAACCTGTACAGCAACAATTTCTGACTCCATCTCTGCC 665
QY 675 CGGAGCTCTGTGACAGACATCGCATGGCTTCGGTACTCACCACACCGGTTGCTGAGC 734
DB 666 CGGAGCTCTGTGACAGACATCGCATGGCTTCGGTACTCACCACACCGGTTGCTGAGC 725
QY 735 GTGCTGGCTATGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 794
DB 726 GTGCTGGCTATGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 785
QY 795 TTCAAGAGAAGACAAGATGCTGCTCTCAAAAGAAACCATATACATATATCATGCTTCA 854
DB 786 TTCAAGAGAAGACAAGATGCTGCTCTCAAAAGAAACCATATACATATATCATGCTTCA 845
QY 855 AGGAACACCCAGCAGCAGAGTCCAGATCTATGATGAATCCTGCACTCCAAAGTGCTT 914
DB 846 AGGAACACCCAGCAGCAGAGTCCAGATCTATGATGAATCCTGCACTCCAAAGTGCTT 905
QY 915 CCCTCAAGGAAGAGCAGTGAACACAGTCTTATTCGGAAGTGCAGTTTCTGCTGATAAGATG 974
DB 906 CCCTCAAGGAAGAGCAGTGAACACAGTCTTATTCGGAAGTGCAGTTTCTGCTGATAAGATG 965
QY 975 GGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGTATGAAATTTGTGATC 1034
DB 966 GGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGTATGAAATTTGTGATC 1025
QY 1035 TAGGCTGCTGGGCTG 1049
DB 1026 TAGGCTGCTGGGCTG 1040
RESULT 13
HSLDADC84 HSLDADC84 1100 bp mRNA linear PRI 04-JAN-2002
LOCUS H.sapiens mRNA for leukocyte differentiation antigen CD84.
ACCESSION Y12632
VERSION Y12632.1 GI:18073112
KEYWORDS leukocyte differentiation antigen.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gaya,A.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1100)
AUTHORS Gaya,A.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
FEATURES
Location/Qualifiers
1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="leukocyte"
/clone_lib="lambda gt10"
70..1089
/codon_start=1
/product="leukocyte differentiation antigen CD84"
/protein_id="CAA73181.1"
/db_xref="GI:18073113"
/db_xref="UniProt/TREMBL:Q8WWI8"
/translation="WAQHLLWLLLCLOTWPEAAKDSIEFTVNGILGESVTFPVNIO
EPQVKLIANTSKTSVAIVTGDSETAPVVTTHRYNYYERIHALGPNVNLISDLRME
DAGDYKADINTQADPYTTTKRYNLQIYRLGPKITQSLMASVNSTCNVLTCSVEKE
EKVNTYNSPLGEEGNVLIQIFQPEDQLTYTCTAQNPNNSDSISARQLCADIAMG
FRHTHTGLSLVLAFFLLVILSSVFLFRKFRQDAASKKTIYTIYIMASRNTOPAES
RIYDEILQSKVLPSEKPEPNTVYSEVQFADKMGKASTQDSKPPGTSSEIYI"
CDS
70..132 sig_peptide
133..1086 mat_peptide
```

ORIGIN		/product="leukocyte differentiation antigen CD84"	
Query Match		31.2%; Score 991; DB 9; Length 1100;	
Best Local Similarity		96.9%; Pred. No. 2.7e-282;	
Matches 1034; Conservative		0; Mismatches 0; Indels 33; Gaps 1;	
QY	15	CGTGCTTTTCCACAGAGGTTAGACCTGGAAGAGTGGCTCAGCACCACCTATGGATC	74
DB	34	CGTGCTTTTCCACAGAGGTTAGACCTGGAAGAGTGGCTCAGCACCACCTATGGATC	93
QY	75	TTGCTCTTTTGGCTGCAACCTGGCGGAGAGCTGGAAGAGCTCAGAAATCTTTCACA	134
DB	94	TTGCTCTTTTGGCTGCAACCTGGCGGAGAGCTGGAAGAGCTCAGAAATCTTTCACA	153
QY	135	GTGAATGGGATTTGGGAGAGTCAGTCATTTTCCCTGTAAATATCCAGAACACGGCAA	194
DB	154	GTGAATGGGATTTGGGAGAGTCAGTCATTTTCCCTGTAAATATCCAGAACACGGCAA	213
QY	195	GTAAATCATTTGCTTGGACTTCTAAACATCTGTTTGTATGTATACACGAGACTCA	254
DB	214	GTAAATCATTTGCTTGGACTTCTAAACATCTGTTTGTATGTATACACGAGACTCA	273
QY	255	GAAACAGCACCGTAGTACTGTGACCCACAGAAATTTATTGAACGGATACATGCTTTA	314
DB	274	GAAACAGCACCGTAGTACTGTGACCCACAGAAATTTATTGAACGGATACATGCTTTA	333
QY	315	GGTCCGAATACAAATCTGGTCAATTTAGCGATCTGAGATGGAAGACCGAGACTCAAA	374
DB	334	GGTCCGAATACAAATCTGGTCAATTTAGCGATCTGAGATGGAAGACCGAGACTCAAA	393
QY	375	GCAGACATAAATACAGAGGTATGCTTCAATCTTCCAGACTCTGAGGACCAACCTGCA	434
DB	394	GCAGACATAAATACAGAGGTATGCTTCAATCTTCCAGACTCTGAGGACCAACCTGCA	453
QY	435	TATCGTCCGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCATCTGTGAACAGC	494
DB	454	TATCGTCCGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCATCTGTGAACAGC	513
QY	495	TGTAATGTCTACACTGATCTCTGTAGAGAAAGAAAGAAATGTGACATCAATTTGG	554
DB	514	TGTAATGTCTACACTGATCTCTGTAGAGAAAGAAAGAAATGTGACATCAATTTGG	573
QY	555	AGTCCCTGGGAGAGAGGTATGCTTCAATCTTCCAGACTCTGAGGACCAACAGAG	614
DB	574	AGTCCCTGGGAGAGAGGTATGCTTCAATCTTCCAGACTCTGAGGACCAACAGAG	633
QY	615	CTGACTTTACAGCTGTACAGCCAGAACCTCTGTCAGCAACAATTTCTGACTCCATCTG	674
DB	634	CTGACTTTACAGCTGTACAGCCAGAACCTCTGTCAGCAACAATTTCTGACTCCATCTG	693
QY	675	CGGAGCTCTGTGACAGATCGCAATGGGCTTCGTAATCCACACCGGGTTGCTGAGC	734
DB	694	CGGAGCTCTGTGACAGATCGCAATGGGCTTCGTAATCCACACCGGGTTGCTGAGC	753
QY	735	GTGCTGCTATGCTTTTCTGCTTCTCATTTCTGCTTCTGCTTCTGCTTCTGCTTCTG	794
DB	754	GTGCTGCTATGCTTTTCTGCTTCTCATTTCTGCTTCTGCTTCTGCTTCTGCTTCTG	813
QY	795	TTCAAGAGAGAGACAAG-----ATGCTGCTCTCA	821
DB	814	TTCAAGAGAGAGACAAGTTCTGCTGTAACACCTTCACTAAGAACCTTTATGCTGCTCA	873
QY	822	AAGAAACCATATACATATATCATGGCTTCAAGGAACACCCAGCCAGAGTCCAGA	881
DB	874	AAGAAACCATATACATATATCATGGCTTCAAGGAACACCCAGCCAGAGTCCAGA	933
QY	882	ATCTATGATGAATCTGAGTCAAGGTGCTTCCCTCCAGGAGAGCCAGTGAACACA	941
DB	934	ATCTATGATGAATCTGAGTCAAGGTGCTTCCCTCCAGGAGAGCCAGTGAACACA	993
QY	942	GTATTATCCGAAGTGCAGTTTGTGATAGATGGGAAAGCCAGCACACAGGACGTAAA	1001

994 GTTATTCCGAAGTGCAGTTTGTGATAGATGGGAAAGCCAGCACACGACAGTAAA 1053

1002 CCTCTCTGGGACTTCAAGCTATGAAATTTGTGATCTAGGCTAGGCTGCTGGCT 1048

1054 CCTCTCTGGGACTTCAAGCTATGAAATTTGTGATCTAGGCTAGGCTGCTGGCT 1100

Db	CR541847	984 bp	mRNA	linear	PRI 29-JUN-2004
QY	Homo sapiens	full open reading frame	CDNA clone	RZPD0834H0132D	for gene CD84, CD84 antigen (leukocyte antigen); complete cds, without stopcodon.
Db	CR541847				
RESULT 14	CR541847.1	GI:49456648			
LOCUS	CR541847				
DEFINITION	Full ORF shuttle clone, Gateway(TM), complete cds.				
ACCESSION	CR541847				
VERSION	1				
KEYWORDS	Full ORF shuttle clone, Gateway(TM), complete cds.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 984)				
AUTHORS	Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S., Neubert, P., Ketrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.				
TITLE	Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 984)				
AUTHORS	Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S., Neubert, P., Ketrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany				
COMMENT	RZPD; RZPD0834H0132D, ORFNo 3790 www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLib; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD Lib No. 834 www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834 www.rzpd.de/products/orfclones/ Contact: Inge Ariart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available from RZPD; Contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD. This CDS has been cloned without stopcodon. The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att.AAAAA GCA GGC TCC ACC (ATG). The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att The clone is validated by full sequence check. Compared to the reference sequence NM_003874 (GI:4502686) we found AA exchange(s) at position (first base of changed triplet): 880 (pro->ser) Clone distribution: http://www.rzpd.de/products/orfclones/.				

FEATURES

source

1. .984

Location/Qualifiers

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

clone="RZPD0834H0132D"

clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"

lab_host="DH5Alpha"

note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"

1. .984

gene

genes="CD84"

CDS	1. -->984 /gene="CD84" /codon_start=1 /protein_id="CAG46645.1" /db_xref="GI:49456649" /translation="MAQHLLWILLCLQIOTWPEAGKDSIFVTNGILGESVFPVNIQ EPKVKIATWTSKTSVAVYTPGSETAPVVTTHRYNRIHALGPNYNLVIDLRME DAGDYADINTQADPYTTTKRYNLQIYRRLGPKITQSLMASVNSDTSARQLCADIAMG EKVNTWNSPLGEGNVLIQIQTPEDELTCTTAQNPVSNNSDSISARQLCADIAMG FRTHHTGLLSVLAMFFLLILSSVFLFRKRODAASKTIYTVIMASRNTQPAES RIYDEILQSKVLPKESVNTVYSEVQFADKMGKASTQDQSKPPTSSVEIVI"	
ORIGIN		
Query Match	31.0%; Score 982.4; DB 9; Length 984;	
Best Local Similarity	99.9%; Pred. No. 9.5e-280;	
Matches 983; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	51	ATGGCTCAGCACCACTATGATCTTGCCTCTGCTGCAAACTCGCGCGGAAGCAGCT 110
DB	1	ATGGCTCAGCACCACTATGATCTTGCCTCTGCTGCAAACTCGCGCGGAAGCAGCT 60
QY	111	GAAAAGACTCAGAAATCTTCAAGTGAATGGGATCTCGGAGAGTCAGTCATTTCCCT 170
DB	61	GAAAAGACTCAGAAATCTTCAAGTGAATGGGATCTCGGAGAGTCAGTCATTTCCCT 120
QY	171	GTAATATCAAGAACACCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTT 230
DB	121	GTAATATCAAGAACACCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTT 180
QY	231	GCTTATGTAAACACCGAGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCAACAGAAAT 290
DB	181	GCTTATGTAAACACCGAGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCAACAGAAAT 240
QY	291	TATTATGAACGATACATGCTTAGTTCGAACTACAATCTGGTCAATTAGCATCTGAGG 350
DB	241	TATTATGAACGATACATGCTTAGTTCGAACTACAATCTGGTCAATTAGCATCTGAGG 300
QY	351	ATGGAAGAGCGAGGAGACTACAAAGCAGACATAAATACACAGCTGATCCCTACACACC 410
DB	301	ATGGAAGAGCGAGGAGACTACAAAGCAGACATAAATACACAGCTGATCCCTACACACC 360
QY	411	ACCAAGCGGTACAACTGTCGAAATCTATCTGGCTTGGGAAACCAAAATATACACAGAT 470
DB	361	ACCAAGCGGTACAACTGTCGAAATCTATCTGGCTTGGGAAACCAAAATATACACAGAT 420
QY	471	TTAATGGCATCTGTGAACAGCACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAA 530
DB	421	TTAATGGCATCTGTGAACAGCACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAA 480
QY	531	GAAAAGAAATGTACATACAAATTTGAGTCCCTCGGAGAGAGGGTAATGTCTTCAAAATC 590
DB	481	GAAAAGAAATGTACATACAAATTTGAGTCCCTCGGAGAGAGGGTAATGTCTTCAAAATC 540
QY	591	TTCCAGACTCTGAGGACCAAGAGCTGATTAAGTGTAAGCCAGCAACCTCTGACG 650
DB	541	TTCCAGACTCTGAGGACCAAGAGCTGATTAAGTGTAAGCCAGCAACCTCTGACG 600
QY	651	AACAATTCGATCCATCTCTCCCGGAGCTCTGTGAGAGATCGCAATGGGCTTCGGT 710
DB	601	AACAATTCGATCCATCTCTCCCGGAGCTCTGTGAGAGATCGCAATGGGCTTCGGT 660
QY	711	ACTACCAACACCGGGTGTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCAATCTG 770
DB	661	ACTACCAACACCGGGTGTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCAATCTG 720
QY	771	TCCTCAGTGTCTTCTGCTTGTCTTCAAGAGACAGAGATGTCCTCAAGAAACACC 830
DB	721	TCCTCAGTGTCTTCTGCTTGTCTTCAAGAGACAGAGATGTCCTCAAGAAACACC 780
QY	831	ATATACATATATCATGGCTTCAAGAGAACACCCAGCAGAGAGTCCAGAAATCTATGAT 890
DB	781	ATATACATATATCATGGCTTCAAGAGAACACCCAGCAGAGAGTCCAGAAATCTATGAT 840
QY	891	GAATCTCTGAGTCCAGAGTCTCCCTCCCAAGGAAGAGCCAGTGAAACACAGTTTATTC 950
DB	841	GAATCTCTGAGTCCAGAGTCTCCCTCCCAAGGAAGAGTCAAGTGAACACAGTTTATTC 900
QY	951	GAAGTGCAGTTTCTGTAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGG 1010
DB	901	GAAGTGCAGTTTCTGTAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGG 960
QY	1011	ACTTCAAGCTATGAAATTTGTGATC 1034
DB	961	ACTTCAAGCTATGAAATTTGTGATC 984
RESULT 15		
AF054816		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
LOCUS		
gene		
CDS		
ORIGIN		
Query Match	30.7%; Score 973; DB 9; Length 1118;	
Best Local Similarity	95.3%; Pred. No. 6e-277;	
Matches 1034; Conservative	0; Mismatches 0; Indels 51; Gaps 1;	
QY	15	CCGTGCTTTTCCACAGAGGTTAGACCTGAAAGAGATGGCTGAGCACCCTATGATC 74
DB	34	CCGTGCTTTTCCACAGAGGTTAGACCTGAAAGAGATGGCTGAGCACCCTATGATC 93
QY	75	TTGCTCTCTTTCCTGCAAACTGGCCGGAAGAGAGCTGAAAGAGCTCAGAAATCTTCACA 134
DB	94	TTGCTCTCTTTCCTGCAAACTGGCCGGAAGAGAGCTGAAAGAGCTCAGAAATCTTCACA 153
QY	135	GTGAATGGGATCTGCGAGAGTCACTCTTCCTGTAATATCCAAAGAACACCGCAA 194
DB	154	GTGAATGGGATCTGCGAGAGTCACTCTTCCTGTAATATCCAAAGAACACCGCAA 213
QY	195	GTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCTTATGTAACACCGAGAGCTCA 254
DB	214	GTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCTTATGTAACACCGAGAGCTCA 273

Qy	255	GAACAGACCCGCTAGCTTACTGTGACCCACAGAAATTAATTATGAACGGATACATGCGCTTA	314
Db	274	GAACAGACCCGCTAGCTTACTGTGACCCACAGAAATTAATTATGAACGGATACATGCGCTTA	333
Qy	315	GGTCCGAACCTACAATCTGGTCAATAGCGATCTGAGGATGGAAGACGACGAGACTACAAA	374
Db	334	GGTCCGAACCTACAATCTGGTCAATAGCGATCTGAGGATGGAAGACGACGAGACTACAAA	393
Qy	375	GCAGACATAAATACACAGAGCTGATCCCTACACACACCAAGCGCTACAACTGGAAATC	434
Db	394	GCAGACATAAATACACAGAGCTGATCCCTACACACACCAAGCGCTACAACTGGAAATC	453
Qy	435	TATCGTCGGCTTGGGAAACCAAAATTAACACAGATTTAATGGCATCTGTGAACAGCACC	494
Db	454	TATCGTCGGCTTGGGAAACCAAAATTAACACAGATTTAATGGCATCTGTGAACAGCACC	513
Qy	495	TGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAATGG	554
Db	514	TGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAATGG	573
Qy	555	AGTCCCTGGGAGAGAGGGTAATGTCTTCAAAATCTTCAGACTCTCGAGGACCAAGAG	614
Db	574	AGTCCCTGGGAGAGAGGGTAATGTCTTCAAAATCTTCAGACTCTCGAGGACCAAGAG	633
Qy	615	CTGACTTACACGCTGACAGCCAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC	674
Db	634	CTGACTTACACGCTGACAGCCAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC	693
Qy	675	CGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACACACCGGGTTGCTGAGC	734
Db	694	CGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACACACCGGGTTGCTGAGC	753
Qy	735	GTGCTGGCTATGTTCTTTCTGCTTGTCTCATTTCTGCTTCAGTGTGTTTGTTCGGTTTG	794
Db	754	GTGCTGGCTATGTTCTTTCTGCTTGTCTCATTTCTGCTTCAGTGTGTTTGTTCGGTTTG	813
Qy	795	TTCAAGAGAGACAAG-----	810
Db	814	TTCAAGAGAGACAAGTAGGATTTCCGAGAGGTTCTGCTTGAACACCTTCACTAAG	873
Qy	811	-----ATGCTGCCTCAAGAAACCATATACATATATCATGGCTTCAAGGAACACC	863
Db	874	AACCCTTATGCTGCCTCAAGAAACCATATACATATATCATGGCTTCAAGGAACACC	933
Qy	864	CAGCAGCAGAGTCCAGAACTATGATGAATCCTGCAGTCCAAAGTGCTTCCCTCCAAG	923
Db	934	CAGCAGCAGAGTCCAGAACTATGATGAATCCTGCAGTCCAAAGTGCTTCCCTCCAAG	993
Qy	924	GAAGAGCCAGTGAACACAGTTTATTCGAAAGTGCAGTTTCTGATAGATGGGGAAGCC	983
Db	994	GAAGAGCCAGTGAACACAGTTTATTCGAAAGTGCAGTTTCTGATAGATGGGGAAGCC	1053
Qy	984	AGCACACAGGACAGTAACCTCTGGGACTTCAAGCTATGAAATGTGATCTAGGCTGCT	1043
Db	1054	AGCACACAGGACAGTAACCTCTGGGACTTCAAGCTATGAAATGTGATCTAGGCTGCT	1113
Qy	1044	GGGCT 1048	
Db	1114	GGGCT 1118	

This Page Blank (uspio)

(uspio)

GenCore version 5.1.6
Copyright (C) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: February 5, 2005, 11:25:41 ; Search time 1603 Seconds
(without alignments)
11717.617 Million cell updates/sec

Title: US-09-882-171-174
Perfect score: 3173
Sequence: 1 tcagaccasggtccgtgc.....gcacatctgtagtccag 3173

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3169.4	99.9	3173	2 AAV59674	AAV59674 Human sec
2	3169.4	99.9	3173	6 ABS73661	ABS73661 Human cdn
3	3169.4	99.9	3173	9 ACD82804	ACD82804 cDNA sequ
4	3169.4	99.9	3173	10 ADI22889	ADI22889 cDNA enco
5	3169.4	99.9	3173	12 ADH73891	ADH73891 Human sec
6	3161.8	99.6	3299	12 ADL82906	ADL82906 Human PRO
7	3161.8	99.6	3299	13 ADP23942	ADP23942 PRO poly
8	3161.8	99.6	3300	6 AAI72383	AAI72383 CD84 codi
9	3159.8	99.6	3687	11 ACN92105	ACN92105 Breast ca
10	3142.2	99.0	3326	12 ADQ23399	ADQ23399 Human sof
11	1034	32.6	1067	12 ADO05707	ADO05707 Human leu
12	1034	32.6	1067	12 ADQ19066	ADQ19066 Human sof
13	1033.4	32.6	1040	6 AAD43563	AAD43563 Human CD8
14	813	25.6	828	2 AAV59796	AAV59796 Human sec
15	813	25.6	828	6 ABS73790	ABS73790 Human cdn
16	813	25.6	828	9 ACD82933	ACD82933 cDNA sequ
17	813	25.6	828	12 ADI23018	ADI23018 cDNA enco
18	813	25.6	828	12 ADH74020	ADH74020 Human sec
19	414.2	13.1	420	9 ACH49562	ACH49562 Human leu
20	312.4	9.8	748	4 AAL24045	AAL24045 Human bre

21	271	8.5	296	2	AAx41382	Aax41382 Human sec
22	236	7.4	301	2	AAx41380	Aax41380 Human sec
23	212.4	6.7	669	4	AAL15199	Aal15199 Human bre
24	212.4	6.7	820	11	ACN85220	Acn85220 Breast ca
C 25	141.4	4.5	3608	4	AAK83192	Aak83192 Human imm
C 26	141.4	4.5	3608	4	AAK74891	Aak74891 Human imm
C 27	141.4	4.5	3608	4	AAK67271	Aak67271 Human imm
C 28	141.2	4.5	8658	4	AAK69231	Aak69231 Human imm
C 29	140.8	4.4	2771	4	AAK91225	Aak91225 Human dig
C 30	140.8	4.4	2776	4	AAK91226	Aak91226 Human dig
C 31	140.8	4.4	19701	4	AAK91227	Aak91227 Human dig
C 32	140	4.4	96592	9	ADA02678	Ada02678 Human TO
C 33	140	4.4	96592	10	ADB72416	Adb72416 Human TIO
C 34	140	4.4	96592	10	ADE95926	Ade95926 Human TOP
C 35	139.6	4.4	552	4	AAK88826	Aak88826 Human dig
C 36	138.4	4.4	173564	13	ABD32953	Abd32953 Human can
C 37	137.8	4.3	17321	10	ADE81091	Ade81091 Human enz
C 38	137	4.3	8892	12	ADQ97695	Adq97695 Human can
C 39	136.8	4.3	25899	12	ADQ59374	Adq59374 Human can
C 40	136	4.3	130244	13	ABD32872	Abd32872 Human can
C 41	136	4.3	131576	11	ACN44890	Acn44890 Human gen
C 42	135.8	4.3	126990	12	ADP13332	Adp13332 Renal cel
C 43	135.6	4.3	1534	12	ADO15882	Ado15882 4 synthet
C 44	135.2	4.3	20015	5	ABA20740	Abaz0740 Human ner
C 45	135	4.3	17996	4	AAL36330	Aal36330 Human mus

ALIGNMENTS

RESULT 1
AAV59674
ID AAV59674 standard; DNA; 3173 BP.

XX AAV59674;

XX 19-JAN-1999 (first entry)

XX Human secreted protein gene 164 clone HSAWF26.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9839448-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004493.

XX 07-MAR-1997; 97US-0038621P.

XX 07-MAR-1997; 97US-0040161P.

XX 07-MAR-1997; 97US-0040162P.

XX 07-MAR-1997; 97US-0040163P.

XX 07-MAR-1997; 97US-0040333P.

XX 07-MAR-1997; 97US-0040334P.

XX 07-MAR-1997; 97US-0040336P.

XX 11-APR-1997; 97US-0043311P.

XX 11-APR-1997; 97US-0043312P.

XX 11-APR-1997; 97US-0043313P.

XX 11-APR-1997; 97US-0043315P.

XX 11-APR-1997; 97US-0043568P.

XX 11-APR-1997; 97US-0043569P.

XX 11-APR-1997; 97US-0043576P.

QY	361	CAGGAGACTACAAGCAGACATAAATACACAGCTGATCCCTACACACCAACCAAGCGCT	420	QY	1441	GGATCAATATTTTGCACACCTGTAAATAGCCANTGGACACACAGCAAGATGCTCTGCTCA	1500
DB	361	CAGGAGACTACAAGCAGACATAAATACACAGCTGATCCCTACACACCAACCAAGCGCT	420	DB	1441	GGATCAATATTTTGCACACCTGTAAATAGCCANTGGACACACAGCAAGATGCTCTGCTCA	1500
QY	421	ACAACCTGCAAACTCTATCGCTGGCTTTGGGAAACCAAAATTAACACAGAGTTTAAATGGCAT	480	QY	1501	CAGTCAGTATGTGTGAAGATCCCTGGTGGCTTCCACACCGATCTTGGAGCAAAATTA	1560
DB	421	ACAACCTGCAAACTCTATCGCTGGCTTTGGGAAACCAAAATTAACACAGAGTTTAAATGGCAT	480	DB	1501	CAGTCAGTATGTGTGAAGATCCCTGGTGGCTTCCACACCGATCTTGGAGCAAAATTA	1560
QY	481	CTGTGAACAGCCTGTAATGTACAACATGATGCTCTGTAGAGAAAGAAAGAAATG	540	QY	1561	GGAAAAATGTACCCTTTCGCTTGAGGCAGATGACAGCCCTTCCCCCGAGTGCATGGCTGGAG	1620
DB	481	CTGTGAACAGCCTGTAATGTACAACATGATGCTCTGTAGAGAAAGAAAGAAATG	540	DB	1561	GGAAAAATGTACCCTTTCGCTTGAGGCAGATGACAGCCCTTCCCCCGAGTGCATGGCTGGAG	1620
QY	541	TGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAAAATTTCCAGACTC	600	QY	1621	AGCAAAATGTGGGCTGCACTATTAAGCACAACCTCATCCCTTTGTCTGGGAATCTTTGTGCAGG	1680
DB	541	TGACATACAAATTTGGAGTCCCTGGGAGAGAGGGTAATGTCTTCAAAATTTCCAGACTC	600	DB	1621	AGCAAAATGTGGGCTGCACTATTAAGCACAACCTCATCCCTTTGTCTGGGAATCTTTGTGCAGG	1680
QY	601	CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTACGACAAATTTCTG	660	QY	1681	GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTCTGTGGGTCTCTGTGCAGAG	1740
DB	601	CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTACGACAAATTTCTG	660	DB	1681	GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTCTGTGGGTCTCTGTGCAGAG	1740
QY	661	ACTCCATCTCTGCCCCGAGCTGTGTGACAGATCGCAATGGGCTTCCGTACTCACCA	720	QY	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTCT	1800
DB	661	ACTCCATCTCTGCCCCGAGCTGTGTGACAGATCGCAATGGGCTTCCGTACTCACCA	720	DB	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTCT	1800
QY	721	CCGGTGTCTGAGCGTGGCTATGTTCTTCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTG	780	QY	1801	GCAGGCTCTAGAGACTGTGGGACACTTTTCTTGGAGTGTCTTCTTGGAGCTTATAGG	1860
DB	721	CCGGTGTCTGAGCGTGGCTATGTTCTTCTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTG	780	DB	1801	GCAGGCTCTAGAGACTGTGGGACACTTTTCTTGGAGTGTCTTCTTGGAGCTTATAGG	1860
QY	781	TTTTTGTCTGCTTCAAGAGAGACAGATGCTGCTCAAAAGAAACCATATACACAT	840	QY	1861	ATTTTCTTCTGCGCAAGATTTCTTCTGATACCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1920
DB	781	TTTTTGTCTGCTTCAAGAGAGACAGATGCTGCTCAAAAGAAACCATATACACAT	840	DB	1861	ATTTTCTTCTGCGCAAGATTTCTTCTGATACCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1920
QY	841	ATATCATGCTTCAAGAAACACCCAGCAGAGTCCAGAACTATATGATGAATCCTGC	900	QY	1921	AGCCATGCCAGTATTTCCACCTCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1980
DB	841	ATATCATGCTTCAAGAAACACCCAGCAGAGTCCAGAACTATATGATGAATCCTGC	900	DB	1921	AGCCATGCCAGTATTTCCACCTCTCCAAAGGAACTGACAGCTTATATTTCTCACACTT	1980
QY	901	AGTCCAGGCTTCCCTCAAGGAGAGCCAGTGAACAGTTTATTCGAAAGTGCAGT	960	QY	1981	CTGGGAACTGGGTATTAATCCAAACCATCAAAATAGAAAGCTTTGCAAGAGCAGAGTCA	2040
DB	901	AGTCCAGGCTTCCCTCAAGGAGAGCCAGTGAACAGTTTATTCGAAAGTGCAGT	960	DB	1981	CTGGGAACTGGGTATTAATCCAAACCATCAAAATAGAAAGCTTTGCAAGAGCAGAGTCA	2040
QY	961	TTGCTGATAGATGGGAAACCCAGCACAGAGCAGTAAACCTCTCGGACCTTCAAGCT	1020	QY	2041	TCTCCAGAAAGAACTTGGGAGATGATGGTGCAGATGATGAACTGAACTGGGTTCATCCAGTTT	2100
DB	961	TTGCTGATAGATGGGAAACCCAGCACAGAGCAGTAAACCTCTCGGACCTTCAAGCT	1020	DB	2041	TCTCCAGAAAGAACTTGGGAGATGATGGTGCAGATGATGAACTGAACTGGGTTCATCCAGTTT	2100
QY	1021	ATGAAATGTGATCTAGGCTGTGGCTGAATTTCTTCTTCTGAAACTGAGTTTACACCA	1080	QY	2101	CAAAAGCTCAGAGAACTAGAGTTTAAAGCTGAGCAGAGTGCAGGCACTTGGCATGCCCC	2160
DB	1021	ATGAAATGTGATCTAGGCTGTGGCTGAATTTCTTCTTCTGAAACTGAGTTTACACCA	1080	DB	2101	CAAAAGCTCAGAGAACTAGAGTTTAAAGCTGAGCAGAGTGCAGGCACTTGGCATGCCCC	2160
QY	1081	CCAATAGTGGAGTCCCTGGATCCAGATCTTCTGCCCCAATCTTACTGGGAGATTG	1140	QY	2161	ACAAAACAGATCACAGCCAGCTTACACAGGCAATTAATCTCTCTCAATGAGGAAAGAAATCAT	2220
DB	1081	CCAATAGTGGAGTCCCTGGATCCAGATCTTCTGCCCCAATCTTACTGGGAGATTG	1140	DB	2161	ACAAAACAGATCACAGCCAGCTTACACAGGCAATTAATCTCTCTCAATGAGGAAAGAAATCAT	2220
QY	1141	CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGT	1200	QY	2221	TCAAACTGAGCAGACATTCATATGATCATTTTAAAGAAAGTGTTCCTCTTATGTTAGC	2280
DB	1141	CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGT	1200	DB	2221	TCAAACTGAGCAGACATTCATATGATCATTTTAAAGAAAGTGTTCCTCTTATGTTAGC	2280
QY	1201	GCCTAAATGGAATGGATGCAATACCTTTCTGAAATGATCTCCCTTCTGAATGAATGAC	1260	QY	2281	AGTATAATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGC	2340
DB	1201	GCCTAAATGGAATGGATGCAATACCTTTCTGAAATGATCTCCCTTCTGAATGAATGAC	1260	DB	2281	AGTATAATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGC	2340
QY	1261	AAAGCAGTTACCTAGTATAGTTTCCAACTTCTCCATCATATAGCAGATGTAGAAA	1320	QY	2341	TGCAATTTAGGCAGATAAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCAC	2400
DB	1261	AAAGCAGTTACCTAGTATAGTTTCCAACTTCTCCATCATATAGCAGATGTAGAAA	1320	DB	2341	TGCAATTTAGGCAGATAAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCAC	2400
QY	1321	TAATATTTTATGACACTGGGATAAAGCAAGATGCTCACTTCTGGAAAGCTGCAT	1380	QY	2401	CAACTACCATAGCAGATTTAGGAGCTGCAAGGCCCAAGAGTAGAGATGTGCATAAT	2460
DB	1321	TAATATTTTATGACACTGGGATAAAGCAAGATGCTCACTTCTGGAAAGCTGCAT	1380	DB	2401	CAACTACCATAGCAGATTTAGGAGCTGCAAGGCCCAAGAGTAGAGATGTGCATAAT	2460
QY	1381	ATGACTAGAGGCTCTTGTGACTGGAGGTAAACACCTGCGCCAGTAACTGTGGGAGAGG	1440	QY	2461	GTCTGCTCTTGTAGCTCAGGAGACAAATTCAGCAGACAGACACTACAGTTTAAAGCTGAAC	2520
DB	1381	ATGACTAGAGGCTCTTGTGACTGGAGGTAAACACCTGCGCCAGTAACTGTGGGAGAGG	1440	DB	2461	GTCTGCTCTTGTAGCTCAGGAGACAAATTCAGCAGACAGACACTACAGTTTAAAGCTGAAC	2520
				QY	2521	TGCAGCTGCAAGTAATAGCATGAACAGTACAGAAAAATACCTTATGAGGGGGAGGCTGA	2580

[illegible]

PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.
PR 06-MAR-1998; 98WU-US0004493.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
PI Bednarik DR, Endress GA, Yu G, Mi J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 2002-634796/68.
DR P-PSDB; ABG95343.
XX
XX New isolated human secreted protein for diagnosing, preventing, treating
PT or ameliorating medical conditions and used as a food additive or
PT preservative.
XX
XX Example 1; SEQ ID NO 174; 129pp; English.
XX
XX The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of 309 cDNA
CC sequences also given in the specification. The protein is used in a
CC pharmaceutical composition used to prevent, treat or ameliorate a medical
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
CC chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents a cDNA derived from a gene
CC encoding one of the novel human secreted proteins of the invention. Note:
CC This sequence did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=642052681
XX
SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
Query Match 99.9%; Score 3169.4; DB 6; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCCGCGCTCCGTGCTTTTCCACAGAGGTTAGACCTCGTAAAGAGATGGCTCAGC 60
DB 1 TCGACCCCGCGCTCCGTGCTTTTCCACAGAGGTTAGACCTCGTAAAGAGATGGCTCAGC 60
QY 61 ACCACCTATGATCTTGTCTCTTTGCTGCGCAACCTGGCCGGAAGCAGCTGGAAGAGACT 120
DB 61 ACCACCTATGATCTTGTCTCTTTGCTGCGCAACCTGGCCGGAAGCAGCTGGAAGAGACT 120
QY 121 CAGAAATCTTACAGTGAATGGATTTCTGGGAGAGTCACTCTTCCCTGTAATAATCC 180
DB 121 CAGAAATCTTACAGTGAATGGATTTCTGGGAGAGTCACTCTTCCCTGTAATAATCC 180
QY 181 AAGAACCACGCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTGCTTATGTAA 240
DB 181 AAGAACCACGCGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTGCTTATGTAA 240
QY 241 CACCGAGAGACTCAGAAACAGACACCGGTAGTTTCTGTGACCCACAGAAATTTATGAAC 300
DB 241 CACCGAGAGACTCAGAAACAGACACCGGTAGTTTCTGTGACCCACAGAAATTTATGAAC 300
QY 301 GGATACATGCTTAGTCCGAACCTACAATCTGCTATTAGCGATCTGAGGATGGAAGACG 360
DB 301 GGATACATGCTTAGTCCGAACCTACAATCTGCTATTAGCGATCTGAGGATGGAAGACG 360
QY 361 CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCAACCAAGCGCT 420
DB 361 CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCAACCAAGCGCT 420
QY 421 ACAACCTGCAATCTATCTGCGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCAT 480
DB 421 ACAACCTGCAATCTATCTGCGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCAT 480
QY 481 CTGTGAACAGCAGCTGTAATGTACACTGCTCTGTAGAGAAAGAAAGAAAGATG 540
DB 481 CTGTGAACAGCAGCTGTAATGTACACTGCTCTGTAGAGAAAGAAAGAAAGATG 540
QY 541 TGACATACAAATTTGGAGTCCCTGGGAGAGAGGTTAATGTCTTCAAAATCTTCCAGACTC 600
DB 541 TGACATACAAATTTGGAGTCCCTGGGAGAGAGGTTAATGTCTTCAAAATCTTCCAGACTC 600
QY 601 CTGAGGACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCCCTGTGAGCAACAAATCTG 660
DB 601 CTGAGGACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCCCTGTGAGCAACAAATCTG 660
QY 661 ACTCCATCTCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACA 720
DB 661 ACTCCATCTCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACA 720
QY 721 CCGGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTTGTCTCAATCTCTCTCAGTGT 780
DB 721 CCGGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTTGTCTCAATCTCTCTCAGTGT 780
QY 781 TTTTGTTCGTTTTCAGAGAAGACCAAGATCTGCTTCAAGAAACCATATACACAT 840
DB 781 TTTTGTTCGTTTTCAGAGAAGACCAAGATCTGCTTCAAGAAACCATATACACAT 840
QY 841 ATATCATGGCTTCAAGAAACCAAGATCTGCTTCAAGAAACCATATACACAT 900
DB 841 ATATCATGGCTTCAAGAAACCAAGATCTGCTTCAAGAAACCATATACACAT 900
QY 901 AGTCCAAAGTGTCTTCCCTTCAAGAAAGAGCAGTGAACACAGTTTATTCGAAAGTGCAGT 960
DB 901 AGTCCAAAGTGTCTTCCCTTCAAGAAAGAGCAGTGAACACAGTTTATTCGAAAGTGCAGT 960
QY 961 TTCTGTATAGATGGGAAAGCCAGCAGACAGTAAACCTCTCGGAGACTTCAAGCT 1020
DB 961 TTCTGTATAGATGGGAAAGCCAGCAGACAGTAAACCTCTCGGAGACTTCAAGCT 1020
QY 1021 ATCAAAATTTGATCTAGGCTGCTGAGTAAATTTCTCCCTCTGGAAACTGAGTTTACAACCA 1080
DB 1021 ATCAAAATTTGATCTAGGCTGCTGAGTAAATTTCTCCCTCTGGAAACTGAGTTTACAACCA 1080
QY 1081 CCAATACTGCGAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTG 1140

1081 DB CCAATCTGGCAGTTCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATG 1140
1141 QY CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGTGGGCATAGCTTGT 1200
1141 DB CAAACTGCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGTGGGCATAGCTTGT 1200
1201 QY GCTTAATGGCAAAATGGATGATACCTTCTCTGAAATGACTCCCTTCTGAAATGAATGAC 1260
1201 DB GCTTAATGGCAAAATGGATGATACCTTCTCTGAAATGACTCCCTTCTGAAATGAATGAC 1260
1261 QY AAAGCAGGTACTAGTATAGTTTCCCAAACTTCTTCCCATCATAGACATGTAGAAA 1320
1261 DB AAAGCAGGTACTAGTATAGTTTCCCAAACTTCTTCCCATCATAGACATGTAGAAA 1320
1321 QY TAATATTTTTATGGCAGCTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCAT 1380
1321 DB TAATATTTTTATGGCAGCTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCAT 1380
1381 QY ATGACTAGAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
1381 DB ATGACTAGAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
1441 QY GGATCAATATTTTGCACACCTGTATAGGCCATGGCACACCAAGATGCTCTGCTCA 1500
1441 DB GGATCAATATTTTGCACACCTGTATAGGCCATGGCACACCAAGATGCTCTGCTCA 1500
1501 QY CAGTCAGTATGTGAAGATCCCTGGTGGCGCTTCAACGCGATCTTGGAGCAAAATTA 1560
1501 DB CAGTCAGTATGTGAAGATCCCTGGTGGCGCTTCAACGCGATCTTGGAGCAAAATTA 1560
1561 QY GGAAATGTACCTTGGCTTGGAGCAGATGAGCCCTTCCCGAGTGCATGGCTGGAG 1620
1561 DB GGAAATGTACCTTGGCTTGGAGCAGATGAGCCCTTCCCGAGTGCATGGCTGGAG 1620
1621 QY AGCAGAAATGTGGCTGCATATAAGACACTCTATCCCTTGTCTGGGAATCTTGTGCAGG 1680
1621 DB AGCAGAAATGTGGCTGCATATAAGACACTCTATCCCTTGTCTGGGAATCTTGTGCAGG 1680
1681 QY GCATACAGGCTTAGTAACTGCAATTAAGACACTCTATCCCTTGTCTGGGAATCTTGTGCAGG 1740
1681 DB GCATACAGGCTTAGTAACTGCAATTAAGACACTCTATCCCTTGTCTGGGAATCTTGTGCAGG 1740
1741 QY TTGTGGCTCTAGGACTGCTGGGACACTTTTCTTGGAGTGTCTACTTCAGAAAGCTTATAGG 1800
1741 DB TTGTGGCTCTAGGACTGCTGGGACACTTTTCTTGGAGTGTCTACTTCAGAAAGCTTATAGG 1800
1801 QY GCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTCTACTTCAGAAAGCTTATAGG 1860
1801 DB GCAGGCTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGTCTACTTCAGAAAGCTTATAGG 1860
1861 QY ATTTCTTTCTGGCCAAAGATTTCCTTCTGTATCACTTCCAAAGCAGCTCAGCAGAGAGC 1920
1861 DB ATTTCTTTCTGGCCAAAGATTTCCTTCTGTATCACTTCCAAAGCAGCTCAGCAGAGAGC 1920
1921 QY AGCCATGCCAGTATTCACACTCTCCAAAGGACTGACAGCTATATTTCTCAGCTT 1980
1921 DB AGCCATGCCAGTATTCACACTCTCCAAAGGACTGACAGCTATATTTCTCAGCTT 1980
1981 QY CTGGGAACTGGGTATAATCCAACTCAAAATAGAAAGCTTGCAGAGCAGAGTCAAT 2040
1981 DB CTGGGAACTGGGTATAATCCAACTCAAAATAGAAAGCTTGCAGAGCAGAGTCAAT 2040
2041 QY TCTCAGAAAGAACTGGGAGATGATGGTGAGATGAATGAATCCAGGTTTCATCCAGTTC 2100
2041 DB TCTCAGAAAGAACTGGGAGATGATGGTGAGATGAATGAATCCAGGTTTCATCCAGTTC 2100
2101 QY CAAAGACTCAGAGAACTAGAGTTTAAGCTTGGCAGAGTGGCCACCTTGGCATGGCCC 2160
2101 DB CAAAGACTCAGAGAACTAGAGTTTAAGCTTGGCAGAGTGGCCACCTTGGCATGGCCC 2160
2161 QY ACAACAGATCAACCCAGCTTACACAGGCAATTAACCTCTCTCAATAGGAAGATCAT 2220
2161 DB ACAACAGATCAACCCAGCTTACACAGGCAATTAACCTCTCTCAATAGGAAGATCAT 2220

2161 DB ACAACAGATCAACCCAGCTTACACAGGCAATTAACCTCTCTCAATAGGAAGATCAT 2220
2221 QY TCACAACTGAGCAGACATTCATATGATCATTTTAAGGAAGTGTTCCTTATGTGTAGC 2280
2221 DB TCACAACTGAGCAGACATTCATATGATCATTTTAAGGAAGTGTTCCTTATGTGTAGC 2280
2281 QY AAGTATTAATCGGCTAACTCCTAAATCCCAATGAATAGTCCCTAGGCTGACAGCAATGGC 2340
2281 DB AAGTATTAATCGGCTAACTCCTAAATCCCAATGAATAGTCCCTAGGCTGACAGCAATGGC 2340
2341 QY TGCATTAAGGAGATTAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCAC 2400
2341 DB TGCATTAAGGAGATTAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCAC 2400
2401 QY CAACTACATTTAGCAGCTATGTAGAGCTGCAAGGCCCAAGTAAAGTAAAGATGTGATTAAT 2460
2401 DB CAACTACATTTAGCAGCTATGTAGAGCTGCAAGGCCCAAGTAAAGTAAAGATGTGATTAAT 2460
2461 QY GTCTGCTCTTGTGTAGCTCAGGAGCAATCCAGCAGACACTACAGTTAACGCTGAAC 2520
2461 DB GTCTGCTCTTGTGTAGCTCAGGAGCAATCCAGCAGACACTACAGTTAACGCTGAAC 2520
2521 QY TGCAGCTCAAGTAAATAGCATCAACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGA 2580
2521 DB TGCAGCTCAAGTAAATAGCATCAACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGA 2580
2581 QY AGCTGGGCTTGAAGGATGGATGAAATTTGGATAGAGAAATGAGGAAGCAGGGCCCTCC 2640
2581 DB AGCTGGGCTTGAAGGATGGATGAAATTTGGATAGAGAAATGAGGAAGCAGGGCCCTCC 2640
2641 QY AAGTCAGAGAAAGCATGAAAAATGAGCAGGGCCCTGGATCAGTGGGGTGTATTTCAGAGCAC 2700
2641 DB AAGTCAGAGAAAGCATGAAAAATGAGCAGGGCCCTGGATCAGTGGGGTGTATTTCAGAGCAC 2700
2701 QY CTCTCAGATGCACCATGCATCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCAG 2760
2701 DB CTCTCAGATGCACCATGCATCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCAG 2760
2761 QY CCAGATGTGTGCCCCCAGCCCATGTCATTTACATGTCCTTCAATGCCCACTCAAAAGG 2820
2761 DB CCAGATGTGTGCCCCCAGCCCATGTCATTTACATGTCCTTCAATGCCCACTCAAAAGG 2820
2821 QY TACCTCTTCTGTAAAGCTTTCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2821 DB TACCTCTTCTGTAAAGCTTTCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2881 QY CACTGCTTTTTTCTCTTTGGTCTTCTATCACTAAACTCATCTCATTCAGGCTTAC 2940
2881 DB CACTGCTTTTTTCTCTTTGGTCTTCTATCACTAAACTCATCTCATTCAGGCTTAC 2940
2941 QY AGCATAACTTAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3000
2941 DB AGCATAACTTAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3000
3001 QY GAAGCKCTGGGGTGGTGGCTCAGCCCTGTAATCCCAACACTTTGGGAGGCGCAAGGCGAG 3060
3001 DB GAAGCKCTGGGGTGGTGGCTCAGCCCTGTAATCCCAACACTTTGGGAGGCGCAAGGCGAG 3060
3061 QY GCGGATACCTGAGGTCAGGATTCGAGATTARTCTGGCCCAACATGTGTGAACCCCATNT 3120
3061 DB GCGGATACCTGAGGTCAGGATTCGAGATTARTCTGGCCCAACATGTGTGAACCCCATNT 3120
3121 QY NTACTTAAATACGAAATTTAGCCAGTGTGGCAGACATCTGTAGTCCCGAG 3173
3121 DB NTACTTAAATACGAAATTTAGCCAGTGTGGCAGACATCTGTAGTCCCGAG 3173

RESULT 3

ACD82804

ID ACD82804 standard; cdna; 3173 BP.

XX

AC ACD82804;

XX

DT 22-SEP-2003 (first entry)
XX cDNA sequence #164 containing coding region of a human secreted protein.
DE
XX
KW Human; secreted protein; hyperproliferative disorder; leukaemia;
KW breast cancer; wound; reproductive disorder; blood-related disorder;
KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;
KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;
KW Graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;
KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;
KW angina pectoris; cerebral ischaemia; congenital heart defect;
KW Parkinson's disease; inflammation; Crohn's disease; vulvexary;
KW immunosuppressive; antibacterial; haemostatic; thrombolytic;
KW anticoagulant; neuroprotective; thyromimetic; antiallergic;
KW antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;
KW cerebroprotective; cardiant; nootropic; antiparkinsonian;
XX antiinflammatory; gene; ss.
OS Homo sapiens.
XX
PN US2003049618-A1.
XX
PD 13-MAR-2003.
XX
PF 16-MAR-2001; 2001US-00809391.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040335P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047422P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 16-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057659P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 19-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.

PA (OLSE//) OLSEN H S.
PA (FISC//) FISCHER C L.
PA (EBNE//) EBNER R.
PA (BREW//) BREWER L A.
PA (MOOR//) MOORE P A.
PA (SHIY//) SHI Y.
PA (LAFL//) LAFLAUR D W.
PA (LIYY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Laflaur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 2003-521800/49.
DR P-PSDB; ABO34537.
XX
XX New genes and its encoded prostate cancer antigen proteins, useful for
PT preventing, treating, ameliorating or diagnosing e.g. prostate cancers,
PT thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
PT ischemia.
XX
PS Claim 4; SEQ ID NO 174; 260pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC proteins and the polynucleotide sequences encoding them. The invention
CC also discloses vectors, host cells, antibodies, and recombinant methods
CC for producing human secreted proteins. The polypeptide and polynucleotide
CC sequences for the secreted proteins are useful for preventing, treating,
CC ameliorating or diagnosing medical conditions such as hyperproliferative
CC disorders (e.g. leukemia or breast cancers), wounds, reproductive
CC disorders, blood-related disorders (e.g. haemophilia or
CC thrombocytopaenia), immunodeficiencies (e.g. Wiskott-Aldrich syndrome or
CC thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease,
CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma,
CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
CC pectoris, cerebral ischemia or congenital heart defects), respiratory
CC disorders, neurological disorders (e.g. Alzheimer's disease or
CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The
CC polynucleotide or polypeptide may also be used as vaccine adjuvants.
CC ACD82641-ACD82950 encode human secreted proteins or their fragments.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipdb/Entry.html
XX
SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Query Match 99.9%; Score 3169.4; DB 9; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCASGGGTCGGTCTTTTCCACAGAGAGGTAGACCCCTGAAAGAGATGGCTCAGC 60
DB 1 TCGACCCASGGGTCGGTCTTTTCCACAGAGAGGTAGACCCCTGAAAGAGATGGCTCAGC 60

QY 61 ACCACTATGGATCTTGGCTCTCTTTGGCTGCAACCTGGCCGGAAGCAGCTGGAAAGACT 120
DB 61 ACCACTATGGATCTTGGCTCTCTTTGGCTGCAACCTGGCCGGAAGCAGCTGGAAAGACT 120

QY 121 CAGAAATCTTCAGTGAATGGGATCTCGGAGAGTCAGTCACTTCCCTGTAATATCC 180
DB 121 CAGAAATCTTCAGTGAATGGGATCTCGGAGAGTCAGTCACTTCCCTGTAATATCC 180

QY 181 AAGAACCCGCGGAAGTTAAATCAATTCCTTGGACTTCTAAACATCTGTTGCTATGTAA 240
DB 181 AAGAACCCGCGGAAGTTAAATCAATTCCTTGGACTTCTAAACATCTGTTGCTATGTAA 240

QY 241 CACGAGGAGCTCAGAAAACAGACCCGATGTTACTGTGACCCACAGAAATTTATGAAC 300
DB 241 CACGAGGAGCTCAGAAAACAGACCCGATGTTACTGTGACCCACAGAAATTTATGAAC 300

QY 301 GGATACATGCTTAGGTCCGAACCTACAATCTGGTCAATTTAGCGATCTGAGGATGAAGACG 360
DB 301 GGATACATGCTTAGGTCCGAACCTACAATCTGGTCAATTTAGCGATCTGAGGATGAAGACG 360

QY 361 CAGGAGACTACAAAGCAGACATAAATAACACAGGCTGATCCCTACACCAACCAAGCGCT 420
DB 361 CAGGAGACTACAAAGCAGACATAAATAACACAGGCTGATCCCTACACCAACCAAGCGCT 420

QY 421 ACAACCTGCAATCTATGCTGGCTTGGGAAACCAAAAATTACACAGAGTTTATGGCAT 480
DB 421 ACAACCTGCAATCTATGCTGGCTTGGGAAACCAAAAATTACACAGAGTTTATGGCAT 480

QY 481 CTGTGAACAGCACCTGTAAATGCTACACACTGACATCTCTGTAGAGAAAGAAAGAAATG 540
DB 481 CTGTGAACAGCACCTGTAAATGCTACACACTGACATCTCTGTAGAGAAAGAAAGAAATG 540

QY 541 TGACATACAATTTGAGTCCCTGGGAGAGAGGTAATGTCTCTTCAAAATCTTCCAGACTC 600
DB 541 TGACATACAATTTGAGTCCCTGGGAGAGAGGTAATGTCTCTTCAAAATCTTCCAGACTC 600

QY 601 CTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTGTGACGACCAATTCG 660
DB 601 CTGAGGACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCTGTGACGACCAATTCG 660

QY 661 ACTCCATCTGCTGCGGCGAGCTCTGTGCAGACATCGCAATGGGCTTCGGTACTCACCA 720
DB 661 ACTCCATCTGCTGCGGCGAGCTCTGTGCAGACATCGCAATGGGCTTCGGTACTCACCA 720

QY 721 CCGGGTGTCTGAGCGTGTGCTATGTTCTTCTGCTTGTCTCATTTCTGCTCAGTGT 780
DB 721 CCGGGTGTCTGAGCGTGTGCTATGTTCTTCTGCTTGTCTCATTTCTGCTCAGTGT 780

QY 781 TTTTGTTCGTTTGTTCAGAGAGACAGAGTCTGCTCAAGAAAACCAATATACAT 840
DB 781 TTTTGTTCGTTTGTTCAGAGAGACAGAGTCTGCTCAAGAAAACCAATATACAT 840

QY 841 ATATCATGGCTTCAAGGAAACCCAGCCAGCAGAGTCCAGAAATCTATGATGAAATCTTCG 900
DB 841 ATATCATGGCTTCAAGGAAACCCAGCCAGCAGAGTCCAGAAATCTATGATGAAATCTTCG 900

QY 901 AGTCAAGTGTCTTCCCTTCAAGGAAAGCAGTGAAACACAGATTTTATTCGGAAGTGCAGT 960
DB 901 AGTCAAGTGTCTTCCCTTCAAGGAAAGCAGTGAAACACAGATTTTATTCGGAAGTGCAGT 960

QY 961 TTGCTGATAAGTGGGAAACCCAGCAGAGGACAGTAAACCTCTCGGACTTCAAGCT 1020
DB 961 TTGCTGATAAGTGGGAAACCCAGCAGAGGACAGTAAACCTCTCGGACTTCAAGCT 1020

QY 1021 ATGAAATTTGATCTTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACCA 1080
DB 1021 ATGAAATTTGATCTTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACCA 1080

QY 1081 CCAATATCGGAGGTTCCCTGGATCCAGATCTTCTGCGCCAACTCTTACTTGGGAGATG 1140
DB 1081 CCAATATCGGAGGTTCCCTGGATCCAGATCTTCTGCGCCAACTCTTACTTGGGAGATG 1140

QY 1141 CAAACTGCGCATCTCAGCCTGTAAGCAAGCAGGAAACCTTTCTGCTGGGATAGCTTGT 1200
DB 1141 CAAACTGCGCATCTCAGCCTGTAAGCAAGCAGGAAACCTTTCTGCTGGGATAGCTTGT 1200

QY 1201 GCCTAAATGGACAAATGGATGCATACCTTCTGAAATGACTCCCTTCTGAAATGAATGAC 1260
DB 1201 GCCTAAATGGACAAATGGATGCATACCTTCTGAAATGACTCCCTTCTGAAATGAATGAC 1260

QY 1261 AAGCAGGTTACCTAGTATAGTTTTTCCAAACTCTTCCCATCATAGCACATGTAGAAA 1320
DB 1261 AAGCAGGTTACCTAGTATAGTTTTTCCAAACTCTTCCCATCATAGCACATGTAGAAA 1320

QY 1321 TAAATATTTTATGGCACACTGGATTAACCAAGCAAGATGTCTCACTTCTGGAAGCTGCAT 1380
DB 1321 TAAATATTTTATGGCACACTGGATTAACCAAGCAAGATGTCTCACTTCTGGAAGCTGCAT 1380

PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040826P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043586P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P B.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EGNE/) EGENER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LIY/) LI Y.
PA (LAPL/) LAFLEUR D W.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM; Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; WPI; 2003-898535/82.
DR P-PSDB; ADI23198.
XX
New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.
XX
Claim 1; SEQ ID NO 174; 256pp; English.
PS
The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the cDNA sequence; a polynucleotide sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a

CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The sequence encodes a novel human secreted
CC protein of the invention.

XX SQ Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Query Match 99.9%; Score 3169.4; DB 10; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCGACCCAGCGCTCCGTCGCTTTTCCACAGAGAGTTAGACCCCTGAAAGAGATGGCTCAGC	60
DB	1	TCGACCCAGCGCTCCGTCGCTTTTCCACAGAGAGTTAGACCCCTGAAAGAGATGGCTCAGC	60
QY	61	ACCACCTATGGATCTTGCTCTCTTTCGCTGCAACCTGGCCGGAAGCAGCTGGAAAGACT	120
DB	61	ACCACCTATGGATCTTGCTCTCTTTCGCTGCAACCTGGCCGGAAGCAGCTGGAAAGACT	120
QY	121	CAGAAATCTTCAGTGAATGGGATCTCGGAGAGTCAGTCACCTTCCCTGTAAATATCC	180
DB	121	CAGAAATCTTCAGTGAATGGGATCTCGGAGAGTCAGTCACCTTCCCTGTAAATATCC	180
QY	181	AAGAACCACGGCAAGTTAAATCACTGCTTGGACTCTTAAACATCTGTTGCTTATGTAA	240
DB	181	AAGAACCACGGCAAGTTAAATCACTGCTTGGACTCTTAAACATCTGTTGCTTATGTAA	240
QY	241	CACGAGAGACTCAGAAACAGCACCGTAGTTACTGTGACCCACAGAAATTAATGAAC	300
DB	241	CACGAGAGACTCAGAAACAGCACCGTAGTTACTGTGACCCACAGAAATTAATGAAC	300
QY	301	GGATACATGCTTAGGTCGCAATACAACTCTGCTGATTTAGCGATCTGAGGATGGAAGCG	360
DB	301	GGATACATGCTTAGGTCGCAATACAACTCTGCTGATTTAGCGATCTGAGGATGGAAGCG	360
QY	361	CAGGAGACTCAAAAGCAGACATAAATACACAGCTGATCCCTACACACCAAGCGCT	420
DB	361	CAGGAGACTCAAAAGCAGACATAAATACACAGCTGATCCCTACACACCAAGCGCT	420
QY	421	ACAACCTGCAATCTATCGTCGGCTTGGGAAACCAAAATTAACAGAGTTTAAATGGCAT	480
DB	421	ACAACCTGCAATCTATCGTCGGCTTGGGAAACCAAAATTAACAGAGTTTAAATGGCAT	480
QY	481	CTGTGAACACACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATG	540
DB	481	CTGTGAACACACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATG	540
QY	541	TGACATACAAATGGAGTCCCTCGGAGAGAGGTAATGTCCTTCAAACTTCCAGACTC	600
DB	541	TGACATACAAATGGAGTCCCTCGGAGAGAGGTAATGTCCTTCAAACTTCCAGACTC	600
QY	601	CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCGAGAACCTGTGTCAGCAATTCG	660
DB	601	CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCGAGAACCTGTGTCAGCAATTCG	660
QY	661	ACTCCATCTCTGCCCGGAGCTGTGTCAGACATCGCAATGGGCTTCCGTACTCACCACA	720
DB	661	ACTCCATCTCTGCCCGGAGCTGTGTCAGACATCGCAATGGGCTTCCGTACTCACCACA	720
QY	721	CCGGGTTGCTGAGCGTCTGGCTATGTTCTTTCTGTTGTTCTCATTTCTGTTTCAGTGT	780
DB	721	CCGGGTTGCTGAGCGTCTGGCTATGTTCTTTCTGTTGTTCTCATTTCTGTTTCAGTGT	780
QY	781	TTTTGTTCCGTTTGTTCAGGAAGACAAGATGCTGCTCAAGAAACCATATACACAT	840
DB	781	TTTTGTTCCGTTTGTTCAGGAAGACAAGATGCTGCTCAAGAAACCATATACACAT	840
QY	841	ATATCATGGCTTCAAGGAACACCCAGCAGAGTCCAGATCTATGATGAATCTCTGC	900
DB	841	ATATCATGGCTTCAAGGAACACCCAGCAGAGTCCAGATCTATGATGAATCTCTGC	900
QY	901	AGTCCAAAGGTGCTTCCCTTCCAAAGGAAGAGCCAGTGAACACAGTTTATTCGAAGTGCAGT	960
DB	901	AGTCCAAAGGTGCTTCCCTTCCAAAGGAAGAGCCAGTGAACACAGTTTATTCGAAGTGCAGT	960

QY	961	TTGCTGATTAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGACTTCAAGCT	1020
DB	961	TTGCTGATTAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGACTTCAAGCT	1020
QY	1021	ATGAAATTTGTGATCTAGGCTGTGGCTGAAATCTCCCTCTGGAAACTGAGTTACAACTA	1080
DB	1021	ATGAAATTTGTGATCTAGGCTGTGGCTGAAATCTCCCTCTGGAAACTGAGTTACAACTA	1080
QY	1081	CAAACTCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCCAACTCTTACTGGGAGATTG	1140
DB	1081	CAAACTCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCCAACTCTTACTGGGAGATTG	1140
QY	1141	CAAACTCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCCAACTCTTACTGGGAGATTG	1200
DB	1141	CAAACTCTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCCAACTCTTACTGGGAGATTG	1200
QY	1201	GCTAAATGGCAAAATGGATGATACCTTCTGAAATGACTCCCTTCTGAATGAATGAC	1260
DB	1201	GCTAAATGGCAAAATGGATGATACCTTCTGAAATGACTCCCTTCTGAATGAATGAC	1260
QY	1261	AAAGCAGGTTACTAGTATAGTTTCCCAACTTCTTCCCATCATAGCATGTAGAAA	1320
DB	1261	AAAGCAGGTTACTAGTATAGTTTCCCAACTTCTTCCCATCATAGCATGTAGAAA	1320
QY	1321	TAATATTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACCTTCTGGAAAGTGCAT	1380
DB	1321	TAATATTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACCTTCTGGAAAGTGCAT	1380
QY	1381	ATGACTAGAGGCTCTTTGTGACTGGAGGTAACAACCTGCCCCAGTAATCTGTGGAGAGG	1440
DB	1381	ATGACTAGAGGCTCTTTGTGACTGGAGGTAACAACCTGCCCCAGTAATCTGTGGAGAGG	1440
QY	1441	GGATCAATATTTGGCACACTGTAATAGGCAATGCGCATCCCTGCGTGGGCTTCAACGCAATTA	1500
DB	1441	GGATCAATATTTGGCACACTGTAATAGGCAATGCGCATCCCTGCGTGGGCTTCAACGCAATTA	1500
QY	1501	CAGTCAATATTTGGCACACTGTAATAGGCAATGCGCATCCCTGCGTGGGCTTCAACGCAATTA	1560
DB	1501	CAGTCAATATTTGGCACACTGTAATAGGCAATGCGCATCCCTGCGTGGGCTTCAACGCAATTA	1560
QY	1561	GGAAATGTACCTTCCCTTGGAGGAGATGAGCCCTTCCCTGAGTGCATGGCTGGAG	1620
DB	1561	GGAAATGTACCTTCCCTTGGAGGAGATGAGCCCTTCCCTGAGTGCATGGCTGGAG	1620
QY	1621	AGCAGATCTGGGCTGCATATAGCACACTCATCCCTTCTGTTGGGAACTCTTGTGTCAGG	1680
DB	1621	AGCAGATCTGGGCTGCATATAGCACACTCATCCCTTCTGTTGGGAACTCTTGTGTCAGG	1680
QY	1681	GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTTCAGAG	1740
DB	1681	GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTTCAGAG	1740
QY	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTCT	1800
DB	1741	TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTCT	1800
QY	1801	GCAGGCTCTAGACACTGAGGACACTTTTCTTGGAGTGTCTTCTCAGAGCCCTTATAGG	1860
DB	1801	GCAGGCTCTAGACACTGAGGACACTTTTCTTGGAGTGTCTTCTCAGAGCCCTTATAGG	1860
QY	1861	ATTTCTTCTTCTGGCCCAAGATTCTCTGTATCATCTCCAAAGCCTCAGCAGAAAGC	1920
DB	1861	ATTTCTTCTTCTGGCCCAAGATTCTCTGTATCATCTCCAAAGCCTCAGCAGAAAGC	1920
QY	1921	AGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACAGCTTATTTCTCACACTT	1980
DB	1921	AGCCATGCCAGTATTTCCCACTCTCCAAAGGAACTGACAGCTTATTTCTCACACTT	1980
QY	1981	CTGGGNACTGGGCTATTAATCCAACTCAAAATAGAGACTCTTCCAAAGAGCAGTGCAT	2040
DB	1981	CTGGGNACTGGGCTATTAATCCAACTCAAAATAGAGACTCTTCCAAAGAGCAGTGCAT	2040

2041 TCTCCAGAGGAACCTGGGAGATGATGGTGACAGATCAAACTGGGTTTCATCCAGTTC 2100
2041 TCTCCAGAGGAACCTGGGAGATGATGGTGACAGATCAAACTGGGTTTCATCCAGTTC 2100
2101 CAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCGAGTGCGGCCACCCCTGGCATGCCCC 2160
2101 CAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCGAGTGCGGCCACCCCTGGCATGCCCC 2160
2161 ACAAACAGATCAACCCAGCAGCTTACACAGGCATTAACCTCTCAATGAGGAAGATCAT 2220
2161 ACAAACAGATCAACCCAGCAGCTTACACAGGCATTAACCTCTCAATGAGGAAGATCAT 2220
2221 TCACAACTCAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGC 2280
2221 TCACAACTCAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGC 2280
2281 AAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGGC 2340
2281 AAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGGC 2340
2341 TGCATATTAGGCGAGATAAGACATCAGTCCCGAGTAAATGAATCCATAGACTCATCTAGCAC 2400
2341 TGCATATTAGGCGAGATAAGACATCAGTCCCGAGTAAATGAATCCATAGACTCATCTAGCAC 2400
2401 CAACCTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATAT 2460
2401 CAACCTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATAT 2460
2461 GTCTGCTCTTGTAGTCTCAGGAGACAATCCAGACAGACACTACAGTTAAACGCTGAAC 2520
2461 GTCTGCTCTTGTAGTCTCAGGAGACAATCCAGACAGACACTACAGTTAAACGCTGAAC 2520
2521 TGCAGCTGCAAGTAATAGCATCAACAGTCCAGAAATACTTTAGGGGGCAGAGGCTGA 2580
2521 TGCAGCTGCAAGTAATAGCATCAACAGTCCAGAAATACTTTAGGGGGCAGAGGCTGA 2580
2581 AGCTGGGCCCTTGAAGAGTGAATGAAATTTGGATAGAGATGAGGAAGCAGAGGCGCTCC 2640
2581 AGCTGGGCCCTTGAAGAGTGAATGAAATTTGGATAGAGATGAGGAAGCAGAGGCGCTCC 2640
2641 AAGTGAGAGAAGCATGAAATAATGAGCAGGGGCTGGATCAGTGGGGTGTATTCAGAGCAC 2700
2641 AAGTGAGAGAAGCATGAAATAATGAGCAGGGGCTGGATCAGTGGGGTGTATTCAGAGCAC 2700
2701 CTCTCAGATGACCATGATGCTCAGCTCCCTTGCCTATGCTGTCAGAGAGTGTCCAG 2760
2701 CTCTCAGATGACCATGATGCTCAGCTCCCTTGCCTATGCTGTCAGAGAGTGTCCAG 2760
2761 CCAGATGTGTGCCCCACCCCATGTCATTTATCATGTCCTTCAATGCCACCTCAAAAGG 2820
2761 CCAGATGTGTGCCCCACCCCATGTCATTTATCATGTCCTTCAATGCCACCTCAAAAGG 2820
2821 TACCTCTCTGTAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2821 TACCTCTCTGTAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
2881 CACTGCTGTTTTTCTCTTTGGTCTCTTATCACTTAAACCTCATCTCAGGCTTAC 2940
2881 CACTGCTGTTTTTCTCTTTGGTCTCTTATCACTTAAACCTCATCTCAGGCTTAC 2940
2941 AGCATAACTAATATTTGTTTTTCTCCTACATATGTTGAGATGAGGAATTTACAGATAAAG 3000
2941 AGCATAACTAATATTTGTTTTTCTCCTACATATGTTGAGATGAGGAATTTACAGATAAAG 3000
3001 GAAGCKGCTGGGTGGTGGCTCAGCGCTGTAATCCACACTTTTGGGAGGCCAAGGAG 3060
3001 GAAGCKGCTGGGTGGTGGCTCAGCGCTGTAATCCACACTTTTGGGAGGCCAAGGAG 3060
3061 GCGGATCAGCTCAGGATTCAGGATTTCTGGCCAACTAGTGTGAACCCCAATNT 3120
3061 GCGGATCAGCTCAGGATTCAGGATTTCTGGCCAACTAGTGTGAACCCCAATNT 3120
3121 NTACTAAAAATAGAAATTTAGCCAGGTGGTGGCAGACATCTGTAGTCCAG 3173

Db 3121 NTACTAAAAATAGAAATTTAGCCAGGTGGTGGCAGACATCTGTAGTCCAG 3173
RESULT 5
ADH73891
ID ADH73891 standard; cDNA; 3173 BP.
XX
AC ADH73891;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human secreted protein cDNA #164.
XX
KW human; secreted protein; cancer; haematopoietic disorder;
KW endocrine disorder; immune system disease; inflammatory disorder; ss;
KW gene.
XX
OS Homo sapiens.
XX
PN US2003225248-A1.
XX
PD 04-DEC-2003.
XX
PF 10-JUN-2002; 2002US-00164861.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.

QY 721 CCGGGTGTGCTGAGCGTCTGGCTATGTTCTTTCTGCTTGTTCTCATTTCTGCTCTTCAGTGT 780
Db 721 CCGGGTGTGCTGAGCGTCTGGCTATGTTCTTTCTGCTTGTTCTCATTTCTGCTCTTCAGTGT 780
QY 781 TTTTGTTCCTGTTTCAAGAGAGAGACAAGATGCTGCCTCAAGAAAAACCATATACACAT 840
Db 781 TTTTGTTCCTGTTTCAAGAGAGAGACAAGATGCTGCCTCAAGAAAAACCATATACACAT 840
QY 841 ATATCATGGCTTCAGAGAACACCCAGCAGCAGAGTCCAGAATCTATGATGAATCCTGC 900
Db 841 ATATCATGGCTTCAGAGAACACCCAGCAGCAGAGTCCAGAATCTATGATGAATCCTGC 900
QY 901 AGTCCAAAGTGCTTCCCTCCAAAGAGAGCCAGTGAACACAGTTTATTCGGAAGTCCAGT 960
Db 901 AGTCCAAAGTGCTTCCCTCCAAAGAGAGCCAGTGAACACAGTTTATTCGGAAGTCCAGT 960
QY 961 TTGCTGATAAGATGGGGAAGCCAGCACACAGACAGTAAACCTCTCGGACCTTCAAGCT 1020
Db 961 TTGCTGATAAGATGGGGAAGCCAGCACACAGACAGTAAACCTCTCGGACCTTCAAGCT 1020
QY 1021 ATGAATTTGTGATCTAGGCTGTGGGTGATTTCTCCCTCTGGAAACTGAGTTACACCA 1080
Db 1021 ATGAATTTGTGATCTAGGCTGTGGGTGATTTCTCCCTCTGGAAACTGAGTTACACCA 1080
QY 1081 CCAATCTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTG 1140
Db 1081 CCAATCTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTG 1140
QY 1141 CAAACTGGCCACATCTCAGCTCTGAAGCAAGCAAGAAACCTTCTGCTGGCCATAGCTTGT 1200
Db 1141 CAAACTGGCCACATCTCAGCTCTGAAGCAAGCAAGAAACCTTCTGCTGGCCATAGCTTGT 1200
QY 1201 GCCTAAATGACAAATGGATGCATCCCTTCTGTAATGACTCCCTTCTGTAATGATGAC 1260
Db 1201 GCCTAAATGACAAATGGATGCATCCCTTCTGTAATGACTCCCTTCTGTAATGATGAC 1260
QY 1261 AAAGCAGGTACTAGTATAGTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAAA 1320
Db 1261 AAAGCAGGTACTAGTATAGTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAAA 1320
QY 1321 TAATATTTTATGGCACCTGGATAAACAAGCAAGATGCTCAGTTCTGGAAGCTGCAT 1380
Db 1321 TAATATTTTATGGCACCTGGATAAACAAGCAAGATGCTCAGTTCTGGAAGCTGCAT 1380
QY 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACCCCTGCCAGTAACTGTGGGAGAAGG 1440
Db 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACCCCTGCCAGTAACTGTGGGAGAAGG 1440
QY 1441 GGATCAATATTTTGCACCTGTATAGGCCATGGCACACCAAGCAAGTCTCTGCTCA 1500
Db 1441 GGATCAATATTTTGCACCTGTATAGGCCATGGCACACCAAGCAAGTCTCTGCTCA 1500
QY 1501 CAGTCAGTATGTGAAGATCCCTGGTGGCTGCTTCCACACGCTCTTGGAGCAATTA 1560
Db 1501 CAGTCAGTATGTGAAGATCCCTGGTGGCTGCTTCCACACGCTCTTGGAGCAATTA 1560
QY 1561 GGAAAAATGTACCTTTCGCTTGAAGCAGATGCAAGCCCTTCCCGAGTGCATGGCTGGAG 1620
Db 1561 GGAAAAATGTACCTTTCGCTTGAAGCAGATGCAAGCCCTTCCCGAGTGCATGGCTGGAG 1620
QY 1621 AGCAGATGTGGGCTGCATATAGCACACTCATCTTGTGCTGGGAATCTTGTGCAAG 1680
Db 1621 AGCAGATGTGGGCTGCATATAGCACACTCATCTTGTGCTGGGAATCTTGTGCAAG 1680
QY 1681 GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTCTGTGAGTCTGTGCAG 1740
Db 1681 GCATAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTCTGTGAGTCTGTGCAG 1740
QY 1741 TTGTGGCTCTAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTCT 1800
Db 1741 TTGTGGCTCTAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTCT 1800
QY 1801 GCAGGCTCTAGAGACTGTCTGGGACACTTTTCTTGGAGTGCTACTTCAGAGCCCTATAGG 1860

Db 1801 GCAGGCTCTAGAGACTGTCTGGGACACTTTTCTTGGAGTGCTACTTCAGAGCCCTTATAGG 1860
QY 1861 ATTTTCTTTCTGGCCCAAGATTTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAAGC 1920
Db 1861 ATTTTCTTTCTGGCCCAAGATTTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAAGC 1920
QY 1921 AGCCATGCCAGTATPCCCACTCTCCAAAAGAACTGACCCAGCTTATATTTCTCACACTT 1980
Db 1921 AGCCATGCCAGTATPCCCACTCTCCAAAAGAACTGACCCAGCTTATATTTCTCACACTT 1980
QY 1981 CTGGGGAACTGGGTATTAATCCAACCATCAAAATAGAAGACCTTCAAGAAGCAGATCAT 2040
Db 1981 CTGGGGAACTGGGTATTAATCCAACCATCAAAATAGAAGACCTTCAAGAAGCAGATCAT 2040
QY 2041 TCTCCAGAAGAACTTGGGAGATGATGGTGAGATGATGATGAATCTGGGTTCATCCAGTTC 2100
Db 2041 TCTCCAGAAGAACTTGGGAGATGATGGTGAGATGATGATGAATCTGGGTTCATCCAGTTC 2100
QY 2101 CAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCATGGCC 2160
Db 2101 CAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCAGCATGGCC 2160
QY 2161 ACAACACATCACCAGCAGCTTACACAGGCAATTAATCTCTCAATGAGGAAGAAATCAT 2220
Db 2161 ACAACACATCACCAGCAGCTTACACAGGCAATTAATCTCTCAATGAGGAAGAAATCAT 2220
QY 2221 TCACAACTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTTAGC 2280
Db 2221 TCACAACTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTTAGC 2280
QY 2281 AAGTATTAATCGGCTAACTTCTTAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGGC 2340
Db 2281 AAGTATTAATCGGCTAACTTCTTAATCCCAATGAATAGTCTAGGCTGGACAGCAATGGGC 2340
QY 2341 TGCAATTAGGCAGATAAAGACATCAGTCCCAAGTAAATGAATCCAATAGACTCATAGCAC 2400
Db 2341 TGCAATTAGGCAGATAAAGACATCAGTCCCAAGTAAATGAATCCAATAGACTCATAGCAC 2400
QY 2401 CAACATCACTTAGCAGTATGTTAGGAGTGCAGGCCCCAAAGTAGAAGTAGTGCATAAT 2460
Db 2401 CAACATCACTTAGCAGTATGTTAGGAGTGCAGGCCCCAAAGTAGAAGTAGTGCATAAT 2460
QY 2461 GTCTGCTCTTGTGAGCTCAGGAGACAAATCCAGCAGACACTTACAGTTAACTCGAAC 2520
Db 2461 GTCTGCTCTTGTGAGCTCAGGAGACAAATCCAGCAGACACTTACAGTTAACTCGAAC 2520
QY 2521 TGCAAGTGCAGTAATAGCATGAACAGTCAAGAAAAATACCTTATAGGGGGCAGGGCTGA 2580
Db 2521 TGCAAGTGCAGTAATAGCATGAACAGTCAAGAAAAATACCTTATAGGGGGCAGGGCTGA 2580
QY 2581 AGCTGGGCTTGAAGGATGATGAATTTGGATAGAGATGAAGGAAGACAGAGGGCTCC 2640
Db 2581 AGCTGGGCTTGAAGGATGATGAATTTGGATAGAGATGAAGGAAGACAGAGGGCTCC 2640
QY 2641 AAGTGAGAGAGCATGAATTAAGTGAAGTGAATTTGGATAGAGATGAAGGAAGACAGAGGGCTCC 2700
Db 2641 AAGTGAGAGAGCATGAATTAAGTGAAGTGAATTTGGATAGAGATGAAGGAAGACAGAGGGCTCC 2700
QY 2701 CTCTCCAGATGCACATGCATGCATCCCTTGCCTATGTTGGCAGAGTGTCCAG 2760
Db 2701 CTCTCCAGATGCACATGCATGCATCCCTTGCCTATGTTGGCAGAGTGTCCAG 2760
QY 2761 CCAGATGTGGCCCCCACCCTTCCATTTTACATGCTTCCATGCTTCAATGCCACCTCAAAAGG 2820
Db 2761 CCAGATGTGGCCCCCACCCTTCCATTTTACATGCTTCCATGCTTCAATGCCACCTCAAAAGG 2820
QY 2821 TACCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
Db 2821 TACCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
QY 2881 CACTGCTGTTTCTTCTTGGTCTTCTATCACTAAACTCATCTCATTCAGCTTAC 2940

2881	DB	CACGCTGTTTTTTTCTCTTTGGTCCTTCTATACATAAAACTCATCTCATTCAGCCCTTAC	2940
2941	QY	AGCATAACTAATTAATTTGTTTTCTCTACTACATTGTACATGTGGGAATTA	3000
2941	DB	AGCATAACTAATTAATTTGTTTTTCTCTACTACATTGTACATGTGGGAATTA	3000
3001	QY	GAAGCCCKGTGGGGTGGCTCACGCCCTGTAATCCAAACACTTTGGGAGGCCAAGCAG	3060
3001	DB	GAAGCCCKGTGGGGTGGCTCACGCCCTGTAATCCAAACACTTTGGGAGGCCAAGCAG	3060
3061	QY	CGCGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAAACATGTTGAAACCCCATNT	3120
3061	DB	CGCGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAAACATGTTGAAACCCCATNT	3120
3121	QY	NTACTAAAATAAGCAAAATTAAGCCAGGTGCGTGGGCACACATCTGTAGTCCGAG	3173
3121	DB	NTACTAAAATAAGCAAAATTAAGCCAGGTGCGTGGGCACACATCTGTAGTCCGAG	3173

RESULT 6
ADL82906
ID ADL82906 standard; cDNA; 3299 BP.

AC ADL82906;

17-JUN-2004 (first entry)

Human PRO24934 cDNA, SEQ ID 108.

Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 Gene Therapy; PRO; B cell related disorder; cancer;
 Immune-mediated inflammatory disease; human; gene; ss.

OS Homo sapiens.

WO2004024097-A2.

25-MAR-2004.

15-SEP-2003; 2003WO-US029097.

PR 16-SEP-2002; 2002US-0411392P.

AA
PA
(GETH) GENENTECH INC.

PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;

WPI; 2004-329389/30.
P-PSDB: ADL82907.

New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX
PS
Claim 2: Fig 108: 695pp: English.

The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgM deficiency, selective deficiency of IgG subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, intermedate lymphoma, follicular lymphoma, type II hyperensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development

Db 961 |||||ATPAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTGGGACTTCAAGCTATGAAA 1020
QY 1027 TTTGTGATCTAGGCTGTGGCTGGAATTTCTCCCTCTGGAAAATGAGTTACAAACCAATPA 1086
Db 1021 TTTGTGATCTAGGCTGTGGCTGGAATTTCTCCCTCTGGAAAATGAGTTACAAACCAATPA 1080
QY 1087 CTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTGCAACT 1146
Db 1081 CTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTGCAACT 1140
QY 1147 GCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTTTGTGCTTAA 1206
Db 1141 GCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTTTGTGCTTAA 1200
QY 1207 ATGGACAAATGATGATACCTTCTCTGAAATGATCTCCCTCTGTAATGATGACAAAGCA 1266
Db 1201 ATGGACAAATGATGATACCTTCTCTGAAATGATCTCCCTCTGTAATGATGACAAAGCA 1260
QY 1267 GGTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAAATATAT 1326
Db 1261 GGTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAAATATAT 1320
QY 1327 TTTTATGGCACACTGGGATPAAACAGCAAGATTGCTCACTTCTGGAAGCTGCATATGACT 1386
Db 1321 TTTTATGGCACACTGGGATPAAACAGCAAGATTGCTCACTTCTGGAAGCTGCATATGACT 1380
QY 1387 AGAGGCTCTTGTGACTGAGGTAAACACCCCTGCCAGTAACTGTGGGAAGGGGATCA 1446
Db 1381 AGAGGCTCTTGTGACTGAGGTAAACACCCCTGCCAGTAACTGTGGGAAGGGGATCA 1440
QY 1447 ATATTTTGCACACCTGTATAGCCATGCGCATGCCACACAGCCAAAGTCTCTGCTCACAGTCA 1506
Db 1441 ATATTTTGCACACCTGTATAGCCATGCGCATGCCACACAGCCAAAGTCTCTGCTCACAGTCA 1500
QY 1507 GTATGTGTGAAGATCCCTGGTGCCTTCCCAACGCACTTTGAGCAAAATTTAGGAAAA 1566
Db 1501 GTATGTGTGAAGATCCCTGGTGCCTTCCCAACGCACTTTGAGCAAAATTTAGGAAAA 1560
QY 1567 TGTACCTTCTGCTTGGGAGAGATGAGCCCTTCCCGGAGTGCATGGCTTGGAGAGCAGA 1626
Db 1561 TGTACCTTCTGCTTGGGAGAGATGAGCCCTTCCCGGAGTGCATGGCTTGGAGAGCAGA 1620
QY 1627 ATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGAGGGGCATAA 1686
Db 1621 ATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGAGGGGCATAA 1680
QY 1687 CAGGCTTAGTAAAGTCCAAACACAGATGACAGTGCCTGTGGGTCTCTGTACAGATTGTGG 1746
Db 1681 CAGGCTTAGTAAAGTCCAAACACAGATGACAGTGCCTGTGGGTCTCTGTACAGATTGTGG 1740
QY 1747 CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTCTGCAGGG 1806
Db 1741 CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTCTGCAGGG 1800
QY 1807 TCTAGAGACTGTGGGACACTTTTCTTGGAGTGCCTTCTTCAAGAGCCCTTATAGGATTTTC 1866
Db 1801 TCTAGAGACTGTGGGACACTTTTCTTGGAGTGCCTTCTTCAAGAGCCCTTATAGGATTTTC 1860
QY 1867 TTTCTGGCCAAAGTTTCTTCTGTATCACTTCAAGAGCCCTCAGCAGAAAGAGCCAT 1926
Db 1861 TTTCTGGCCAAAGTTTCTTCTGTATCACTTCAAGAGCCCTCAGCAGAAAGAGCCAT 1920
QY 1927 GCCCAGTATTTCCACTCTCTCAAAAGAACTGACACAGCTTATATTTCTCACACTTCTGGGG 1986
Db 1921 GCCCAGTATTTCCACTCTCTCAAAAGAACTGACACAGCTTATATTTCTCACACTTCTGGGG 1980
QY 1987 AACTGGGTATAATCCAAACCATCAAAATAGAGACCTTGCAGAAAGCAGATCAITCTCCA 2046
Db 1981 AACTGGGTATAATCCAAACCATCAAAATAGAGACCTTGCAGAAAGCAGATCAITCTCCA 2040
QY 2047 GAGGACTTGGGAGATGATGGTCAGATGATGAACCTGGGTTCCAGTTCACAGTTCACAGA 2106

Db 2041 GAAGAACTTGGGAGATGATGGTCAGATGATGAACCTGGGTTTATCCAGTTCACAGA 2100
QY 2107 TCTCAGAACTTAGAGTTTAAAGCTGAGCAGAGTGCCTGCAACCTTGGCATGCCCAACAAC 2166
Db 2101 TCTCAGAACTTAGAGTTTAAAGCTGAGCAGAGTGCCTGCAACCTTGGCATGCCCAACAAC 2160
QY 2167 AGATCACCAGCCAGCTTACAGAGCATTAACCTCTCAATGAGGAAGAAATCAATTCACAA 2226
Db 2161 AGATCACCAGCCAGCTTACAGAGCATTAACCTCTCAATGAGGAAGAAATCAATTCACAA 2220
QY 2227 CTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTTAGCAAGTAT 2286
Db 2221 CTGAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTTAGCAAGTAT 2280
QY 2287 AATGGCTTAACCTTAAATCCCAATGAATAGTCTTAGGCTGCACAGCAATGGGCTGCAAT 2346
Db 2281 AATGGCTTAACCTTAAATCCCAATGAATAGTCTTAGGCTGCACAGCAATGGGCTGCAAT 2340
QY 2347 TAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTA 2406
Db 2341 TAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTA 2400
QY 2407 CCATTAGCACTATGTTAGGAGCTCAAGGCCCCCAAGTAGAAGATGTGCAATAATGTCTGC 2466
Db 2401 CCATTAGCACTATGTTAGGAGCTCAAGGCCCCCAAGTAGAAGATGTGCAATAATGTCTGC 2460
QY 2467 TCTTGTGTAGCTCAGGAGACAAATCCAGCACAGACACTACAGTTAAACCTGAACTGCAGC 2526
Db 2461 TCTTGTGTAGCTCAGGAGACAAATCCAGCACAGACACTACAGTTAAACCTGAACTGCAGC 2520
QY 2527 TGCAAGTAAATAGCATGAACAGTCAAGAAAATACCTTATAGGGGGCAGGGCTGAAGCTGG 2586
Db 2521 TGCAAGTAAATAGCATGAACAGTCAAGAAAATACCTTATAGGGGGCAGGGCTGAAGCTGG 2580
QY 2587 GCCTTGAAGGATGATGAAATTTGGATAGAAATTTGAGAAAGACAGAGGGCTTCAAGTGA 2646
Db 2581 GCCTTGAAGGATGATGAAATTTGGATAGAAATTTGAGAAAGACAGAGGGCTTCAAGTGA 2640
QY 2647 GAGAGCATGAAATGAGCAGGGCTGGATCAGTGGGGTATTCAGAGCAGCTCTCC 2706
Db 2641 GAGAGCATGAAATGAGCAGGGCTGGATCAGTGGGGTATTCAGAGCAGCTCTCTCC 2700
QY 2707 AGATGCACCATGCTACAGTCCCTTGGCTATGTGTGGCAGAGTGTCCAGCCAGAT 2766
Db 2701 AGATGCACCATGCTACAGTCCCTTGGCTATGTGTGGCAGAGTGTCCAGCCAGAT 2760
QY 2767 GTGTGCCCCACCCCATGTCCATTTACATGCTTCAATGCCCACCTCAAAAGGTACCTC 2826
Db 2761 GTGTGCCCCACCCCATGTCCATTTACATGCTTCAATGCCCACCTCAAAAGGTACCTC 2820
QY 2827 TTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC 2886
Db 2821 TTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC 2880
QY 2887 TGTTTTTTCTCTTTTGGTCTTCTATCACTAAAACTCATCTCATTTACAGCCTTACAGCATA 2946
Db 2881 TGTTTTTTCTCTTTTGGTCTTCTATCACTAAAACTCATCTCATTTACAGCCTTACAGCATA 2940
QY 2947 ACTAATTAATTTTGTCTTCTCTACTACATTTGATGTGGGAATACAGATAAACGGAAGCC 3006
Db 2941 ACTAATTAATTTTGTCTTCTCTACTAATTTGATGTGGGAATACAGATAAACGGAAGCC 3000
QY 3007 KGCTGGGGTGTGGCTCACGCTCTGAATCCCAACACTTTTGGGAGGCCAAGCAGGCGGAT 3066
Db 3001 GGCTGGGGTGTGGCTCACGCTCTGAATCCCAACACTTTTGGGAGGCCAAGCAGGCGGAT 3060
QY 3067 CACTGTAGGTCAGGATTCGAGATTATCTGGCCAAACATGGTGAAACCCCATNTNTACTA 3126
Db 3061 CACTGTAGGTCAGGATTCGAGATTATCTGGCCAAACATGGTGAAACCCCATCTCTACTA 3120
QY 3127 AAAATACGAATTAAGCAGGTTGGTGGCACACATCTGTAGTCCAG 3173
Db 3121 AAAATACGAATTAAGCAGGTTGGTGGCACACATCTGTAGTCCAG 3167

Best Local Similarity 99.8%; Pred. No.: 0;
Matches 3160: Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	7	CCASGGCTCGTGCTTTTCCACAGAAAGTTAGACCCCTGAAAGAGATGGCTCAGCACACC	66
Db	1	CCACGGCTCGTGCTTTTCCACAGAAAGTTAGACCCCTGAAAGAGATGGCTCAGCACACC	60
Qy	67	TATGGATCTTGCTCCTTTGGCTCGCAACCTGGCGGGAAGCAGCTGGNAAGAGCTCAGAAA	126
Db	61	TATGGATCTTGCTCCTTTGGCTCGCAACCTGGCGGGAAGCAGCTGGNAAGAGCTCAGAAA	120
Qy	127	TCCTTCACAGTGAATGGATTCGGGAGAGTCAGTCACCTTCCCTGTAAATATCCAAGAAC	186
Db	121	TCCTTCACAGTGAATGGATTCGGGAGAGTCAGTCACCTTCCCTGTAAATATCCAAGAAC	180
Qy	187	CACGGCAAGTTAAATCATTTGCTGGACTCTTAAACATCTGTGCTTTATGTAAACACAG	246
Db	181	CACGGCAAGTTAAATCATTTGCTGGACTCTTAAACATCTGTGCTTTATGTAAACACAG	240
Qy	247	GAGACTCAGAAAAGCACCCTGATTTACTGTGACCCACAGAAATATATTGAACGGATAC	306
Db	241	GAGACTCAGAAAAGCACCCTGATTTACTGTGACCCACAGAAATATATTGAACGGATAC	300
Qy	307	ATGCTTTAGGTCGGAATCAAACTGGCTATTAGCGATCTGAGGATGGAAGACGAGGAG	366
Db	301	ATGCTTTAGGTCGGAATCAAACTGGCTATTAGCGATCTGAGGATGGAAGACGAGGAG	360
Qy	367	ACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACACCAAGGCTTACAACC	426
Db	361	ACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACACCAAGGCTTACAACC	420
Qy	427	TGCNAATCTATCGTCGGCTTTGGGAAACCAAAAATTTACACAGAGTTTAAATGSCATCTGTGA	486
Db	421	TGCNAATCTATCGTCGGCTTTGGGAAACCAAAAATTTACACAGAGTTTAAATGSCATCTGTGA	480
Qy	487	ACAGCACTGTAAATGTACACTGACCTGCTCTGTAGAGAAAGAAAGAAATGTGACAT	546
Db	481	ACAGCACTGTAAATGTACACTGACCTGCTGTAGAGAAAGAAAGAAATGTGACAT	540
Qy	547	ACAATTTGGAGTCCCTGGGAGAGAGGTAATGTCTTCAAACTTCCAGACTCCTGAGG	606
Db	541	ACAATTTGGAGTCCCTGGGAGAGAGGTAATGTCTTCAAACTTCCAGACTCCTGAGG	600
Qy	607	ACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCTGTCTGACTCTCA	666
Db	601	ACCAAGAGCTGACTTACACGCTGTACAGCCAGAACCTGTCTGACTCTCA	660
Qy	667	TCTCTGCCCGGACGCTCTGTGCAGACATCGCAATGGGCTTCGTACTCACACACCGGT	726
Db	661	TCTCTGCCCGGACGCTCTGTGCAGACATCGCAATGGGCTTCGTACTCACACACCGGT	720
Qy	727	TGCTGAGGCTGCTGCTATGTTCTTTCTGCTGTTCTCATTTCTGCTTTCAGTGTGTTTTGT	786
Db	721	TGCTGAGGCTGCTGCTATGTTCTTTCTGCTGTTCTCATTTCTGCTTTCAGTGTGTTTTGT	780
Qy	787	TCGGTTGTTTCAAGAGAAACAGATGCTGCTCAAGAAACCATATACATATATCA	846
Db	781	TCCGTTTGTTCAGAGAAACAGATGCTGCTCAAGAAACCATATACATATATCA	840
Qy	847	TGGCTTCAAGGAACCCAGCCAGCAGAGTCAGAAATCTATGATGAATTCCTGCACTCA	906
Db	841	TGGCTTCAAGGAACCCAGCCAGCAGAGTCAGAAATCTATGATGAATTCCTGCACTCA	900
Qy	907	AGGTGCTTCCCTCCAGGAAGCCAGTGAACACAGTTTATTTCCGAAGTGCAGTTTGTCTG	966
Db	901	AGGTGCTTCCCTCCAGGAAGCCAGTGAACACAGTTTATTTCCGAAGTGCAGTTTGTCTG	960
Qy	967	ATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGCTATGAAA	1026
Db	961	ATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGCTATGAAA	1020
Qy	1027	TTGTGATCTAGGCTGCTGGGCTGAATTCCTCTGGAACCTGAGTTTCAACCAACCAATA	1086

RESULT 7
ADP23942
IID ADP23942 standard; cDNA; 3299 BP.
XX
XX ADP23942;
18-NOV-2004 (first entry)
PRO polypeptide encoding cDNA SEQ ID NO:1120.
ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
immunosuppressive; osteopathic; antidiabetic; dermatological;
antipruritic; antiallergic; antiasthmatic; hepatotropic; respiratory;
gene therapy; immune system.
Unidentified.
OS
WO2004041170-A2.
PN
21-MAY-2004.
XX
30-OCT-2003; 2003WO-US034312.
XX
01-NOV-2002; 2002US-0423394P.
XX (GETH) GENENTECH INC.
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI: 2004-419628/39.
XX P-PSDB; ADP23943.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 1; SEQ ID NO 1120; 2940pp; English.
PS
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipruritic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX disease, asthma, allergic rhinitis, atopic dermatitis, food
XX hypersensitivity, urticaria, an immunologic disease of the lung,
XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX pneumonitis, a transplantation associated disease, graft rejection or
XX graft-versus-host disease. The present sequence encodes a PRO protein of
XX the invention.
XX
XX Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;
XX

Db 1021 TTGTGATCTAGGCTGCTGGGTGAATTTCTCCCTCTGGAACTGAGTTACACCACCAATA 1080
Qy 1087 CTGGCAGGTTCCCTGGATCCAGATCTTCTTGCCCAAATCTTTACTTGGGAGATTGCAAACT 1146
Db 1081 CTGGCAGGTTCCCTGGATCCAGATCTTCTTGCCCAAATCTTTACTTGGGAGATTGCAAACT 1140
Qy 1147 GCCACATCTCAGCCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1206
Db 1141 GCCACATCTCAGCCTGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1200
Qy 1207 ATGGCAAAATGGATGATACATACCTTCTCGAAATGACTCCCTTCTGAATGAATGACAAAGCA 1266
Db 1201 ATGGCAAAATGGATGATACATACCTTCTCGAAATGACTCCCTTCTGAATGAATGACAAAGCA 1260
Qy 1267 GGTACCTAGTATAGTTTCCCAAATCTTCTCCCAATCATAGACATGTCAGTAAATATATAT 1326
Db 1261 GGTACCTAGTATAGTTTCCCAAATCTTCTCCCAATCATAGACATGTCAGTAAATATATAT 1320
Qy 1327 TTTTATGGCACACTGGGATTAACCAAGCAAGATTGCTCACTTCTGGAAGCTCATATGACT 1386
Db 1321 TTTTATGGCACACTGGGATTAACCAAGCAAGATTGCTCACTTCTGGAAGCTCATATGACT 1380
Qy 1387 AGAGGCCCTCTTGACTGGAGTAAACAACTCCCTGCCAGTAACTGTGGGAGAGGGGATCA 1446
Db 1381 AGAGGCCCTCTTGACTGGAGTAAACAACTCCCTGCCAGTAACTGTGGGAGAGGGGATCA 1440
Qy 1447 ATATTTTGGCACACTGTATAGGCCATGGGCACACAGCCAGATGCTCTGCTCACAGTCA 1506
Db 1441 ATATTTTGGCACACTGTATAGGCCATGGGCACACAGCCAGATGCTCTGCTCACAGTCA 1500
Qy 1507 GTATGTGTAAGATCCCTGGTCCGTGGCTTCCACACAGCATCTTCAGCAAAATTTAGCAAAA 1566
Db 1501 GTATGTGTAAGATCCCTGGTCCGTGGCTTCCACACAGCATCTTCAGCAAAATTTAGCAAAA 1560
Qy 1567 TGTACCCCTTGCCTGAGGCAGATGAGCCCTTCCCTCCAGTGCATGCTGTGGAGAGCAGA 1626
Db 1561 TGTACCCCTTGCCTGAGGCAGATGAGCCCTTCCCTCCAGTGCATGCTGTGGAGAGCAGA 1620
Qy 1627 ATGTGGCTGCAATATAAGCACACTATCCCTTTGTCTGGGATCTTTGTGAGGGCATAA 1686
Db 1621 ATGTGGCTGCAATATAAGCACACTATCCCTTTGTCTGGGATCTTTGTGAGGGCATAA 1680
Qy 1687 CAGGCTTAGTAAAGTCAAAACACAGATGACAGTGTCTGTGGGTCTCTGTACAGATTGTGG 1746
Db 1681 CAGGCTTAGTAAAGTCAAAACACAGATGACAGTGTCTGTGGGTCTCTGTACAGATTGTGG 1740
Qy 1747 CTCTCAGCCATGAGACACACTCTCCAAATGAGTGTGGAAATGTTCTTTCTGAGGG 1806
Db 1741 CTCTCAGCCATGAGACACACTCTCCAAATGAGTGTGGAAATGTTCTTTCTGAGGG 1800
Qy 1807 TCTAGAGACTGTGGGACACTTTCTTGAGTGCTACTTCAAGCCCTTATAGGATTTTC 1866
Db 1801 TCTAGAGACTGTGGGACACTTTCTTGAGTGCTACTTCAAGCCCTTATAGGATTTTC 1860
Qy 1867 TTTCTGGCCCAAGATTCTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAGAGAGCCAT 1926
Db 1861 TTTCTGGCCCAAGATTCTCTTCTGTATCACTCCAAGCAGCTCAGCAGAGAGAGAGCCAT 1920
Qy 1927 GCCAGTATTCCTCACTCCAAAGGAACTGACAGCTATATATTTCTCACTTCTGGGG 1986
Db 1921 GCCAGTATTCCTCACTCCAAAGGAACTGACAGCTATATATTTCTCACTTCTGGGG 1980
Qy 1987 AACTGGGTATATCCAAACCATCAAAATAGAGACCTTGAAGAGCAGAGTCAATCTCCA 2046
Db 1981 AACTGGGTATATCCAAACCATCAAAATAGAGACCTTGAAGAGCAGAGTCAATCTCCA 2040
Qy 2047 GAAGGAACTTGGGAGATGATGTGTCAGATCATCAAACTGGGTTCATCCAGTTCCAAAGA 2106
Db 2041 GAAGGAACTTGGGAGATGATGTGTCAGATCATCAAACTGGGTTCATCCAGTTCCAAAGA 2100
Qy 2107 CTCAGAGAACTAGATTTAAGCTGAGGCAGATGCGCCACCCCTGCGATGCCCAAC 2166
Db 2101 CTCAGAGAACTAGATTTAAGCTGAGGCAGATGCGCCACCCCTGCGATGCCCAAC 2160

Qy 2167 AGATCACAGCCAGCTTACAGGCAATTAATCTCTCAATGAGGAAGAATCATTCACAA 2226
Db 2161 AGATCACAGCCAGCTTACAGGCAATTAATCTCTCAATGAGGAAGAATCATTCACAA 2220
Qy 2227 CTGAGCAAGCAATTCATATGATCATTTAAGGAAGTGTTCCTTTATGTGTAGCAAGTAT 2286
Db 2221 CTGAGCAAGCAATTCATATGATCATTTAAGGAAGTGTTCCTTTATGTGTAGCAAGTAT 2280
Qy 2287 AATCGGCTAACTCCTAAATCCCAATGATAGTCTTAGCTGGACAGCAATGGGCTGCAT 2346
Db 2281 AATCGGCTAACTCCTAAATCCCAATGATAGTCTTAGCTGGACAGCAATGGGCTGCAT 2340
Qy 2347 TAGCAGATTAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGACCAACTA 2406
Db 2341 TAGCAGATTAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGACCAACTA 2400
Qy 2407 CCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAAAGTGAAGATGTGCATPAATGTCTGC 2466
Db 2401 CCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAAAGTGAAGATGTGCATPAATGTCTGC 2460
Qy 2467 TCTTGTGATGCTCAGGAGCAATTCAGACAGACACTACAGTTAAACGCTGAACCTGCAGC 2526
Db 2461 TCTTGTGATGCTCAGGAGCAATTCAGACAGACACTACAGTTAAACGCTGAACCTGCAGC 2520
Qy 2527 TGCAAGTAAATAGCATGAACAGTCAAGAAATAACCTTATAGGGGGCAGGGCTGAAGCTGG 2586
Db 2521 TGCAAGTAAATAGCATGAACAGTCAAGAAATAACCTTATAGGGGGCAGGGCTGAAGCTGG 2580
Qy 2587 GCCTTGAAGGATGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGCTCCAAAGTGA 2646
Db 2581 GCCTTGAAGGATGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGCTCCAAAGTGA 2640
Qy 2647 GAGAGCATGAATAATGAGCAGGGCCCTGGATCAGTGGGGTGTATTCAGAGCACTCTCC 2706
Db 2641 GAGAGCATGAATAATGAGCAGGGCCCTGGATCAGTGGGGTGTATTCAGAGCACTCTCC 2700
Qy 2707 AGATGCACATGCTATGCTCACAGTCCCTTGCTTGTGTGGCAGAGTGTCCAGCCAGAT 2766
Db 2701 AGATGCACATGCTATGCTCACAGTCCCTTGCTTGTGTGGCAGAGTGTCCAGCCAGAT 2760
Qy 2767 GTGTGCCCCCACCACATGCTCATTTACATGCTTCAATGCCCACCTCAAAAGGTACCTC 2826
Db 2761 GTGTGCCCCCACCACATGCTCATTTACATGCTTCAATGCCCACCTCAAAAGGTACCTC 2820
Qy 2827 TTCTGTAAGCTTTCCCTGCTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC 2886
Db 2821 TTCTGTAAGCTTTCCCTGCTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC 2880
Qy 2887 TGTTTTTTCTCTTTGCTCTTCTATCACTAAAACTCATCTCATTCAGCCCTTACAGCATA 2946
Db 2881 TGTTTTTTCTCTTTGCTCTTCTATCACTAAAACTCATCTCATTCAGCCCTTACAGCATA 2940
Qy 2947 ACTAATATTTGTTTTTCTCTCATCTACATGTTGAGGAATTACAGATAACCGAAGCC 3006
Db 2941 ACTAATATTTGTTTTTCTCTCATCTACATGTTGAGGAATTACAGATAACCGAAGCC 3000
Qy 3007 KGCTGGGTGTGGCTCAGCCTGTGAATCCCAACATTTGGGAGGCCAAGGAGGCGGAT 3066
Db 3001 GGCTGGGTGTGGCTCAGCCTGTGAATCCCAACATTTGGGAGGCCAAGGAGGCGGAT 3060
Qy 3067 CACTGAGGTGAGGATTCGAGATTGCTCTGGCCAACTGTTGTAACCCCAATNTACTA 3126
Db 3061 CACTGAGGTGAGGATTCGAGATTGCTCTGGCCAACTGTTGTAACCCCAATNTACTA 3120
Qy 3127 AAAATACGAATTAGCCAGGTGTGGTGGCACACATCTCTAGTCCCGAG 3173
Db 3121 AAAATACGAATTAGCCAGGTGTGGTGGCACACATCTCTAGTCCCGAG 3167

RESULT 8

AAI72383

ID AAI72383 standard; cDNA; 3300 BP.

XX AAI72383;
 AC 02-MAY-2002 (first entry)
 DT CD84 coding sequence.
 XX SCZ; gene; CD84; platelet; monocyte; circulating B cell; schizophrenia;
 KW allele; polymorphic marker; chromosome 1q22; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 45..1031
 FT CDS /*tag= a
 FT /product= "SCZ"
 FT
 XX WO200202054-A2.
 XX 10-JAN-2002.
 XX 23-APR-2001; 2001WO-US013040.
 XX 21-APR-2000; 2000US-0198873P.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA Brzustowicz LM, Bassett AS;
 XX WPI; 2002-171605/22.
 DR P-PSDB; AAB47878.
 XX Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by
 PT determining presence or absence of an allele of a linked polymorphic
 PT marker present on chromosome 1q22, where the marker is linked to a variant
 PT form of the SCZ gene.
 XX Claim 19; Page 68-70; 82pp; English.
 XX This sequence was isolated using the method of the invention as the SCZ
 CC gene. This sequence has been previously identified as CD84, GenBank
 CC Accession No: NM 003874. CD84 is a 73 kDa antigen present on platelets,
 CC monocytes and circulating B cells. The proteins encoded by this sequence
 CC may be involved in the processes by which the brain responds to
 CC biological stimuli. Therefore they may provide targets for therapeutic
 CC intervention in the treatment of schizophrenia. The SCZ sequence may be
 CC used in a new method of diagnosing susceptibility to schizophrenia in a
 CC patient. The method comprises determining the presence or absence of an
 CC allele of a linked polymorphic marker in the DNA of the patient. The
 CC polymorphic marker is present in chromosome 1q22 and is linked to a gene
 CC (SCZ) having a variant form associated with a phenotype of schizophrenia
 XX Sequence 3300 BP; 957 A; 802 C; 750 G; 791 T; 0 U; 0 Other;
 SQ
 Query Match 99.68; Score 3161.8; DB 6; Length 3300;
 Best Local Similarity 99.88; Pred. No. 0;
 Matches 3160; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CCAGCGCTCCGCTGCTTTTCCACAGAGGTTAGACCCCTGGAAGAGATGGCTCAGCACCACC 66
 DB 1 CCAGCGCTCCGCTGCTTTTCCACAGAGGTTAGACCCCTGGAAGAGATGGCTCAGCACCACC 60
 QY 67 TATGGATCTTGCTCTCTTTGGCTGCAAACTCTGGCGGGAAGCAGCTGGAAAAAGACTCAGAAA 126
 DB 61 TATGGATCTTGCTCTCTTTGGCTGCAAACTCTGGCGGGAAGCAGCTGGAAAAAGACTCAGAAA 120
 QY 127 TCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTAATATCCAGAAC 186
 DB 121 TCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGTAATATCCAGAAC 180
 QY 187 CACGGCAAGTTAAATCATCTGCTGGACTTCTAAACATCTGTTGCTTATGTAACACAG 246
 DB 181 CACGGCAAGTTAAATCATCTGCTGGACTTCTAAACATCTGTTGCTTATGTAACACAG 240

QY 247 GAGACTCAGAAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATTTATTATGAACGATAC 306
 DB 241 GAGACTCAGAAAACAGCACCCGCTAGTTACTGTGACCCACAGAAATTTATTATGAACGATAC 300
 QY 307 ATGCGCTTAGTCCGAACTACATCTGGTCACTTAGCGATCTGAGGATGGAGAGCGCAGGAG 366
 DB 301 ATGCGCTTAGTCCGAACTACATCTGGTCACTTAGCGATCTGAGGATGGAGAGCGCAGGAG 360
 QY 367 ACTCAGAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACCAAGCGCTACAACC 426
 DB 361 ACTCAGAAAGCAGACATAAATACACAGGCTGATCCCTACACACCACCAAGCGCTACAACC 420
 QY 427 TGCAAATCTATCTCGGCTTGGGAAACCAAAAATTACACAGAGTTTAAATGGCATCTGTGA 486
 DB 421 TGCAAATCTATCTCGGCTTGGGAAACCAAAAATTACACAGAGTTTAAATGGCATCTGTGA 480
 QY 487 ACAGCACCTGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGCAT 546
 DB 481 ACAGCACCTGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGCAT 540
 QY 547 ACAATTGGAGTCCCTGGGAGAGAGGGTAATGTCTCTCAAATCTTCCAGACTCTCTGAGG 606
 DB 541 ACAATTGGAGTCCCTGGGAGAGAGGGTAATGTCTCTCAAATCTTCCAGACTCTCTGAGG 600
 QY 607 ACCAAGAGCTGACTTACAGTGTACAGCCAGAACCTCTGTCAGCAACAATTTCTGACTCCA 666
 DB 601 ACCAAGAGCTGACTTACAGTGTACAGCCAGAACCTCTGTCAGCAACAATTTCTGACTCCA 660
 QY 667 TCTTGTCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCGTACTCACCACACCGGGT 726
 DB 661 TCTTGTCCCGGAGCTCTGTGACAGATCGCAATGGGCTTCGTACTCACCACACCGGGT 720
 QY 727 TCGTGAGCGTGTGGCTATGTTCTTCTGCTGTTCTCATTTCTGCTTCTCAGTGTCTTTGT 786
 DB 721 TCGTGAGCGTGTGGCTATGTTCTTCTGCTGTTCTCATTTCTGCTTCTCAGTGTCTTTGT 780
 QY 787 TCGGTTTGTTCAGAGAGACAGAGATGCTGCTCTCAAAGAAAACCATATACATATATCA 846
 DB 781 TCGGTTTGTTCAGAGAGACAGAGATGCTGCTCTCAAAGAAAACCATATACATATATCA 840
 QY 847 TGGCTTCAAGGAAACACCCAGCCAGCAGAGTCCAGAAATCTATGATGAATCTCTGAGTCCA 906
 DB 841 TGGCTTCAAGGAAACACCCAGCCAGCAGAGTCCAGAAATCTATGATGAATCTCTGAGTCCA 900
 QY 907 AGGTGCTTCCCTCCAGAGGAGCCAGTGAACAGCTTTATTCGGAAGTGCAGTTTGTCTG 966
 DB 901 AGGTGCTTCCCTCCAGAGGAGCCAGTGAACAGCTTTATTCGGAAGTGCAGTTTGTCTG 960
 QY 967 ATAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTCTGGGACTTCAAGCTATGAAA 1026
 DB 961 ATAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTCTGGGACTTCAAGCTATGAAA 1020
 QY 1027 TTGTGATCTAGGCTGTGGGCTGAATTTCTCCCTCTCGAAACTGAGTTAACAACCAATA 1086
 DB 1021 TTGTGATCTAGGCTGTGGGCTGAATTTCTCCCTCTCGAAACTGAGTTAACAACCAATA 1080
 QY 1087 CTGGCAGGTTCCCTGATCCAGATCTTCTCTGCGCAACTCTTACTGGGAGATTCGCAACT 1146
 DB 1081 CTGGCAGGTTCCCTGATCCAGATCTTCTCTGCGCAACTCTTACTGGGAGATTCGCAACT 1140
 QY 1147 GCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCTAGCTTTGTGCCCTAA 1206
 DB 1141 GCCACATCTCAGCCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGCTAGCTTTGTGCCCTAA 1200
 QY 1207 ATGGCAAAATGGATGATACCTTTCTCTGAAATGACTCCCTTCTGAAATGAATGAACAGCA 1266
 DB 1201 ATGGCAAAATGGATGATACCTTTCTCTGAAATGACTCCCTTCTGAAATGAATGAACAGCA 1260
 QY 1267 GGTTCCTAGTAGTATTTTCCCAAACTTTCTTCCCATCATAGCAGCATGTAGAAATATAT 1326
 DB 1261 GGTTCCTAGTAGTATTTTCCCAAACTTTCTTCCCATCATAGCAGCATGTAGAAATATAT 1320

QY 1327 TTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCATAGACT 1386
DB 1321 TTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCATAGACT 1380
QY 1387 AGAGGCTCTTGTGACTGAGGTAAACAACCTGGCCAGTAACAGTGTGGGAGAAAGGGGATCA 1446
DB 1381 AGAGGCTCTTGTGACTGAGGTAAACAACCTGGCCAGTAACAGTGTGGGAGAAAGGGGATCA 1440
QY 1447 ATATTTTGCACACCTGTAAATAGCCATGGCACACAGCCCAAGATCTCTGCTCACAGTCA 1506
DB 1441 ATATTTTGCACACCTGTAAATAGCCATGGCACACAGCCCAAGATCTCTGCTCACAGTCA 1500
QY 1507 GTATGTGTGAAGATCCCTGGTGGCCCTTCCACACGATCTTTCAGCAAAATTTAGAAATA 1566
DB 1501 GTATGTGTGAAGATCCCTGGTGGCCCTTCCACACGATCTTTCAGCAAAATTTAGAAATA 1560
QY 1567 TGTACCTTTCGCTTGGGAGATGAGAGCCCTTCCCGAGTGATGCTTGGAGAGCAGA 1626
DB 1561 TGTACCTTTCGCTTGGGAGATGAGAGCCCTTCCCGAGTGATGCTTGGAGAGCAGA 1620
QY 1627 ATGTGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTTGTGCAAGGCGATAA 1686
DB 1621 ATGTGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTTGTGCAAGGCGATAA 1680
QY 1687 CAGGCTTAGTAAGTCCAAACACAGATGACAGTGTCTGTGGGTCTCTGTCAAGTGTGG 1746
DB 1681 CAGGCTTAGTAAGTCCAAACACAGATGACAGTGTCTGTGGGTCTCTGTCAAGTGTGG 1740
QY 1747 CTCTCAGCATGTAGACACA CTCTCCAAATGAGTGTGGAAATGTTCTTCTCAGGG 1806
DB 1741 CTCTCAGCATGTAGACACA CTCTCCAAATGAGTGTGGAAATGTTCTTCTCAGGG 1800
QY 1807 TCTAGAGCTGTGGGACACTTTCTTGGAGTGCTACTTTCAGAGCTTTATAGGAATTTTC 1866
DB 1801 TCTAGAGCTGTGGGACACTTTCTTGGAGTGCTACTTTCAGAGCTTTATAGGAATTTTC 1860
QY 1867 TTTCTGGCCAAAGATTTCCTTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGACGCCAT 1926
DB 1861 TTTCTGGCCAAAGATTTCCTTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGACGCCAT 1920
QY 1927 GCCAGATATCCCATCTCTCCAAAGAACTGACAGCTTATATTTCTACACTTCTGGGG 1986
DB 1921 GCCAGATATTCCTCTCTCCAAAGAACTGACAGCTTATATTTCTCACACTTCTGGGG 1980
QY 1987 AACTGGGTATAATCCAAACCATCAAAATAGAACCTTGCAGAGCAGAGTCACTTCTCCA 2046
DB 1981 AACTGGGTATAATCCAAACCATCAAAATAGAACCTTGCAGAGCAGAGTCACTTCTCCA 2040
QY 2047 GAAGGAACCTGGGAGATGATGTGACAGATGATGAAACTGGGTTTCATCCAGTTCCAAAGA 2106
DB 2041 GAAGGAACCTGGGAGATGATGTGACAGATGATGAAACTGGGTTTCATCCAGTTCCAAAGA 2100
QY 2107 CTCAGAGAACTAGATTTAAGCTGAGGAGAGTGCGGCCACCTGGCATGCCCCCAAAAC 2166
DB 2101 CTCAGAGAACTAGATTTAAGCTGAGGAGAGTGCGGCCACCTGGCATGCCCCCAAAAC 2160
QY 2167 AGATCACAGCAGCTTACACAGGCAATTAACCTCTCTCAATGAGGAAGATCACTTCAAA 2226
DB 2161 AGATCACAGCAGCTTACACAGGCAATTAACCTCTCTCAATGAGGAAGATCACTTCAAA 2220
QY 2227 CTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTAT 2286
DB 2221 CTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTAT 2280
QY 2287 AATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAAT 2346
DB 2281 AATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAAT 2340
QY 2347 TAGGCAGATAAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTA 2406
DB 2341 TAGGCAGATAAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCACCAACTA 2400
QY 2407 CCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCAATATGCTGTC 2466

DB 2401 CCATTAGCACTATGTTAGGAGCTCAAGGCCCAAGTAGAAGATGTGCAATATGCTGTC 2460
QY 2467 TCTTGTGTAGCTCAGGAGACAATTTCCAGCACAGACACTACAGTTAAACGCTCAACTGCAGC 2526
DB 2461 TCTTGTGTAGCTCAGGAGACAATTTCCAGCACAGACACTACAGTTAAACGCTCAACTGCAGC 2520
QY 2527 TGCAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGGCTGAAGCTGG 2586
DB 2521 TGCAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGGCTGAAGCTGG 2580
QY 2587 GCCTTGAAGGATGATGAATAATTTGGATAGAGAAATGAGGAAGACAGAGGCCCTCCAAAGTGA 2646
DB 2581 GCCTTGAAGGATGATGAATAATTTGGATAGAGAAATGAGGAAGACAGAGGCCCTCCAAAGTGA 2640
QY 2647 GAGAGCATGAAATGAGCAGGGGCTGAGTACAGTGGGTGTATTACAGACCACTCTCC 2706
DB 2641 GAGAGCATGAAATGAGCAGGGGCTGAGTACAGTGGGTGTATTACAGACCACTCTCC 2700
QY 2707 AGATGCACATGCTATGCTCACAGTCCCTTGTCTATGTGTGGCAGAGTGTCCAGCCAGAT 2766
DB 2701 AGATGCACATGCTATGCTCACAGTCCCTTGTCTATGTGTGGCAGAGTGTCCAGCCAGAT 2760
QY 2767 GTGTGCCCCCAACCCCATGTCTTCAATGTCTTCAATGCCCACTCAAAGGTACCTC 2826
DB 2761 GTGTGCCCCCAACCCCATGTCTTCAATGTCTTCAATGCCCACTCAAAGGTACCTC 2820
QY 2827 TTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTTCACACTGC 2886
DB 2821 TTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTTCACACTGC 2880
QY 2887 TGTTTTTTCCCTTTTGGTCTTCTATCACTAAAACTCATCTCATTCAGCCTTACAGCATA 2946
DB 2881 TGTTTTTTCCCTTTTGGTCTTCTATCACTAAAACTCATCTCATTCAGCCTTACAGCATA 2940
QY 2947 ACTAATATTTGTTTTTCTCTCATCACTTGTATGTGGGAATTAAGATAACCGAAGCC 3006
DB 2941 ACTAATATTTGTTTTTCTCTCATCACTTGTATGTGGGAATTAAGATAACCGAAGCC 3000
QY 3007 KGCTGGGTGTGGCTCACGCTGTAAATCCCAACACTTTGGAGGCCAAGGCGCGGAT 3066
DB 3001 GGCTGGGTGTGGCTCACGCTGTAAATCCCAACACTTTGGAGGCCAAGGCGCGGAT 3060
QY 3067 CACCTGAGGTGAGGATTTGAGATTTCTGCGCAACATGTGTGAACCCCAATNTNTACTA 3126
DB 3061 CACCTGAGGTGAGGATTTGAGATTTCTGCGCAACATGTGTGAACCCCAATNTNTACTA 3120
QY 3127 AAAATACGAAATTAGCAGGTGTGGTGGCACACATCTGTAGTCCAG 3173
DB 3121 AAAATACGAAATTAGCAGGTGTGGTGGCACACATCTGTAGTCCAG 3167

RESULT 9

ACN92105

ID ACN92105 standard; DNA; 3687 BP.

XX

AC ACN92105;

XX

DT 02-DEC-2004 (first entry)

XX

DE Breast cancer related marker, seq id 13255.

XX

KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX

OS Homo sapiens.

XX

PN US2003099974-A1.

XX

PD 29-MAY-2003.

XX

PF 18-JUL-2002; 2002US-00198846.

XX

PR 18-JUL-2001; 2001US-0306220P.

Db 2071 GGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGTGGTCTCTGTCTGACAGATTGTGGCT 2130
Qy 1749 CTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTTCTGCGAGGTCT 1808
Db 2131 CTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTTCTGCGAGGTCT 2190
Qy 1809 TAGAGACTGTGGGACACTTTTCTTGGAGTGTCTTCTCAGAGCCCTTATAGGATTTCTT 1868
Db 2191 TAGAGACTGTGGGACACTTTTCTTGGAGTGTCTTCTCAGAGCCCTTATAGGATTTCTT 2250
Qy 1869 TCTGGCAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAGCAGCCATGC 1928
Db 2251 TCTGGCAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAGAGCAGCCATGC 2310
Qy 1929 CCAGTATTTCCCACTCTCCAAAGGAACTGACCAAGCTTATTTCTCAGACTTTCTGGGAA 1988
Db 2311 CCAGTATTTCCCACTCTCCAAAGGAACTGACCAAGCTTATTTCTCAGACTTTCTGGGAA 2370
Qy 1989 CTGGGTATTAATCCAAACCATCAAAATAGAAGACTTGCAGAGAGCAGAGTCATTCTCCAGA 2048
Db 2371 CTGGGTATTAATCCAAACCATCAAAATAGAAGACTTGCAGAGAGCAGAGTCATTCTCCAGA 2430
Qy 2049 AGGAATCTGGGAGATGATGGTGAGATGATGAATCTGAGTGTTCATCCAGTTCCTCAAGACT 2108
Db 2431 AGGAATCTGGGAGATGATGGTGAGATGATGAATCTGAGTGTTCATCCAGTTCCTCAAGACT 2490
Qy 2109 CAGAGAACTAGAGTTTAACTGAGGAGAGTGGCGCCACCTGGCATGCGCCCAACAACAG 2168
Db 2491 CAGAGAACTAGAGTTTAACTGAGGAGAGTGGCGCCACCTGGCATGCGCCCAACAACAG 2550
Qy 2169 ATCACCAGCAGCTTACACAGGATTAATCTCTCTCAATGAGAGAGAAATCAATTCACAACT 2228
Db 2551 ATCACCAGCAGCTTACACAGGATTAATCTCTCTCAATGAGAGAGAAATCAATTCACAACT 2610
Qy 2229 GAGCAAGACATTCATATGATCAATTAAGAAAGTGTTCCTTATGTGTAGCAAGTATAA 2288
Db 2611 GAGCAAGACATTCATATGATCAATTAAGAAAGTGTTCCTTATGTGTAGCAAGTATAA 2670
Qy 2289 TGGCTAACTCTTAATCCCAATGATAGTCTAGGCTGGAGAGCAATGGGCTGCAATTA 2348
Db 2671 TGGCTAACTCTTAATCCCAATGATAGTCTAGGCTGGAGAGCAATGGGCTGCAATTA 2730
Qy 2349 GGCAGATAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCACACTACC 2408
Db 2731 GGCAGATAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCACACTACC 2790
Qy 2409 ATTAGCACTATGTTAGGAGCTGAGGCCCCAAAGTAGAAGATGTGCATATGTCTGCTC 2468
Db 2791 ATTAGCACTATGTTAGGAGCTGAGGCCCCAAAGTAGAAGATGTGCATATGTCTGCTC 2850
Qy 2469 TTGTGTAGCTCAGGAGACAAATCCAGCAGACACACTACAGTTTAAACGCTGAACCTGCAGCTG 2528
Db 2851 TTGTGTAGCTCAGGAGACAAATCCAGCAGACACACTACAGTTTAAACGCTGAACCTGCAGCTG 2910
Qy 2529 CAAGTAATAGCATGAACAGTCAGAAAATAACCTTATGAGGGGCGAGGCTGAAGCTGGGC 2588
Db 2911 CAAGTAATAGCATGAACAGTCAGAAAATAACCTTATGAGGGGCGAGGCTGAAGCTGGGC 2970
Qy 2589 CTTGAAGATGATGAAATTTGGATAGAGAAATGAGAGAGAGAGAGGCGCTCCAAAGTGAGA 2648
Db 2971 CTTGAAGATGATGAAATTTGGATAGAGAAATGAGAGAGAGAGGCGCTCCAAAGTGAGA 3030
Qy 2649 GAAGCATGAAAATGAGCAGGGGCGCTGGATCAGTGGGTGTTATTCAGAGCACTCTCCAG 2708
Db 3031 GAAGCATGAAAATGAGCAGGGGCGCTGGATCAGTGGGTGTTATTCAGAGCACTCTCCAG 3090
Qy 2709 ATGCACCATGCTCAGTCCCTTGTGCTATGTGTGGCAGAGTGTCCAGCCAGATGT 2768
Db 3091 ATGCACCATGCTCAGTCCCTTGTGCTATGTGTGGCAGAGTGTCCAGCCAGATGT 3150
Qy 2769 GTGCCCCCAGCCCATGTCAATTTACATGTCTTCAATGCCCACTCAAAAGTACTCTTT 2828
Db 3151 GTGCCCCCAGCCCATGTCCATTTACATGTCTTCAATGCCCACTCAAAAGTACTCTTT 3210

RESULT 10

ADQ23399

ID ADQ23399 standard; DNA; 3326 BP.

XX AC ADQ23399;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6219.

XX KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; ds.

XX OS Homo sapiens.

XX PN WO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnik A;

XX DR WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

XX Example 2; SEQ ID NO 6219; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated

|||||
2069 AAGAACTTGGGAGATGATGGTGACAGATGATGAACCTGGGTTTCATCCCGATGTTCCAAAGAC 2128
|||||
2108 TCAGAGAACTAGAGTTTAAAGCTGAGGAGAGAGTGGCCACCTGGCATGCCCAACAAACA 2167
|||||
2129 TCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGGCCACCTGGCATGCCCAACAAACA 2188
|||||
2168 GATCACCAGGAGCTTACACAGGCATTAACTCTCTCAATGAGGAAGAAATCATTCACAAC 2227
|||||
2189 GATCACCAGGAGCTTACACAGGCATTAACTCTCTCAATGAGGAAGAAATCATTCACAAC 2248
|||||
2228 TGAGCAAGACATTTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTGTACCAAGTATA 2287
|||||
2249 TGAGCAAGACATTTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTGTACCAAGTATA 2308
|||||
2288 ATCGGCTAACTCCTAAATCCCAATGAATAGTCTCTAGGCTGGACAGCAATGGGCTGCAATT 2347
|||||
2309 ATCGGCTAACTCCTAAATCCCAATGAATAGTCTCTAGGCTGGACAGCAATGGGCTGCAATT 2368
|||||
2348 AGGCAGATAAGACATCAGTCCAGTAATGAATCCATAGACTCATCTAGCAACCAACTAC 2407
|||||
2369 AGGCAGATAAGACATCAGTCCAGTAATGAATCCATAGACTCATCTAGCAACCAACTAC 2428
|||||
2408 CATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATATATGCTGCT 2467
|||||
2429 CATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATATATGCTGCT 2488
|||||
2468 CTTGTAGCTCAGGAGACAAATCCAGCAAGACACTACAGTTAAACGCTGAACTCAGCT 2527
|||||
2489 CTTGTAGCTCAGGAGACAAATCCAGCAAGACACTACAGTTNNNNNNNNNNNNNNNN 2548
|||||
2528 GCAAGTAATAGCATGAACAGTCCAGAAATACCTTATGAGGGGCGAGGCTGCAAGCTGGG 2587
|||||
2549 GCAAGTAATAGCATGAACAGTCCAGAAATACCTTATGAGGGGCGAGGCTGCAAGCTGGG 2608
|||||
2588 CTTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGCCTCCAAAGTCAG 2647
|||||
2609 CTTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGCCTCCAAAGTCAG 2668
|||||
2648 AGAAGCATGAAAATAGCAGGGGCTGGATCAGTGGGGTGATTTACAGACACCTCTCCA 2707
|||||
2669 AGAAGCATGAAAATAGCAGGGGCTGGATCAGTGGGGTGATTTACAGACACCTCTCCA 2728
|||||
2708 GATGACCATGATGCTCAGCTCCCTGCTATGTTGGCAGAGTGTCCAGACCCAGATG 2767
|||||
2729 GATGACCATGATGCTCAGCTCCCTGCTATGTTGGCAGAGTGTCCAGACCCAGATG 2788
|||||
2768 TGTGCCCCCACCCTCATGTTCAATTTACATGTCCTTCAATGCCACCTCAAAAGGTACCTCT 2827
|||||
2789 TGTGCCCCCACCCTCATGTTCAATTTACATGTCCTTCAATGCCACCTCAAAAGGTACCTCT 2848
|||||
2828 TCTGTAAGCTTTCCTGATCAGGAATCAAAATTAATCAGGGATCTTTTACACTGCT 2887
|||||
2849 TCTGTAAGCTTTCCTGATCAGGAATCAAAATTAATCAGGGATCTTTTACACTGCT 2908
|||||
2888 GTTTTTCCTCTTGGTCTCTATCACTAAACTCATCTCAATCAGCTTACAGCATAA 2947
|||||
2909 GTTTTTCCTCTTGGTCTCTATCACTAAACTCATCTCAATCAGCTTACAGCATAA 2968
|||||
2948 CTAATATTTGTTTTCCTCACTACATTTGATGTTGGAATTTACAGATAAAACGGAAGCC 3007
|||||
2969 CTAATATTTGTTTTCCTCACTACATTTGATGTTGGAATTTACAGATAAAACGGAAGCC 3028
|||||
3008 GCTGGGGTGGGCTCAGCCCTGTAATCCACACTTTGGGAGCCAGGAGGCGATC 3067
|||||
3029 GCTGGGGTGGGCTCAGCCCTGTAATCCACACTTTGGGAGCCAGGAGGCGGATC 3088
|||||
3068 ACCTGAGGTCAGGATTTGAGATTTCTGGCAACATGTTGCAACCCCATTTTACTAA 3127
|||||
3089 ACCTGAGGTCAGGATTTGAGATTTCTGGCAACATGTTGCAACCCCATTTTACTAA 3148
|||||
3128 AATACGAAATAGCCAGGTGGTGCCACACATCTGTAGTCCGAG 3173
|||||

Db 3149 AATACGAAATAGCCAGGTGGTGCCACACATCTGTAGTCCGAG 3194

RESULT 11
ADO05707
ID ADO05707 standard; DNA; 1067 BP.
XX ADO05707;
AC ADO05707;
DT 15-JUL-2004 (first entry)
XX Human leukocyte differentiation antigen CD84 encoding DNA.
XX T cell; antiallergic; immunosuppressive; virucide; antibacterial;
KW antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds;
KW leukocyte differentiation antigen.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 70..1056
FT /*tag= a
FT /product= "CD84"
FT
XX WO2004032867-A2.
XX 22-APR-2004.
XX 09-OCT-2003; 2003WO-US032065.
XX 09-OCT-2002; 2002US-0417102P.
XX 09-OCT-2002; 2002US-0417103P.
XX 09-OCT-2002; 2002US-0417243P.
XX 18-OCT-2002; 2002US-0419575P.
XX 08-NOV-2002; 2002US-0424777P.
XX 08-NOV-2002; 2002US-0424881P.
XX (TOLE-) TOLERRX INC.
XX Rao P, Szymanska G;
XX WPI; 2004-340801/31.
XX P-PSDB; ADO05708.
XX GENBANK; 6650105.
XX
PT Treating a condition that benefits from modulating regulatory or effector
PT T cell function comprises administering an agent that modulates the
PT expression or activity of a gene or polypeptide (e.g. PTER2, TGFbeta1,
PT Jagged-1 or GPR-32).
XX
PS Example; SEQ ID NO 7; 161pp; English.
XX
XX The invention relates to treating a subject having a condition that
XX benefits from modulating the balance of regulatory T cell function
XX relative to effector T cell function, or vice versa, in a subject. The
XX method involves administering an agent that modulates the expression or
XX activity of a molecule selected from PTER2 and TGFbeta1, or Jagged-1,
XX GPR-32, CD83, CD84, CD89, serotonin R, B155, serotonin R2C, GPR63,
XX histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PDE-4d, and PI-
XX 3-related kinase to the subject, such that treatment occurs. The methods
XX are useful for diagnosing, preventing or treating conditions
XX characterized by a too-vigorous or weak effector T cell or regulatory T
XX cell response to antigens associated with the condition, such as in an
XX allergic response, an autoimmune disorder, a viral infection, a microbial
XX infection, a parasitic infection or a tumour. The present sequence
XX represents a DNA encoding a human leukocyte differentiation CD84 antigen,
XX preferentially expressed in regulatory T cells.
SQ Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;

Query Match 32.6%; Score 1034; DB 12; Length 1067;
Best Local Similarity 100.0%; Pred. No. 4.4e-307;
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 CCGTCTTTTCCACAGAGGTTAGACCTGGAAGAGATGGCTCAGACACACCTATGGATC 74
34 CCGTCTTTTCCACAGAGGTTAGACCTGGAAGAGATGGCTCAGACACACCTATGGATC 93
75 TTGCTCTTTGCTGCAAACTGGCGGAAGCAGCTGGAAGAGACTCAGAAATCTTTCACA 134
94 TTGCTCTTTGCTGCAAACTGGCGGAAGCAGCTGGAAGAGACTCAGAAATCTTTCACA 153
135 GTGAATGGGATTTGGAGAGTCACTCTTCCCTGTTAAATATATCAAGAACACCGGCAA 194
154 GTGAATGGGATTTGGAGAGTCACTCTTCCCTGTTAAATATATCAAGAACACCGGCAA 213
195 GTTAAATCATTTGCTGGAGTCTTAAACATCTGTTGCTTATGTATCAACACGAGACTCA 254
214 GTTAAATCATTTGCTGGAGTCTTAAACATCTGTTGCTTATGTATCAACACGAGACTCA 273
255 GAAACAGACCCGTAGTTACTGTGACCCACAGAAATTTATGAAACGATACATGCTTTA 314
274 GAAACAGACCCGTAGTTACTGTGACCCACAGAAATTTATGAAACGATACATGCTTTA 333
315 GGTCCGAATCAATCTGTCATTTAGCGATCTGAGATGGAAGACCGAGAGACTACAAA 374
334 GGTCCGAATCAATCTGTCATTTAGCGATCTGAGATGGAAGACCGAGAGACTACAAA 393
375 GCAGACATTAATACAGAGTGTATCCCTACACACCAAGCGCTACACCTGCAAAATC 434
394 GCAGACATTAATACAGAGTGTATCCCTACACACCAAGCGCTACACCTGCAAAATC 453
435 TATCGTCGGCTTGGGAAACCAAAATTTACACAGATTTTAAATGGCATCTGTGAACAGCACC 494
454 TATCGTCGGCTTGGGAAACCAAAATTTACACAGATTTTAAATGGCATCTGTGAACAGCACC 513
495 TGTAAATGTCACTGATCTCTGTAGAGAAAGAAAGAAATGTGACATCAATTTGG 554
514 TGTAAATGTCACTGATCTCTGTAGAGAAAGAAAGAAATGTGACATCAATTTGG 573
555 AGTCCCTGGGAGAGAGGTTATGCTTCAATCTTCCAGACTCTCGAGGACCAAGAG 614
574 AGTCCCTGGGAGAGGTTATGCTTCAATCTTCCAGACTCTCGAGGACCAAGAG 633
615 CTGACTTTACAGTGTACAGCCAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC 674
634 CTGACTTTACAGTGTACAGCCAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC 693
675 CGGAGCTCTGTGCAGACATCGCAATGGGCTTCGTAATCCGTAATCCGAGTCCGAGC 734
694 CGGAGCTCTGTGCAGACATCGCAATGGGCTTCGTAATCCGTAATCCGAGTCCGAGC 753
735 GTGCTGGCTATGTTCTTCTGCTGTTCTCAATCTGCTTCACTGTTTGTTCGTTTG 794
754 GTGCTGGCTATGTTCTTCTGCTGTTCTCAATCTGCTTCACTGTTTGTTCGTTTG 813
795 TTCAAGAGAGACAGAGTGTGCTCAAGAAACCAATATACATATATCATGGCTTCA 854
814 TTCAAGAGAGACAGAGTGTGCTCAAGAAACCAATATACATATATCATGGCTTCA 873
855 AGGAACACCCAGCCAGAGAGTCCAGAAATCTATGATGAATCTCTGAGTCCAGAGTGTCT 914
874 AGGAACACCCAGCCAGAGAGTCCAGAAATCTATGATGAATCTCTGAGTCCAGAGTGTCT 933
915 CCCTCCAGAGAGAGCCAGTGAACACAGTTTATTCGAGTGCAGTTTGTGATGAAGATG 974
934 CCCTCCAGAGAGAGCCAGTGAACACAGTTTATTCGAGTGCAGTTTGTGATGAAGATG 993
975 GGGAAAGCCAGACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGATC 1034
994 GGGAAAGCCAGACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGATC 1053
1035 TAGGCTCTGGCT 1048
1054 TAGGCTCTGGCT 1067

RESULT 12
ADQ19066
ID ADQ19066 standard; DNA; 1067 BP.
XX
AC ADQ19066;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1885.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
XX WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
of a gene in a first soft tissue sample and a normal soft tissue sample
and comparing the gene expression, also useful in treating soft tissue
sarcoma.
XX
PS Example 2; SEQ ID NO 1885; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
which comprises obtaining a first soft tissue sample from an individual
and a normal soft tissue sample from the same or different individual,
determining the expression of a gene in both samples and comparing the
expression of the gene in both soft tissue samples, where a higher level
of protein expression in the first soft tissue sample indicates the
presence of soft tissue sarcoma. The method of the invention has
cytostatic applications and may be useful for detecting soft tissue
sarcoma, possibly via gene therapy or vaccine production. The nucleic
acid sequences may be useful in diagnostic and screening applications.
The current sequence is that of a human soft tissue sarcoma-upregulated
DNA of the invention. The current sequence is not shown within the
specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;
Query Match 32.6%; Score 1034; DB 12; Length 1067;
Best Local Similarity 100.0%; Pred. No. 4-4e-307;
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CCGTCTTTTCCACAGAGGTTAGACCTGGAAGAGATGGCTCAGACACACCTATGGATC 74
DB 34 CCGTCTTTTCCACAGAGGTTAGACCTGGAAGAGATGGCTCAGACACACCTATGGATC 93
QY 75 TTGCTCTTTGCTGCAAACTGGCGGAAGCAGCTGGAAGAGACTCAGAAATCTTTCACA 134
DB 94 TTGCTCTTTGCTGCAAACTGGCGGAAGCAGCTGGAAGAGACTCAGAAATCTTTCACA 153
QY 135 GTGAATGGGATTTGGAGAGTCACTCTTCCCTGTTAAATATATCAAGAACACCGGCAA 194
DB 154 GTGAATGGGATTTGGAGAGTCACTCTTCCCTGTTAAATATATCAAGAACACCGGCAA 213
QY 195 GTTAAATCATTTGCTGGAGTCTTAAACATCTGTTGCTTATGTATCAACACGAGACTCA 254
DB 214 GTTAAATCATTTGCTGGAGTCTTAAACATCTGTTGCTTATGTATCAACACGAGACTCA 273

```
QY 255 GAAACAGCAGCCCGTACTGTGACCCACAGAAATTTATGAAACGGATACATGCTTGA 314
|
|
|
Db 274 GAAACAGCAGCCCGTACTGTGACCCACAGAAATTTATGAAACGGATACATGCTTGA 333
|
|
|
QY 315 GGTCCGAATACAAATCTGGTTCATTTAGCGATCTGAGGATGGAAGACCGACGAGACTACAAA 374
|
|
|
Db 334 GGTCCGAATACAAATCTGGTTCATTTAGCGATCTGAGGATGGAAGACCGACGAGACTACAAA 393
|
|
|
QY 375 GCAGACATAAATACACAGCTGTATCCCTACACACCAACGCGCTACAACTGCAAAATC 434
|
|
|
Db 394 GCAGACATAAATACACAGCTGTATCCCTACACACCAACGCGCTACAACTGCAAAATC 453
|
|
|
QY 435 TATCGTCGGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCATCTGTGACAGCACC 494
|
|
|
Db 454 TATCGTCGGCTTGGGAAACCAAAATTTACACAGAGTTTAAATGGCATCTGTGACAGCACC 513
|
|
|
QY 495 TGTAAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAATGTGACATACAAATGG 554
|
|
|
Db 514 TGTAAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAATGTGACATACAAATGG 573
|
|
|
QY 555 AGTCCCTCGGAGAGAGGGTAAATGTCCTTCAAAATCTTCCAGACTCTGAGGACCAAGAG 614
|
|
|
Db 574 AGTCCCTCGGAGAGAGGGTAAATGTCCTTCAAAATCTTCCAGACTCTGAGGACCAAGAG 633
|
|
|
QY 615 CTGACTTACACGCTGACAGCCAGACCCCTGTGACGACCAATTTCTGACTCCATCTCGCC 674
|
|
|
Db 634 CTGACTTACACGCTGACAGCCAGACCCCTGTGACGACCAATTTCTGACTCCATCTCGCC 693
|
|
|
QY 675 CGGAGCTCTGTGCAGACATCGCAATGGCTTCCGTACTCACACACCGGGTTGCTGAGC 734
|
|
|
Db 694 CGGAGCTCTGTGCAGACATCGCAATGGCTTCCGTACTCACACACCGGGTTGCTGAGC 753
|
|
|
QY 735 GTGCTGGCTATGTTCTTCTGCTGTTCTCATTCTGCTTCAAGTGTGTTTGTTCGGTTG 794
|
|
|
Db 754 GTGCTGGCTATGTTCTTCTGCTGTTCTCATTCTGCTTCAAGTGTGTTTGTTCGGTTG 813
|
|
|
QY 795 TTCAAGAGAGCAAGATCGCTCCAAAGAAACCATATACATATATCATGCTTCA 854
|
|
|
Db 814 TTCAAGAGAGCAAGATCGCTCCAAAGAAACCATATACATATATCATGCTTCA 873
|
|
|
QY 855 AGGAACACCCAGCCAGCAGATCCAGAAATCTATGATGAATCTTGCAGTCCAAAGTGTCT 914
|
|
|
Db 874 AGGAACACCCAGCCAGCAGATCCAGAAATCTATGATGAATCTTGCAGTCCAAAGTGTCT 933
|
|
|
QY 915 CCTTCAAGAGAGCCAGTGAACAGATTTATTCGAGTGCAGTTCGCTGATGAATG 974
|
|
|
Db 934 CCTTCAAGAGAGCCAGTGAACAGATTTATTCGAGTGCAGTTCGCTGATGAATG 993
|
|
|
QY 975 GGGAAAGCCAGCACAGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC 1034
|
|
|
Db 994 GGGAAAGCCAGCACAGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC 1053
|
|
|
QY 1035 TAGGCTGTGGGT 1048
|
|
|
Db 1054 TAGGCTGTGGGT 1067
|
|
|
```

RESULT 13

AAD43563

ID AAD43563 standard; DNA; 1040 BP.

XX

AC AAD43563;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human CD84 DNA.

XX

Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatocellular carcinoma; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis;

diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; anti-inflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 42..1028

/*tag= a

/product= "Human CD84 protein"

EP1223218-A1.

17-JUL-2002.

02-NOV-2001; 2001EP-00309339.

03-NOV-2000; 2000US-00706167.

(MILL-) MILLENNIUM PHARM INC.

Fraser CC;

WPI; 2002-620680/67.

P-PSDB; AAE26238.

Novel isolated polypeptide containing immunoglobulin and immunoglobulin-like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders.

Disclosure; Page 76; 138pp; English.

The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. asthma and psoriasis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is used in gene therapy. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 DNA used in the invention

Sequence 1040 BP; 308 A; 256 C; 231 G; 245 T; 0 U; 0 Other;

Query Match

Best Local Similarity 32.6%; Score 1033.4; DB 6; Length 1040;

Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CCGTGCCTTTCCACAGAGGTTAGACCCCTGGAAGAGATGGCTACGCCACCTATGATC 74

Db 6 CGGTGCTTTTCCACAGAGGTTAGACCCCTGGAAGAGATGGCTACGCCACCTATGATC 65

QY 75 TTGTCCTCTTCCCTGCAAACTGCGGAGACAGCTGGAAGAGACTCAGAATCTTACA 134

Db 66 TTGTCCTCTTCCCTGCAAACTGCGGAGACAGCTGGAAGAGACTCAGAATCTTACA 125

QY 135 GTGAATGGGATTCGGGAGAGTCACTTCCCTCTTAAATATCCAAAGACACCGCAA 194

PR	06-JUN-1997;	97US-0048964P.
PR	06-JUN-1997;	97US-0048974P.
PR	13-JUN-1997;	97US-0049610P.
PR	08-JUL-1997;	97US-0051928P.
PR	16-JUL-1997;	97US-0052874P.
PR	18-AUG-1997;	97US-0055724P.
PR	22-AUG-1997;	97US-0056630P.
PR	22-AUG-1997;	97US-0056631P.
PR	22-AUG-1997;	97US-0056632P.
PR	22-AUG-1997;	97US-0056636P.
PR	22-AUG-1997;	97US-0056637P.
PR	22-AUG-1997;	97US-0056662P.
PR	22-AUG-1997;	97US-0056664P.
PR	22-AUG-1997;	97US-0056845P.
PR	22-AUG-1997;	97US-0056862P.
PR	22-AUG-1997;	97US-0056864P.
PR	22-AUG-1997;	97US-0056872P.
PR	22-AUG-1997;	97US-0056874P.
PR	22-AUG-1997;	97US-0056875P.
PR	22-AUG-1997;	97US-0056877P.
PR	22-AUG-1997;	97US-0056878P.
PR	22-AUG-1997;	97US-0056879P.
PR	22-AUG-1997;	97US-0056880P.
PR	22-AUG-1997;	97US-0056881P.
PR	22-AUG-1997;	97US-0056882P.
PR	22-AUG-1997;	97US-0056884P.
PR	22-AUG-1997;	97US-0056886P.
PR	22-AUG-1997;	97US-0056887P.
PR	22-AUG-1997;	97US-0056888P.
PR	22-AUG-1997;	97US-0056889P.
PR	22-AUG-1997;	97US-0056892P.
PR	22-AUG-1997;	97US-0056893P.
PR	22-AUG-1997;	97US-0056894P.
PR	22-AUG-1997;	97US-0056903P.
PR	22-AUG-1997;	97US-0056908P.
PR	22-AUG-1997;	97US-0056909P.
PR	22-AUG-1997;	97US-0056910P.
PR	22-AUG-1997;	97US-0056911P.
PR	05-SEP-1997;	97US-0057650P.
PR	05-SEP-1997;	97US-0057663P.
PR	05-SEP-1997;	97US-0057761P.
PR	12-SEP-1997;	97US-0058785P.
PR	02-OCT-1997;	97US-0061060P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;	
PI	Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;	
PI	Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;	
PI	Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H,	
XX		
DR	WPI; 1998-506364/43.	
DR	P-PSDB; AAW75010.	
XX		
PT	New isolated human genes and the secreted polypeptide(s) they encode -	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
XX	Claim 1; Page 526-527; 721pp; English.	
XX		
CC	This sequence represents a nucleic acid molecule designated Gene 164 from	
CC	the human cDNA clone HSAW26 (deposited as clone ATCC 97903 and ATCC	
CC	209049) which encodes a secreted human protein. The gene can be used to	
CC	generate fusion proteins by linking to the gene to a human immunoglobulin	
CC	Fc portion (e.g. AAV59502) for increasing the stability of the fused	
CC	protein as compared to the human protein only. The invention relates to	
CC	186 novel genes and their fragments (nucleic acid sequences: AAV59511-	
CC	V59812; amino acid sequences AAW74731-W75026) which are useful for	
CC	preventing, treating or ameliorating medical conditions e.g. by protein	
CC	or gene therapy. Also, pathological conditions can be diagnosed by	
CC	determining the amount of the new polypeptides in a sample or by	
CC	determining the presence of mutations in the new polynucleotides.	

CC	Specific uses are described for each of the 186 polynucleotides, based on		
CC	which tissues they are most highly expressed in (see AAV59511 for		
CC	described uses)		
XX			
SQ	Sequence 828 BP; 247 A; 198 C; 172 G; 204 T; 0 U; 7 Other;		
	Query Match 25.6%; Score 813; DB 2; Length 828;		
	Best Local Similarity 99.2%; Pred. No. 4.7e-239;		
	Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;		
Qy	2146 ACCCTGGCATGCCCAACAGATACACGAGCTTACACAGGCATTAATCTCTCA	2205	
Db	1 ACCCTGGCATGCCCAACAGATACACGAGCTTACACAGGCATTAATCTCTCA	60	
Qy	2206 ATGAGGAAGATCAATTCACAACTGAGCAAGATTCATATGATCATTTAAGGAAGTGT	2265	
Db	61 ATGAGGAAGATCAATTCACAACTGAGCAAGATTCATATGATCATTTAAGGAAGTGT	120	
Qy	2266 CCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGC	2325	
Db	121 CCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATGAATAGTCTAGGC	180	
Qy	2326 TGGACAGCAATGGCTGCAATTTAGGAGATTAAGACATCAGTCCAGTAAATGATCCAT	2385	
Db	181 TGGACAGCAATGGCTGCAATTTAGGAGATTAAGACATCAGTCCAGTAAATGATCCAT	240	
Qy	2386 AGACTCATCTAGCAACCACTACCACTATGTTAGGAGCTGCAAGGCCCAAGTA	2445	
Db	241 AGACTCATCTAGCAACCACTACCACTATGTTAGGAGCTGCAAGGCCCAAGTA	300	
Qy	2446 GAAGATGTGCATAATGTCTCTTGTGTAGCTCAGGAGACAATTCACAGCACACACTA	2505	
Db	301 GAAGATGTGCATAATGTCTCTTGTGTAGCTCAGGAGACAATTCACAGCACACACTA	360	
Qy	2506 CAGTTAACGCTGAATCGAGCTGCAAGTAAATAGATGAACAGTACAGAAAATACCTTATG	2565	
Db	361 CAGTTAACGCTGAATCGAGCTGCAAGTAAATAGATGAACAGTACAGAAAATACCTTATG	420	
Qy	2566 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGATGGATGAAATTTGGATAGAGATGAGGA	2625	
Db	421 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGATGGATGAAATTTGGATAGAGATGAGGA	480	
Qy	2626 AGACAGAGGGCTCCAAAGTGAGAGAAGCATGAAAATGAGCAGGGGCTGAGTACAGTGGG	2685	
Db	481 AGACAGAGGGCTCCAAAGTGAGAGAAGCATGAAAATGAGCAGGGGCTGAGTACAGTGGG	540	
Qy	2686 GTGTATTACAGACACCTCTCCAGATGCACCATGCTCAGTCCCTCCCTTCCCTATGTGT	2745	
Db	541 GTGTATTACAGACACCTCTCCAGATGCACCATGCTCAGTCCCTCCCTTCCCTATGTGT	600	
Qy	2746 GGCAGAGTGTCCAGCAGCATGTGTGCCCCCACCACCCATGTCCATTTACATGTCTTCAAT	2805	
Db	601 GGCAGAGTGTCCAGCAGCATGTGTGCCCCCACCACCCATGTCCATTTACATGTCTTCAAT	660	
Qy	2806 GCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCTTCCCTTCCCTTCAAAATTA	2864	
Db	661 GCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCTTCCCTTCCCTTCAAAATTA	720	
Qy	2865 ATCAGGAGTCTTTTTCACACTGCTGTTTTTCTTGGTCTTCTTATCAGTAAACTCA	2924	
Db	721 ATCAGGAGTCTTTTTCACACTGCTGTTTTTCTTGGTCTTCTTATCAGTAAACTCA	780	
Qy	2925 TCTCATTCAGGCTTACAGCATAAATTAATTTTGTTCCTTCCCTCACTACA	2972	
Db	781 TCTCATTCAGGCTTACAGCATAAATTAATTTTGTTCCTTCCCTCACTACA	828	
RESULT 15			
ABS73790			
ID	ABS73790 standard; cDNA; 828 BP.		
XX	ABS73790;		
XX	XX		

CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents a cDNA derived from a gene
CC encoding one of the novel human secreted proteins of the invention. Note:
CC This sequence did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=6420526B1
XX
SQ Sequence 828 BP; 247 A; 198 C; 172 G; 204 T; 0 U; 7 Other;

Query Match 25.6%; Score 813; DB 6; Length 828;
Best Local Similarity 99.2%; Pred. No. 4.7e-239;
Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2146 ACCCTGGCATGCCCAACACAGATCACCGCCAGCTTACACAGGCATTAACTCTCCTCA 2205
Db 1 ACCTGGCATGCCCAACACAGATCACCGCCAGCTTACACAGGCATTAACTCTCCTCA 60

QY 2206 ATGAGGAAGAATCATTCAACACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGT 2265
Db 61 ATGAGGAAGAATCATTCAACACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGT 120

QY 2266 CCCTTATGTTAGCAAGTATTAATCGGCTAACTCCCTAAATCCCAATGAATAGTCTTAGGC 2325
Db 121 CCCTTATGTTAGCAAGTATTAATCGGCTAACTCCCTAAATCCCAATGAATAGTCTTAGGC 180

QY 2326 TGGACAGCAATGGCTGCAATTAGGCAGATAAGACATCAGTCCAGTAATAATGAATCCAT 2385
Db 181 TGGACAGCAATGGCTGCAATTAGGCAGATAAGACATCAGTCCAGTAATAATGAATCCAT 240

QY 2386 AGACTCATCTAGACCAACTACCATTTAGCACTATGTTAGAGCTGCAAGGCCCAAGTA 2445
Db 241 AGACTCATCTAGACCAACTACCATTTAGCACTATGTTAGAGCTGCAAGGCCCAAGTA 300

QY 2446 GAAGATGTGCATTAATCTCTGCTCTGTGTAGCTCAGGACACAATCCAGCACAGACACTA 2505
Db 301 GAAGATGTGCATTAATCTCTGCTCTGTGTAGCTCAGGACACAATCCAGCACAGACACTA 360

QY 2506 CAGTTAACGCTGAACCTGCAGCTCCAAGTAATAGCATGAACAGTCAGAAAAATACCTTAG 2565
Db 361 CAGTTAACGCTGAACCTGCAGCTCCAAGTAATAGCATGAACAGTCAGAAAAATACCTTAG 420

QY 2566 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGA 2625
Db 421 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGA 480

QY 2626 AGACAGAGGGCTCCCAAGTCAGAGAGACATGAAAAATGACAGGGGCTGGATCAGTGGG 2685
Db 481 AGACAGAGGGCTCCCAAGTCAGAGAGACATGAAAAATGACAGGGGCTGGATCAGTGGG 540

QY 2686 GTGTATTACAGACACCTCTCCAGATGCCATGCGATGCTCAGAGTCCCTTGCCTTAGTGT 2745
Db 541 GTGTATTACAGACACCTCTCCAGATGCCATGCGATGCTCAGAGTCCCTTGCCTTAGTGT 600

QY 2746 GGCAGAGTGTCCAGCCAGATGTGCCCCACCCCATGTCCATTTACATGTCCTTCAAT 2805
Db 601 GGCAGAGTGTCCAGCCAGATGTGCCCCACCCCATGTCCATTTACATGTCCTTCAAT 660

QY 2806 GCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCT -GGTATCAGGAATCAAAATTA 2864
Db 661 GCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCTKGGTATCAGGAATCAAAATTA 720

QY 2865 ATCAGGATCTTTTACAGCTGTGTTTTTTCCTTTTGGTCTCTATCACTAAACTCA 2924

Db 721 ATCAGGGATCTTTTCACACTGTGTTTTTTTCCCTCTTTGGTCTTCTATCACTAAACTCA 780
QY 2925 TCTCATTCAGCCTTACAGCATAACTAATATTTTGTCTTCTCACTACA 2972
Db 781 TCTCATTCAGCCTTACAGCATAACTAATATTTTGTCTTCTCACTACA 828

Search completed: February 5, 2005, 14:34:42
Job time : 1608 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2005, 14:34:44 ; Search time 504 Seconds
(without alignments)
10301.401 Million cell updates/sec

Title: US-09-882-171-174
Perfect score: 3173
Sequence: 1 tcgacccacagcgctcggtgc.....gcacacatctgtagtcctccag 3173

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3169.4	99.9	3173	3	US-09-149-476-174 Sequence 174, App
2	3161.8	99.6	3299	4	US-09-949-016-557 Sequence 557, App
3	3155.8	99.5	3296	4	US-09-949-016-1456 Sequence 1456, Ap
4	2202.8	69.4	37475	4	US-09-949-016-12299 Sequence 12299, A
5	2202.8	69.4	37492	4	US-09-949-016-13198 Sequence 13198, A
6	813	25.6	828	3	US-09-149-476-303 Sequence 303, App
C 7	600.6	18.9	601	4	US-09-949-016-28971 Sequence 28971, A
C 8	600.6	18.9	601	4	US-09-949-016-28972 Sequence 28972, A
C 9	600.6	18.9	601	4	US-09-949-016-28973 Sequence 28973, A
C 10	600.6	18.9	601	4	US-09-949-016-28974 Sequence 28974, A
C 11	600.6	18.9	601	4	US-09-949-016-28975 Sequence 28975, A
C 12	600.6	18.9	601	4	US-09-949-016-49962 Sequence 49962, A
C 13	600.6	18.9	601	4	US-09-949-016-49963 Sequence 49963, A
C 14	600.6	18.9	601	4	US-09-949-016-49964 Sequence 49964, A
C 15	600.6	18.9	601	4	US-09-949-016-49965 Sequence 49965, A
C 16	600.6	18.9	601	4	US-09-949-016-49966 Sequence 49966, A
C 17	597.4	18.8	601	4	US-09-949-016-28976 Sequence 28976, A
C 18	597.4	18.8	601	4	US-09-949-016-49967 Sequence 49967, A
C 19	138	4.3	601	4	US-09-949-016-139467 Sequence 139467, A
C 20	138	4.3	601	4	US-09-949-016-139468 Sequence 139468, A
C 21	138	4.3	117001	4	US-09-949-016-15684 Sequence 15684, A
C 22	137.8	4.3	11338	4	US-09-949-016-16583 Sequence 16583, A
C 23	137	4.3	601	4	US-09-949-016-145725 Sequence 145725, A
C 24	137	4.3	601	4	US-09-949-016-145993 Sequence 145993, A
C 25	137	4.3	601	4	US-09-949-016-146261 Sequence 146261, A
C 26	137	4.3	205044	4	US-09-949-016-15851 Sequence 15851, A
C 27	137	4.3	205044	4	US-09-949-016-15852 Sequence 15852, A

C 28	137	4.3	205044	4	US-09-949-016-15853 Sequence 15853, A
C 29	137	4.3	223471	4	US-09-949-016-12387 Sequence 12387, A
C 30	137	4.3	223471	4	US-09-949-016-12724 Sequence 12724, A
C 31	137	4.3	223471	4	US-09-949-016-12725 Sequence 12725, A
C 32	136.6	4.3	601	4	US-09-949-016-145724 Sequence 145724, A
C 33	136.6	4.3	601	4	US-09-949-016-145992 Sequence 145992, A
C 34	136.6	4.3	601	4	US-09-949-016-146260 Sequence 146260, A
C 35	136.4	4.3	96845	4	US-09-949-016-13658 Sequence 13658, A
C 36	136	4.3	841	5	PCT-US93-06251-80 Sequence 80, Appl
C 37	136	4.3	841	5	PCT-US93-06251-81 Sequence 81, Appl
C 38	136	4.3	91279	4	US-09-949-016-15146 Sequence 15146, A
C 39	136	4.3	346112	4	US-09-949-016-13165 Sequence 13165, A
C 40	135.8	4.3	64813	4	US-09-949-016-11957 Sequence 11957, A
C 41	135.8	4.3	70131	4	US-09-949-016-16064 Sequence 16064, A
C 42	135.2	4.3	601	4	US-09-949-016-139466 Sequence 139466, A
C 43	135.2	4.3	15222	4	US-09-949-016-11916 Sequence 11916, A
C 44	135.2	4.3	15223	4	US-09-949-016-16912 Sequence 16912, A
C 45	135.2	4.3	63319	4	US-09-949-016-16579 Sequence 16579, A

ALIGNMENTS

RESULT 1
US-09-149-476-174
; Sequence 174, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23

[illegible]

1	EARLIER	FILING DATE:	1997-08-22
2	EARLIER	APPLICATION NUMBER:	60/056,894
3	EARLIER	FILING DATE:	1997-08-22
4	EARLIER	APPLICATION NUMBER:	60/056,911
5	EARLIER	FILING DATE:	1997-08-22
6	EARLIER	APPLICATION NUMBER:	60/056,636
7	EARLIER	FILING DATE:	1997-08-22
8	EARLIER	APPLICATION NUMBER:	60/056,874
9	EARLIER	FILING DATE:	1997-08-22
10	EARLIER	APPLICATION NUMBER:	60/056,910
11	EARLIER	FILING DATE:	1997-08-22
12	EARLIER	APPLICATION NUMBER:	60/056,864
13	EARLIER	FILING DATE:	1997-08-22
14	EARLIER	APPLICATION NUMBER:	60/056,631
15	EARLIER	FILING DATE:	1997-08-22
16	EARLIER	APPLICATION NUMBER:	60/056,845
17	EARLIER	FILING DATE:	1997-08-22
18	EARLIER	APPLICATION NUMBER:	60/056,892
19	EARLIER	FILING DATE:	1997-08-22
20	EARLIER	APPLICATION NUMBER:	60/057,761
21	EARLIER	FILING DATE:	1997-08-22
22	EARLIER	APPLICATION NUMBER:	60/047,595
23	EARLIER	FILING DATE:	1997-05-23
24	EARLIER	APPLICATION NUMBER:	60/047,599
25	EARLIER	FILING DATE:	1997-05-23
26	EARLIER	APPLICATION NUMBER:	60/047,588
27	EARLIER	FILING DATE:	1997-05-23
28	EARLIER	APPLICATION NUMBER:	60/047,585
29	EARLIER	FILING DATE:	1997-05-23
30	EARLIER	APPLICATION NUMBER:	60/047,586
31	EARLIER	FILING DATE:	1997-05-23
32	EARLIER	APPLICATION NUMBER:	60/047,590
33	EARLIER	FILING DATE:	1997-05-23
34	EARLIER	APPLICATION NUMBER:	60/047,594
35	EARLIER	FILING DATE:	1997-05-23
36	EARLIER	APPLICATION NUMBER:	60/047,589
37	EARLIER	FILING DATE:	1997-05-23
38	EARLIER	APPLICATION NUMBER:	60/047,593
39	EARLIER	FILING DATE:	1997-05-23
40	EARLIER	APPLICATION NUMBER:	60/047,614
41	EARLIER	FILING DATE:	1997-05-23
42	EARLIER	APPLICATION NUMBER:	60/043,578
43	EARLIER	FILING DATE:	1997-04-11
44	EARLIER	APPLICATION NUMBER:	60/043,576
45	EARLIER	FILING DATE:	1997-04-11
46	EARLIER	APPLICATION NUMBER:	60/047,501
47	EARLIER	FILING DATE:	1997-05-23
48	EARLIER	APPLICATION NUMBER:	60/043,670
49	EARLIER	FILING DATE:	1997-04-11
50	EARLIER	APPLICATION NUMBER:	60/056,632
51	EARLIER	FILING DATE:	1997-08-22
52	EARLIER	APPLICATION NUMBER:	60/056,664
53	EARLIER	FILING DATE:	1997-08-22
54	EARLIER	APPLICATION NUMBER:	60/056,876
55	EARLIER	FILING DATE:	1997-08-22
56	EARLIER	APPLICATION NUMBER:	60/056,881
57	EARLIER	FILING DATE:	1997-08-22
58	EARLIER	APPLICATION NUMBER:	60/056,909
59	EARLIER	FILING DATE:	1997-08-22
60	EARLIER	APPLICATION NUMBER:	60/056,875
61	EARLIER	FILING DATE:	1997-08-22
62	EARLIER	APPLICATION NUMBER:	60/056,862
63	EARLIER	FILING DATE:	1997-08-22
64	EARLIER	APPLICATION NUMBER:	60/056,887
65	EARLIER	FILING DATE:	1997-08-22
66	EARLIER	APPLICATION NUMBER:	60/056,908
67	EARLIER	FILING DATE:	1997-08-22
68	EARLIER	APPLICATION NUMBER:	60/048,964
69	EARLIER	FILING DATE:	1997-06-06
70	EARLIER	APPLICATION NUMBER:	60/057,650
71	EARLIER	FILING DATE:	1997-09-05
72	EARLIER	APPLICATION NUMBER:	60/056,884
73	EARLIER	FILING DATE:	1997-08-22

```
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      99.9%; Score 3169.4; DB 3; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCGAGCGTCGCTCTTTTCCACAGAGGTTAGACCCTGGAAGAGATGGCTCAGC 60
DB 1 TCGACCCGAGCGTCGCTCTTTTCCACAGAGGTTAGACCCTGGAAGAGATGGCTCAGC 60

QY 61 ACCACCTATGGATCTTGGCTCTTGGCTGCAAAACCTGGCCGAGCAGCTGGAAGACT 120
DB 61 ACCACCTATGGATCTTGGCTCTTGGCTGCAAAACCTGGCCGAGCAGCTGGAAGACT 120

QY 121 CAGAAATCTTCAGTGAATGGGATTCCTGGAGAGTCAGTCACTTCCCTGTAAATATCC 180
DB 121 CAGAAATCTTCAGTGAATGGGATTCCTGGAGAGTCAGTCACTTCCCTGTAAATATCC 180

QY 181 AAGAACCCAGCGCAAGTTAAATCAITTCCTTGGACTCTTAAACATCTGTTCCTTATGTA 240
DB 181 AAGAACCCAGCGCAAGTTAAATCAITTCCTTGGACTCTTAAACATCTGTTCCTTATGTA 240

QY 241 CACGAGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAATGAAC 300
DB 241 CACGAGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAATGAAC 300

QY 301 GGNATACCTCCTTAGCTCGGAATCAATCTGGTCTATTAGCGATCTGAGGATGGAAGCG 360
DB 301 GGNATACCTCCTTAGCTCGGAATCAATCTGGTCTATTAGCGATCTGAGGATGGAAGCG 360

QY 361 CAGGAGACTACAAGCAGACATAAATACAGAGCTGATCCCTACACACCCAGCGCT 420
DB 361 CAGGAGACTACAAGCAGACATAAATACAGAGCTGATCCCTACACACCCAGCGCT 420

QY 421 ACAACCTGCAATCTATCTGTCGCTGGGAAACCAAAATTAACAGAGTTTAATGGCAT 480
DB 421 ACAACCTGCAATCTATCTGTCGCTGGGAAACCAAAATTAACAGAGTTTAATGGCAT 480

QY 481 CTGTGAACAGCACTGTAAATGTCACACTGACATGCTCTGTAGAGAAAGAGAAAGAAATG 540
DB 481 CTGTGAACAGCACTGTAAATGTCACACTGACATGCTCTGTAGAGAAAGAGAAAGAAATG 540

QY 541 TGACATACAATTTGGAGTCCCTCGGAGAGAGGGTAAATGTCTTCAAACTCTCCAGACTC 600
DB 541 TGACATACAATTTGGAGTCCCTCGGAGAGAGGGTAAATGTCTTCAAACTCTCCAGACTC 600

QY 601 CTGAGAACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGACGAAACAATCTG 660
DB 601 CTGAGAACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGACGAAACAATCTG 660

QY 661 ACTCCATCTCTGCCCCGAGCTCTGTGCACACATCGCAATGGGCTCCGTACTCACCACA 720
DB 661 ACTCCATCTCTGCCCCGAGCTCTGTGCACACATCGCAATGGGCTCCGTACTCACCACA 720

QY 721 CCGGGTGTCTGAGGCTCGGCTATGTTCTTCTGCTGTGTTCTCATTCTCTCTTCAGTGT 780
DB 721 CCGGGTGTCTGAGGCTCGGCTATGTTCTTCTGCTGTGTTCTCATTCTCTCTTCAGTGT 780

QY 781 TTTTGTTCCTGTTTTCAGAGAGAACAGATGCTGCTCAAGAAACCATATACACAT 840
DB 781 TTTTGTTCCTGTTTTCAGAGAGAACAGATGCTGCTCAAGAAACCATATACACAT 840

QY 841 ATATCATGGCTTCAAGGAACACCCAGCAGCAGAGTCCAGATCTATGATGAATCCTGC 900
DB 841 ATATCATGGCTTCAAGGAACACCCAGCAGCAGAGTCCAGATCTATGATGAATCCTGC 900

QY 901 AGTCCAAAGGTGCTTCCCTCCAAGGAAGCCAGTGAACACAGTTTATTCGGAAGTGCAGT 960
DB 901 AGTCCAAAGGTGCTTCCCTCCAAGGAAGCCAGTGAACACAGTTTATTCGGAAGTGCAGT 960

901 AGTCCAAAGGTGCTTCCCTCCAAGGAAGCCAGTGAACACAGTTTATTCGGAAGTGCAGT 960
961 TTGCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGGACTTCAAGCT 1020
961 TTGCTGATAAGATGGGAAAGCCAGCACACAGGACAGTAAACCTCTCTGGGACTTCAAGCT 1020
1021 ATGAAATTTGATCTAGGCTGCTGGCTGAAATTTCCCTCTGGAAACTGAGTTACAACCA 1080
1021 ATGAAATTTGATCTAGGCTGCTGGCTGAAATTTCCCTCTGGAAACTGAGTTACAACCA 1080
1081 CCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCAACTTCTTACTGGGAGATTG 1140
1081 CCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCCAACTTCTTACTGGGAGATTG 1140
1141 CAAACTGCGCACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTCTGCGGCATAGCTTGT 1200
1141 CAAACTGCGCACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTCTGCGGCATAGCTTGT 1200
1201 GCCTAAATGGACAAATGGATGCATACCTTCTCTGAAATGAATCCCTTCTGAATGAATGAC 1260
1201 GCCTAAATGGACAAATGGATGCATACCTTCTCTGAAATGAATCCCTTCTGAATGAATGAC 1260
1261 AAGCAGGTTACTAGTATAGTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAA 1320
1261 AAGCAGGTTACTAGTATAGTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAA 1320
1321 TAATATTTTATGGCACACTGGGATAAACAAGCAAGATGTCTCTCTGGAAGCTGCGAT 1380
1321 TAATATTTTATGGCACACTGGGATAAACAAGCAAGATGTCTCTCTGGAAGCTGCGAT 1380
1381 ATGACTAGAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
1381 ATGACTAGAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
1441 GGATCAATATTTTGCACACCTGTATAGGCCATAGGCACACACAGCCAGGATGTCTCTCA 1500
1441 GGATCAATATTTTGCACACCTGTATAGGCCATAGGCACACACAGCCAGGATGTCTCTCA 1500
1501 CAGTCAGTATGTGAAGATCCCTGGTGGTGGCTTACACAGCATCTTGTAGCAAAATTA 1560
1501 CAGTCAGTATGTGAAGATCCCTGGTGGTGGCTTACACAGCATCTTGTAGCAAAATTA 1560
1561 GGAAATATGTAACCTTTCGCTTGGAGCAGATGACAGCCCTTCCCGAGTGTGCTTGGAG 1620
1561 GGAAATATGTAACCTTTCGCTTGGAGCAGATGACAGCCCTTCCCGAGTGTGCTTGGAG 1620
1621 AGCAGATGTGGCTGTCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGTCAGG 1680
1621 AGCAGATGTGGCTGTCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGTCAGG 1680
1681 GCATTAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTCTGTGCGGTCTCTGTGTCAGAG 1740
1681 GCATTAACAGGCTTAGTAAAGTCCAAACACAGATGACAGTCTGTGCGGTCTCTGTGTCAGAG 1740
1741 TTGTGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTCTTCTTCT 1800
1741 TTGTGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTCTTCTTCT 1800
1801 GCAGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTACTTCCAGAGCCTTATAGG 1860
1801 GCAGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTACTTCCAGAGCCTTATAGG 1860
1861 ATTTCTTCTTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGC 1920
1861 ATTTCTTCTTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGC 1920
1921 AGCCATGCCAGTATTTCCCACTCTCCAAAGGAGTGTGACAGCTTATATTTCTCACACTT 1980
1921 AGCCATGCCAGTATTTCCCACTCTCCAAAGGAGTGTGACAGCTTATATTTCTCACACTT 1980
1981 CTGGGAACTGGGTATAATCCCAACCAATCAAAATAGAAAGCTTTGCAAGAGCAGAGTCA 2040
1981 CTGGGAACTGGGTATAATCCCAACCAATCAAAATAGAAAGCTTTGCAAGAGCAGAGTCA 2040
```


QY	607	ACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGACCAACAAATTCCTGACTCCA	666	QY	1687	CAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTGTGTGGGTCTCTGTGACAGAGTTGGG	1746
Db	601	ACCAAGAGCTGACTTACAGCTGTACAGCCAGAACCCCTGTGACCAACAAATTCCTGACTCCA	660	Db	1681	CAGGCTTAGTAAAGTCCAAACACAGATGACAGTGTGTGTGGGTCTCTGTGACAGAGTTGGG	1740
QY	667	TCCTGCTCCGCGAGCTCTGTGAGAGATCGCAATGGGCTTCGGTACTCACACACCGGGT	726	QY	1747	CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTCTTTCTGCGAGG	1806
Db	661	TCCTGCTCCGCGAGCTCTGTGAGAGATCGCAATGGGCTTCGGTACTCACACACCGGGT	720	Db	1741	CTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTCTTTCTGCGAGG	1800
QY	727	TGCTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCATTCGTCTTCAGTGTGTTTTGT	786	QY	1807	TCTAGAGACTGCTGGGACACTTTTCTTGAGTGTCTACTTTCAGAGCCCTTATAGGATTTTC	1866
Db	721	TGCTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCATTCGTCTTCAGTGTGTTTTGT	780	Db	1801	TCTAGAGACTGCTGGGACACTTTTCTTGAGTGTCTACTTTCAGAGCCCTTATAGGATTTTC	1860
QY	787	TCGGTTGTTCAAGAGAACAGAGTCTGCCTCAAGAAACCAATACATATATCA	846	QY	1867	TTTTCTGGCCAGATTTCTTCTGTATCACTCCAGCAGCTCAGCAGAGAGAGAGCCAT	1926
Db	781	TCGGTTGTTCAAGAGAACAGAGTCTGCCTCAAGAAACCAATATATATATCA	840	Db	1861	TTTTCTGGCCAGATTTCTTCTGTATCACTCCAGCAGCTCAGCAGAGAGAGAGCCAT	1920
QY	847	TGCGTTCAAGGAACACCCAGCAGCAGAGTCCAGAACTTATGATGAAATCCTGCGAGTCCA	906	QY	1927	GCCGAGTATTTCCACTCTCCAAAGGAACCTGACCAAGTATATTTCTCACTTTCTGGGG	1986
Db	841	TGCGTTCAAGGAACACCCAGCAGCAGAGTCCAGAACTTATGATGAAATCCTGCGAGTCCA	900	Db	1921	GCCGAGTATTTCCACTCTCCAAAGGAACCTGACCAAGTATATTTCTCACTTTCTGGGG	1980
QY	907	AGGTGCTTCCCTCCAAAGGAAGCCAGTGAAACACAGTTTATTCGGAAGTGCGATTTGCTG	966	QY	1987	AACTCGGTATATCCAAACCATAGAAACCTTGCAAGAGCAGAGTCAATTTCTCCA	2046
Db	901	AGGTGCTTCCCTCCAAAGGAAGCCAGTGAAACACAGTTTATTCGGAAGTGCGATTTGCTG	960	Db	1981	AACTCGGTATATCCAAACCATAGAAACCTTGCAAGAGCAGAGTCAATTTCTCCA	2040
QY	967	ATAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTCGGACTTCAAGCTATGARA	1026	QY	2047	GAAGGAACCTGGGAGATGATGTCAGATGATGAACTGGGTTCATTCAGAGTTCCAAAGA	2106
Db	961	ATAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTCGGACTTCAAGCTATGARA	1020	Db	2041	GAAGGAACCTGGGAGATGATGTCAGATGATGAACTGGGTTCATTCAGAGTTCCAAAGA	2100
QY	1027	TTGTGATCTAGGCTGTGGCTGAAATTCCTCCCTCTGGAACCTGAGTTACAAACCAATA	1086	QY	2107	CTCAGAGAACTAGATTTAAGCTGAGGAGAGTGGCCACCTGGCATGCCCAACAAC	2166
Db	1021	TTGTGATCTAGGCTGTGGCTGAAATTCCTCCCTCTGGAACCTGAGTTACAAACCAATA	1080	Db	2101	CTCAGAGAACTAGATTTAAGCTGAGGAGAGTGGCCACCTGGCATGCCCAACAAC	2160
QY	1087	CTGGCAGGTTCCCTGATCCAGATCTTCTGTGCCCCAACTCTTACTGGGAGATTGCAAACT	1146	QY	2167	AGATCACCAGCCAGCTTACACAGGCAATTAACCTCTCTCAATGAGGAAGAAATCAATTCACAA	2226
Db	1081	CTGGCAGGTTCCCTGATCCAGATCTTCTGTGCCCCAACTCTTACTGGGAGATTGCAAACT	1140	Db	2161	AGATCACCAGCCAGCTTACACAGGCAATTAACCTCTCTCAATGAGGAAGAAATCAATTCACAA	2220
QY	1147	GCCACATCTCAGCTGTAGCAAGCAGGAACCTTCTGTGGGATAGCTTGTGGCTTAA	1206	QY	2227	CTGAGCAAGACATTCATATGATCATTTAAAGGAAGTGTTCCTTATGTGTAGCAAGTAT	2286
Db	1141	GCCACATCTCAGCTGTAGCAAGCAGGAACCTTCTGTGGGATAGCTTGTGGCTTAA	1200	Db	2221	CTGAGCAAGACATTCATATGATCATTTAAAGGAAGTGTTCCTTATGTGTAGCAAGTAT	2280
QY	1207	ATGCAAAATGGATGATACCTTCTGAAATGACTCCCTTCTGAATGAATGATGACAAAGCA	1266	QY	2287	AATCGGCTAACTCCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAAT	2346
Db	1201	ATGCAAAATGGATGATACCTTCTGAAATGACTCCCTTCTGAATGAATGATGACAAAGCA	1260	Db	2281	AATCGGCTAACTCCTTAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAAT	2340
QY	1267	GGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGACATGTAGAAATATAT	1326	QY	2347	TAGGCAAGATAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCAACCACTA	2406
Db	1261	GGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGACATGTAGAAATATAT	1320	Db	2341	TAGGCAAGATAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCAACCACTA	2400
QY	1327	TTTTATGGCACCTGGGATAAACAGCAAGATTCCTCAGTCTTGGAGCTGCATATGACT	1386	QY	2407	CCATTAAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGCATATGTCTGC	2466
Db	1321	TTTTATGGCACCTGGGATAAACAGCAAGATTCCTCAGTCTTGGAGCTGCATATGACT	1380	Db	2401	CCATTAAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGCATATGTCTGC	2460
QY	1387	AGAGGCTCTTGTGACTGGAGGTAAACAAACCTTCCAGTAACCTGTGGGAAGAGGGATCA	1446	QY	2467	TCTTGTGTAGCTCAGAGAGCAATTCAGACACAGACTACAGTTAAGCTGAACTGCAGC	2526
Db	1381	AGAGGCTCTTGTGACTGGAGGTAAACAAACCTTCCAGTAACCTGTGGGAAGAGGGATCA	1440	Db	2461	TCTTGTGTAGCTCAGAGAGCAATTCAGACACAGACTACAGTTAAGCTGAACTGCAGC	2520
QY	1447	ATATTTTGGCACTGTATAGGCCATGGGCACACAGCCAGTAAGTCTCTGCTCAGCTCA	1506	QY	2527	TGCAAGTAAATAGCATCAACAGTCAAGAAATACTTTATAGGGGGGAGGCTGAAAGCTGG	2586
Db	1441	ATATTTTGGCACTGTATAGGCCATGGGCACACAGCCAGTAAGTCTCTGCTCAGCTCA	1500	Db	2521	TGCAAGTAAATAGCATCAACAGTCAAGAAATACTTTATAGGGGGGAGGCTGAAAGCTGG	2580
QY	1507	GTATGTGTAAGATCCCTGGTGGCTTCAACAGCATCTTGAGCAAAATAGGAAA	1566	QY	2587	GCCTTGAAGGATGGATGAAATTTGGATAGAGATAGGAAAGACAGAGGGGCTCAGAGTGA	2646
Db	1501	GTATGTGTAAGATCCCTGGTGGCTTCAACAGCATCTTGAGCAAAATAGGAAA	1560	Db	2581	GCCTTGAAGGATGGATGAAATTTGGATAGAGATAGGAAAGACAGAGGGGCTCAGAGTGA	2640
QY	1567	TGTACCTCTGCTTGGAGCAGATGACAGCCCTTCCCGAGTGCATGCTTGGAGAGCAGA	1626	QY	2647	GAGAAGCATGAAAATGAGCAGGGGCTGGATCAGTGGGGTGTATTTCAGAGCACCTCTCC	2706
Db	1561	TGTACCTCTGCTTGGAGCAGATGACAGCCCTTCCCGAGTGCATGCTTGGAGAGCAGA	1620	Db	2641	GAGAAGCATGAAAATGAGCAGGGGCTGGATCAGTGGGGTGTATTTCAGAGCACCTCTCC	2700
QY	1627	ATGTGGGCTGCATATAAGCAACATCTATCCCTTTCTGTGGGAATCTTTGTGAGGGCATAA	1686	QY	2707	AGATGACCATGATGCTCAGCTCCCTTGTGTCCTTATGTGTGGCAGAGTGTCCCAGGCCAGAT	2766
Db	1621	ATGTGGGCTGCATATAAGCAACATCTATCCCTTTCTGTGGGAATCTTTGTGAGGGCATAA	1680	Db	2701	AGATGACCATGATGCTCAGCTCCCTTGTGTCCTTATGTGTGGCAGAGTGTCCCAGGCCAGAT	2760
				QY	2767	GTGTGGGCTGCATATAAGCAACATCTATCCCTTTCTGTGGGAATCTTTGTGAGGGCATCTC	2826

2761	Db	GTGTGCCCCCACCACCATGTCAATTTATCATGTCTTCAATGCCACCTCAAAGGTACCTC	2820
2827	Qy	TTCTGTAAGCTTTTCCCTGGGTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC	2886
2821	Db	TTCTGTAAGCTTTTCCCTGGGTATCAGGAATCAAAATTAATCAGGGATCTTTTTCACACTGC	2880
2887	Qy	TGTTTTTTCCTCTTTTGGTCCCTTCATCACTAAACTCATCTCATCTCAGCCTTACAGCAT	2946
2881	Db	TGTTTTTTCCTCTTTTGGTCCCTTCATCACTAAACTCATCTCATCTCAGCCTTACAGCAT	2940
2947	Qy	ACTAAATATTGTGTTTTTCTCTACTACATTTGTACATGTGGGAATTACAGATAAAGCAAGCC	3006
2941	Db	ACTAAATATTGTGTTTTTCTCTACTACATTTGTACATGTGGGAATTACAGATAAAGCAAGCC	3000
3007	Qy	KGCTGGGGTGGTGGCTCACGCTCTGTAATCCAAACATTTTGGGAGGCCAAGCAGCGGAT	3066
3001	Db	GGCTGGGGTGGTGGCTCACGCTCTGTAATCCAAACATTTTGGGAGGCCAAGCAGCGGAT	3060
3067	Qy	CACCTGAGGTCAGGARTTCGAGATTAPCTCGGCCAACATGTGTGGAACCCCATNTNTACTA	3126
3061	Db	CACCTGAGGTCAGGARTTCGAGATTAPCTCGGCCAACATGTGTGGAACCCCATNTNTACTA	3120
3127	Qy	AAAAATAGAAATTAGCCAGGTGTGGTGGGCACACATCTGTAGTCCCAAG	3173
3121	Db	AAAAATAGAAATTAGCCAGGTGTGGTGGGCACACATCTGTAGTCCCAAG	3167

RESULT 3
 US-09-949-016-1456
 ; Sequence 1456, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1456
 ; LENGTH: 3296
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-1456

	Query Match	99.5%;	Score 3155.8;	DB 4;	Length 3296;
	Best Local Similarity	99.8%;	Prd. No. 0;		
	Matches 3154;	Conservative	3;	Mismatches 2;	Indels 0; Gaps 0;
QY	15	CCGTGCTTTTCCACAGAAGGTTAGACCCCTGAAAGAGATGGCTCAGCACACCACTATGGATC	74		
DB	7	CCGTGCTTTTCCACAGAAGGTTAGACCCCTGAAAGAGATGGCTCAGCACCACTATGGATC	66		
QY	75	TTGCTCTCTTTGCTGCAAACTGGCGCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA	134		
DB	67	TTGCTCTCTTTGCTGCAAACTGGCGCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA	126		
QY	135	GTGAATGGGATTTCTGGGAGAGTCAGTCATTTCCCTGTAAATATCAAGAAACCACGGCAA	194		
DB	127	GTGAATGGGATTTCTGGGAGAGTCAGTCATTTCCCTGTAAATATCAAGAAACCACGGCAA	186		
QY	195	GTTAAATCAATGCTTTGGACTTCTAAACATCTGTTGCTTATGTAACACCAAGGAGACTCA	254		
DB	187	GTTAAATCAATGCTTTGGACTTCTAAACATCTGTTGCTTATGTAACACCAAGGAGACTCA	246		

Qy	255	GAACACGACCGCTAGTCTACTGTGACCCACAGAAATTTATTATGAACGGATACATGCTCTTA	314
Db	247	GAACACGACCGCTAGTCTACTGTGACCCACAGAAATTTATTATGAACGGATACATGCTCTTA	306
Qy	315	GGTCCGAATCTACAAATCTGGTGCTATTAGCGATCTGAGGATGGAAGACGACGAGACTACAAA	374
Db	307	GGTCCGAATCTACAAATCTGGTGCTATTAGCGATCTGAGGATGGAAGACGACGAGACTACAAA	366
Qy	375	GCAGACATAAATACACAGCGCTGATCCCTTACACACCAACGAGGCTTAAACCTGCGAAATC	434
Db	367	GCAGACATAAATACACAGCGCTGATCCCTTACACACCAACGAGGCTTAAACCTGCGAAATC	426
Qy	435	TATCGTCGGCTTCGGAAACCAAAAAATTACACAGAGTTTAATGGCATCTGTGAACACGACCC	494
Db	427	TATCGTCGGCTTCGGAAACCAAAAAATTACACAGAGTTTAATGGCATCTGTGAACACGACCC	486
Qy	495	TGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAATGTGACATACAATTTGG	554
Db	487	TGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAATGTGACATACAATTTGG	546
Qy	555	AGTCCCTCGGAGAGGAGGTAATGTCCTTCAAAATCTTCCAGACTCTCGAGGACCAAGAG	614
Db	547	AGTCCCTCGGAGAGGAGGTAATGTCCTTCAAAATCTTCCAGACTCTCGAGGACCAAGAG	606
Qy	615	CTGACTTTACACGTGTACAGCCCAAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC	674
Db	607	CTGACTTTACACGTGTACAGCCCAAGAACCCCTGTGAGCAACAAATCTGACTCCATCTCTGCC	666
Qy	675	CGGAGCTCTGTGGAGACATCGCAATGGGCTTCGGTACTCACCACACCGGTTGCTGAGC	734
Db	667	CGGAGCTCTGTGGAGACATCGCAATGGGCTTCGGTACTCACCACACCGGTTGCTGAGC	726
Qy	735	GTGCTGCTATGTTCTTTCTGCTTGTGTTCTCATTTCTGTCTTTCAGTGTGTTTTGTTCCGTTG	794
Db	727	GTGCTGCTATGTTCTTTCTGCTTGTGTTCTCATTTCTGTCTTTCAGTGTGTTTTGTTCCGTTG	786
Qy	795	TTCAAGAGAGACAAAGATGTGCTCTAAAGAAAACCAATATACACATATATCATGGGCTTCA	854
Db	787	TTCAAGAGAGACAAAGATGTGCTCTAAAGAAAACCAATATACACATATATCATGGGCTTCA	846
Qy	855	AGGAACACCCAGCCAGCAGAGTCAGAAATCTATGATGAAATCTCGCAGTCCAAAGGTGCTT	914
Db	847	AGGAACACCCAGCCAGCAGAGTCAGAAATCTATGATGAAATCTCGCAGTCCAAAGGTGCTT	906
Qy	915	CCCTCCAAGGAAGACGAGTGAACACAGTTTATTCGAGTGACGTTTGTGCTGATAGATG	974
Db	907	CCCTCCAAGGAAGACGAGTGAACACAGTTTATTCGAGTGACGTTTGTGCTGATAGATG	966
Qy	975	GGGAAGCCAGCACACAGGACAGTAAACCTCTGGGACTTCAAGCTATGAAATTTGTGATC	1034
Db	967	GGGAAGCCAGCACACAGGACAGTAAACCTCTGGGACTTCAAGCTATGAAATTTGTGATC	1026
Qy	1035	TAGGCTGCTGGGCTGAAATTTCCCTCTCTGGAACCTGAGTTTACCAACCACTACTGGCAGG	1094
Db	1027	TAGGCTGCTGGGCTGAAATTTCCCTCTCTGGAACCTGAGTTTACCAACCACTACTGGCAGG	1086
Qy	1095	TTCCCTGGATCCAGATCTTCTGCCCACCTCTTACGGAGATGTCGAATCTGCCCATC	1154
Db	1087	TTCCCTGGATCCAGATCTTCTGCCCACCTCTTACGGAGATGTCGAATCTGCCCATC	1146
Qy	1155	TCAGCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTGTGCTTAAATTTGACAA	1214
Db	1147	TCAGCTGTAAAGCAAGCAGGAAACCTTCTGCTGGGATAGCTGTGCTTAAATTTGACAA	1206
Qy	1215	ATGATGATACCTTCTGTAATGATCTCCCTTCTGTAATGAAATGACAAACGAGTTACCT	1274
Db	1207	ATGATGATACCTTCTGTAATGATCTCCCTTCTGTAATGAAATGACAAACGAGTTACCT	1266
Qy	1275	AGTATGTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAAAATAATTTTTATGG	1334
Db	1267	AGTATGTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAAAATAATTTTTATGG	1326
Qy	1335	CACACTGGGATTAACAAAGCAAGATTGCTCTCTTGGAGCTGATGACTAGAGGCCT	1394

1327 CACACTGGGATATAACAGCAAGATGCTCATCTTGGAGCTGCATATGACTAGAGGCT 1386
1395 CTTGTGACTGGAGTTAAACCCCTGCCCCAGTAACTGTGTGGAGAAAGGGGATCAATATTTTG 1454
1387 CTTGTGACTGGAGTTAAACCCCTGCCCCAGTAACTGTGTGGAGAAAGGGGATCAATATTTTG 1446
1455 CACACTGTAATAGGCATGACACACAGCCAGGATGCTCTGCTCAGCTCAGTATGTGT 1514
1447 CACACCTGTAATAGGCATGACACACAGCCAGGATGCTCTGCTCAGCTCAGTATGTGT 1506
1515 GAAGATCCCTGTGCTGCTGCTTCCACAGCCATCTTTGAGCAAAATAGGAAAATGTACCCCT 1574
1507 GAAGATCCCTGTGCTGCTGCTTCCACAGCCATCTTTGAGCAAAATAGGAAAATGTACCCCT 1566
1575 TCGCTTGAAGCAGATGACGACCTTCCCGAGTGCATGCTGAGAGCAGAAATGTGGGC 1634
1567 TCGCTTGAAGCAGATGACGACCTTCCCGAGTGCATGCTGAGAGCAGAAATGTGGGC 1626
1635 TGCATATAAGCACACTCATCCCTTCTGCTGGGAATCTTTGTGAGGAGCATAACAGGCTTA 1694
1627 TGCATATAAGCACACTCATCCCTTCTGCTGGGAATCTTTGTGAGGAGCATAACAGGCTTA 1686
1695 GTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGAGTGTGGCTCTTCAGC 1754
1687 GTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGAGAGTGTGGCTCTTCAGC 1746
1755 CATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTTCGAGGGTCTAGAGA 1814
1747 CATGTAGACACACTCTCCAAATGGAGTGTGGAAAATGTTCTTTCGAGGGTCTAGAGA 1806
1815 CTGCTGGGACACTTTCTTGGAGTGTACTTCAAGAGCCCTTATAGGATTTCTTCTGCGC 1874
1807 CTGCTGGGACACTTTCTTGGAGTGTACTTCAAGAGCCCTTATAGGATTTCTTCTGCGC 1866
1875 CAAGATTTCTTCTGATCACTCCAAGAGCCCTCAGCAGAAAGCAGCCATGCCCAGTA 1934
1867 CAAGATTTCTTCTGATCACTCCAAGAGCCCTCAGCAGAAAGCAGCCATGCCCAGTA 1926
1935 TTCCCACTCTCCAAAAGGAACTGACAGCTTATTTCTCACTTCTGAGGAACTGGGT 1994
1927 TTCCCACTCTCCAAAAGGAACTGACAGCTTATTTCTCACTTCTGAGGAACTGGGT 1986
1995 ATAATCCAACCATCAAAATAGAGACTTTCAGAGAGCAGAGTCAATCTCCAGAGAAC 2054
1987 ATAATCCAACCATCAAAATAGAGACTTTCAGAGAGCAGAGTCAATCTCCAGAGAAC 2046
2055 TTGGAGATGATGTCAGATGATGAATCTGGGTTCATCCAGTTCCTCCAGTTCCTCCAGT 2114
2047 TTGGAGATGATGTCAGATGATGAATCTGGGTTCATCCAGTTCCTCCAGTTCCTCCAGT 2106
2115 ACTAGAGTTTAAAGTGAAGCAGAGTGGCCGACCCCTGGCATGCCCAACAAAGATCAAC 2174
2107 ACTAGAGTTTAAAGTGAAGCAGAGTGGCCGACCCCTGGCATGCCCAACAAAGATCAAC 2166
2175 AGCCAGTTTACAGGCAATTAATCTCTCAATGAGGAAAGTCAATCTCCAGTTCCTCCAG 2234
2167 AGCCAGTTTACAGGCAATTAATCTCTCAATGAGGAAAGTCAATCTCCAGTTCCTCCAG 2226
2235 GACATTCATATGATCAATTAAGGAGTGTTCCTTATGTTAGCAAGTATATTCGGCT 2294
2227 GACATTCATATGATCAATTAAGGAGTGTTCCTTATGTTAGCAAGTATATTCGGCT 2286
2295 AACTCTTAAATCCCAATAGTCTTGGCTGGAGCAATGGGCTGCAATAGGAGCA 2354
2287 AACTCTTAAATCCCAATAGTCTTGGCTGGAGCAATGGGCTGCAATAGGAGCA 2346
2355 TAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCACCACTACCATAGC 2414
2347 TAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCACCACTACCATAGC 2406
2415 ACTATGTTAGGAGTGCAGGCCCAAGTAGAGATGTCATATCTGCTCTCTGCT 2474

2407 ACTATGTTAGGAGTGCAGGCCCAAGTGAAGATGTCATATGCTGCTCTGTGT 2466
2475 AGCTCAGGAGCAATTTCCAGCACACACTACAGTTAAAGCTGAACCTGAGCTGCAAGTA 2534
2467 AGCTCAGGAGCAATTTCCAGCACACACTACAGTTAAAGCTGAACCTGAGCTGCAAGTA 2526
2535 ATAGCATGAACAGTGCAGAAAATACCTTATGAGGGGCGAGGCTGAAAGCTGGCCCTTGA 2594
2527 ATAGCATGAACAGTGCAGAAAATACCTTATGAGGGGCGAGGCTGAAAGCTGGCCCTTGA 2586
2595 GGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCCAGTGAAGAGCA 2654
2587 GGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCCAGTGAAGAGCA 2646
2655 TGAATAATGAGCAGGGGCTGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGCAC 2714
2647 TGAATAATGAGCAGGGGCTGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGCAC 2706
2715 CATGATGCTCAGTCCCTTGCCTTATGTCGAGAGTGTCCAGCCAGATGTGTGCC 2774
2707 CATGATGCTCAGTCCCTTGCCTTATGTCGAGAGTGTCCAGCCAGATGTGTGCC 2766
2775 CCACCCCATGTCATTTACATGCTCTTCAATGCCACCTCAAAAGGTACTCTTCTGTAA 2834
2767 CCACCCCATGTCATTTACATGCTCTTCAATGCCACCTCAAAAGGTACTCTTCTGTAA 2826
2835 AGCTTTCCCTGCTATCAGGAATCAAAATTAATCAGGATCTTTTCACTGCTGTTTTT 2894
2827 AGCTTTCCCTGCTATCAGGAATCAAAATTAATCAGGATCTTTTCACTGCTGTTTTT 2886
2895 CTTCTTTGCTCTTCTATCACTAAACCTCATCTTCAAGCCCTTACAGCATAACTAATTA 2954
2887 CTTCTTTGCTCTTCTATCACTAAACCTCATCTTCAAGCCCTTACAGCATAACTAATTA 2946
2955 TTTGTTTTCTCTCATCATGTTGATGTCGGAATTAACAGATAAAGGAGCCGCTGGG 3014
2947 TTTGTTTTCTCTCATCATGTTGATGTCGGAATTAACAGATAAAGGAGCCGCTGGG 3006
3015 TGGTGGCTCAGCCCTGTAATCCCACTTTGGAGGCCCAAGCAGCGGATCACCTGAG 3074
3007 TGGTGGCTCAGCCCTGTAATCCCACTTTGGAGGCCCAAGCAGCGGATCACCTGAG 3066
3075 GTCCAGATTCGAGATTAATCTGGCCCAACATGTCGGAATTAATCTTACTAAAAATACG 3134
3067 GTCCAGATTCGAGATTAATCTGGCCCAACATGTCGGAATTAATCTTACTAAAAATACG 3126
3135 AAATTAGCCAGTGTGGTGGCACACATCTGTAGTCCAG 3173
3127 AAATTAGCCAGTGTGGTGGCACACATCTGTAGTCCAG 3165

RESULT 4

US-09-949-016-12299
; Sequence 12299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12299
; LENGTH: 37475
; TYPE: DNA

; ORGANISM: Human
US-09-949-016-12299

Query Match 69.4%; Score 2202.8; DB 4; Length 37475;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2204; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy	960	TTTGTCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTTAAACCTCTGGGACCTTCAAGC	1019
Db	33147	TCCTCTGCACAGATGGGAAAGCCAGCACACAGGACAGTTAAACCTCTGGGACCTTCAAGC	33206
Qy	1020	TATGAAATTTGTGATCTAGGCTGTGGGCTGAAATTTCTCCCTCTGGAAACTGAGTTTACAACC	1079
Db	33207	TATGAAATTTGTGATCTAGGCTGTGGGCTGAAATTTCTCCCTCTGGAAACTGAGTTTACAACC	33266
Qy	1080	ACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGGCCCAAATCTTTACTTGGGAGATT	1139
Db	33267	ACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGGCCCAAATCTTTACTTGGGAGATT	33326
Qy	1140	GCAAACTGCCACATCTCAGCTCTTAAGCAAAAGCAGGAAACCTTTCTGTCTGGGCATAGCTTTG	1199
Db	33327	GCAAACTGCCACATCTCAGCTCTTAAGCAAAAGCAGGAAACCTTTCTGTCTGGGCATAGCTTTG	33386
Qy	1200	TGCTAAATGGCAAAATGGATGCATACCTCTCTGAAATGACTCCCTTCTGAAATGAATGA	1259
Db	33387	TGCTAAATGGCAAAATGGATGCATACCTCTCTGAAATGACTCCCTTCTGAAATGAATGA	33446
Qy	1260	CAAAAGCAGTTTACTAGTATAGTTTTCCTCAAACTTCTTCCCATCATGACATCATGTAGAAA	1319
Db	33447	CAAAAGCAGTTTACTAGTATAGTTTTCCTCAAACTTCTTCCCATCATGACATCATGTAGAAA	33506
Qy	1320	ATAATATTTTATGCGACACTGGGATAAAACAGCAAGATTGCTCACTTCTGGAAGCTGCA	1379
Db	33507	ATAATATTTTATGCGACACTGGGATAAAACAGCAAGATTGCTCACTTCTGGAAGCTGCA	33566
Qy	1380	TATGACTAGAGGCTCTTTGTGACTGAGGTAAACAACCTTGCCCAATAACTGTGGGAGAG	1439
Db	33567	TATGACTAGAGGCTCTTTGTGACTGAGGTAAACAACCTTGCCCAATAACTGTGGGAGAG	33626
Qy	1440	GGGATCAATATTTTGCACACTCTTAATAGCCATGSCACACAGCAAGATGCTCTGCTC	1499
Db	33627	GGGATCAATATTTTGCACACTCTTAATAGCCATGSCACACAGCAAGATGCTCTGCTC	33686
Qy	1500	ACAGTCAGTATGTGGAAGATCCCTGGTGGGCTTCAACAACGATCTTTGAGCAAAAT	1559
Db	33687	ACAGTCAGTATGTGGAAGATCCCTGGTGGGCTTCAACAACGATCTTTGAGCAAAAT	33746
Qy	1560	AGGAAATGTACCTTTCGCTTGAGGACAGATGAGCCCTTCCCTCCAGTGCATGGCTCGA	1619
Db	33747	AGGAAATGTACCTTTCGCTTGAGGACAGATGAGCCCTTCCCTCCAGTGCATGGCTCGA	33806
Qy	1620	GAGCAGAAATGTGGGCTGCATATAAGCACACTCATCCCTTTGCTGGGAATCTTTGTGAG	1679
Db	33807	GAGCAGAAATGTGGGCTGCATATAAGCACACTCATCCCTTTGCTGGGAATCTTTGTGAG	33866
Qy	1680	GGCATACAGGCTTAGTAAGTCAAACAAGATGACAGTGCCTGTGGGTCTCTGTGAGA	1739
Db	33867	GGCATACAGGCTTAGTAAGTCAAACAAGATGACAGTGCCTGTGGGTCTCTGTGAGA	33926
Qy	1740	GTTCGTGCTCTCAGCCATGAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTC	1799
Db	33927	GTTCGTGCTCTCAGCCATGAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTC	33986
Qy	1800	TGCAGGCTCTAGAGACTGTGGGACACTTTTCTTGAGTGCCTAATCAGAGCCCTTATAG	1859
Db	33987	TGCAGGCTCTAGAGACTGTGGGACACTTTTCTTGAGTGCCTAATCAGAGCCCTTATAG	34046
Qy	1860	GATTTTCTTTCTGGCCAAAGTTTCTCTGTATCACTCCAGAGCCCTCAGCAGAGAG	1919
Db	34047	GATTTTCTTTCTGGCCAAAGTTTCTCTGTATCACTCCAGAGCCCTCAGCAGAGAG	34106
Qy	1920	CAGCCATGCCCAAGTATTTCCCACTCTCTCCAAAGGAACTGACCAAGCTTATATTTCTCACACT	1979

QY 3060 GCGGATCACTCAGCTCAGGATTCAGATTARTCTGCCAACATGGTGAACCCCATN 3119
DB 35247 GCGGATCACTCAGCTCAGGATTCAGATTARTCTGCCAACATGGTGAACCCCATC 35306

QY 3120 TWTACTAAAAATACGAAATTTAGCCAGGTGTGGGACACATCTGTAGTCCCAG 3173
DB 35307 TCTACTAAAAATACGAAATTTAGCCAGGTGTGGGACACATCTGTAGTCCCAG 35360

RESULT 5

US-09-949-016-13198
; Sequence 13198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13198
; LENGTH: 37492
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13198

Query Match 69.4%; Score 2202.8; DB 4; Length 37492;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2204; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 960 TTTCCTGATGAATGGGAAAGCAGCAGACAGAGATGAATCTCTGGGATCTCAAGC 1019
DB 33147 TCTCTGACAGATGGGAAAGCAGCAGACAGAGATGAATCTCTGGGATCTCAAGC 33206
QY 1020 TATGAATTTGATCTAGGCTGTGGCTGAATCTCTGGGATCTCAAGC 1079
DB 33207 TATGAATTTGATCTAGGCTGTGGCTGAATCTCTGGGATCTCAAGC 33266
QY 1080 ACCAATCTGCGAGTTCCCTGGATCCAGATCTCTCTGCCCACTCTTACTGGGAGATT 1139
DB 33267 ACCAATCTGCGAGTTCCCTGGATCCAGATCTCTCTGCCCACTCTTACTGGGAGATT 33326
QY 1140 GCAAACTGCCACATCTCAGCTCTAAGCAAGAGGAAACCTTCTGCTGGGATAGCTTG 1199
DB 33327 GCAAACTGCCACATCTCAGCTCTAAGCAAGAGGAAACCTTCTGCTGGGATAGCTTG 33386
QY 1200 TGCTTAATGGAACAAATGGATGATACCTCTCTGGAATGATCTCTCTGGAATGATGA 1259
DB 33387 TGCTTAATGGAACAAATGGATGATACCTCTCTGGAATGATCTCTCTGGAATGATGA 33446
QY 1260 CAAAGCAGGTTTACCTAGTATAGTTTCTCCCAACTCTTCCCATCATAGCAGATGAGAAA 1319
DB 33447 CAAAGCAGGTTTACCTAGTATAGTTTCTCCCAACTCTTCCCATCATAGCAGATGAGAAA 33506
QY 1320 ATATATTTTTATGGCACCTGGGATGAACAGCAAGATGCTCACTTCTGGAGCTGCA 1379
DB 33507 ATATATTTTTATGGCACCTGGGATGAACAGCAAGATGCTCACTTCTGGAGCTGCA 33566
QY 1380 TATGACTAGGCTCTTGTGACTGGAGGTAAACCTCTGGAATGATCTGCTGGAGAG 1439
DB 33567 TATGACTAGGCTCTTGTGACTGGAGGTAAACCTCTGGAATGATCTGCTGGAGAG 33626
QY 1440 GGGATCAATATTTTGGCACCTGTAATAGGCGATGGCAGACCCAGATGCTCTGCTC 1499

DB 33627 GGGATCAATATTTTGGCACCTGTAATAGGCGATGGCAGACCCAGATGCTCTGCTC 33686
QY 1500 ACAGTCAGTATGTGTAAGATCCCTGGTGGCTTCCACCAAGCATCTTCTGAGCAAAAT 1559
DB 33687 ACAGTCAGTATGTGTAAGATCCCTGGTGGCTTCCACCAAGCATCTTCTGAGCAAAAT 33746
QY 1560 AGGAAATGTATCCCTTCCCTTGGGACAGATGAGCCCTTCCCTGGGATGCTGCTGGA 1619
DB 33747 AGGAAATGTATCCCTTCCCTTGGGACAGATGAGCCCTTCCCTGGGATGCTGCTGGA 33806
QY 1620 GAGCAGATGTGGCTGCTATAGCAGATCCCTTCTGCTGGGATCTTCTGCTGAG 1679
DB 33807 GAGCAGATGTGGCTGCTATAGCAGATCCCTTCTGCTGGGATCTTCTGCTGAG 33866
QY 1680 GGCATAACAGGCTTAGTAAAGTCCAAACAGATGACAGTGTGTGGGCTCTCTGTCAG 1739
DB 33867 GGCATAACAGGCTTAGTAAAGTCCAAACAGATGACAGTGTGTGGGCTCTCTGTCAG 33926
QY 1740 GTTGTGGCTCTCAGCCATGTAGACACATCTCTCAAATGAGGTGTGGGAAATGTTCTTTC 1799
DB 33927 GTTGTGGCTCTCAGCCATGTAGACACATCTCTCAAATGAGGTGTGGGAAATGTTCTTTC 33986
QY 1800 TGCAGGCTTAGAGACTGCTGGGACATCTTCTTGGAGTGTACTTTCAGAGCCTTATAG 1859
DB 33987 TGCAGGCTTAGAGACTGCTGGGACATCTTCTTGGAGTGTACTTTCAGAGCCTTATAG 34046
QY 1860 GATTTTCTTCTGGCAAGATTTCTTCTGTATCACTCAAGCAGCCTCAGCAGAGAAAG 1919
DB 34047 GATTTTCTTCTGGCAAGATTTCTTCTGTATCACTCAAGCAGCCTCAGCAGAGAAAG 34106
QY 1920 CAGCCATGCCAGTATTTCCACTCTCTCAAAGGAACTGACAGCTTATATTTCTCACACT 1979
DB 34107 CAGCCATGCCAGTATTTCCACTCTCTCAAAGGAACTGACAGCTTATATTTCTCACACT 34166
QY 1980 TCTGGGAACTGGGTATATATCAACCAATCAAAATAGAGACTTTCAGAGCAGAGTCA 2039
DB 34167 TCTGGGAACTGGGTATATATCAACCAATCAAAATAGAGACTTTCAGAGCAGAGTCA 34226
QY 2040 TTCTCCAGAAAGAACTTGGGAGATGATGTGAGATGATGAATCTGGGTTTCTATCCAGATT 2099
DB 34227 TTCTCCAGAAAGAACTTGGGAGATGATGTGAGATGATGAATCTGGGTTTCTATCCAGATT 34286
QY 2100 CCAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGGCCACCTGTCATGCCCC 2159
DB 34287 CCAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGGCCACCTGTCATGCCCC 34346
QY 2160 CCAAAACAGATCAGCAGCAGCTTACAGAGCAATTAATCTCTCTCAATGAGGAGAAATCA 2219
DB 34347 CCAAAACAGATCAGCAGCAGCTTACAGAGCAATTAATCTCTCTCAATGAGGAGAAATCA 34406
QY 2220 TTCAAACTGAGCAAGACATTCATATGATCATTTAAAGGAGTGTTCCTTATGTGTAG 2279
DB 34407 TTCAAACTGAGCAAGACATTCATATGATCATTTAAAGGAGTGTTCCTTATGTGTAG 34466
QY 2280 CAAATTAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGAGCAATGGG 2339
DB 34467 CAAATTAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGAGCAATGGG 34526
QY 2340 CTGCAATAGGCAAGATTAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCA 2399
DB 34527 CTGCAATAGGCAAGATTAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCTAGCA 34586
QY 2400 CCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGAGTGAAGATGTGATAA 2459
DB 34587 CCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGAGTGAAGATGTGATAA 34646
QY 2460 TGTCTGCTCTTGTGTAGCTCAGGAGCAATTTCCAGCAGACACACTACAGTTAACGCTGAA 2519
DB 34647 TGTCTGCTCTTGTGTAGCTCAGGAGCAATTTCCAGCAGACACACTACAGTTAACGCTGAA 34706
QY 2520 CTCAGCTGCAAGTAAATAGCATGAACAGTCAAGAAAAATACCTTATAGGGGGGAGGGCTG 2579
DB 34707 CTCAGCTGCAAGTAAATAGCATGAACAGTCAAGAAAAATACCTTATAGGGGGGAGGGCTG 34766

QY 2580 AAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGAAACAGAGGGCCCTC 2639
Db |||||
QY 34767 AAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGAAACAGAGGGCCCTC 34826
Db |||||
QY 2640 CAAGTGAGAGAGCATGAAATAGCAGAGGGCCCTGGATCAGTGGGGTGTATTACAGACA 2699
Db |||||
QY 34827 CAAGTGAGAGAGCATGAAATAGCAGAGGGCCCTGGATCAGTGGGGTGTATTACAGACA 34886
Db |||||
QY 2700 CTTCTCCAGATGCAATCATGATGCTTACAGTCCCTTGGCTATGTGTGCAGAGTGTCCCA 2759
Db |||||
QY 34887 CTTCTCCAGATGCAATCATGATGCTTACAGTCCCTTGGCTATGTGTGCAGAGTGTCCCA 34946
Db |||||
QY 2760 GCCAGATGTGCCCCCACCACCATGCTCAATTTACATGCTCCCTCAATGCCACCTCAAAAG 2819
Db |||||
QY 34947 GCCAGATGTGCCCCCACCACCATGCTCAATTTACATGCTCCCTCAATGCCACCTCAAAAG 35006
Db |||||
QY 2820 GFACCTCTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC 2879
Db |||||
QY 35007 GFACCTCTTCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC 35066
Db |||||
QY 2880 ACATGCTGTTTTTTCCTTTTGGTCTTATATCACTAAATCATCTCATTTACAGCCCTTA 2939
Db |||||
QY 35067 ACATGCTGTTTTTTCCTTTTGGTCTTATATCACTAAATCATCTCATTTACAGCCCTTA 35126
Db |||||
QY 2940 CAGCATTAATAATTTGTTTTTCTCTACTACATTTGATCATGTGGGAATTAACAGATAAC 2999
Db |||||
QY 35127 CAGCATTAATAATTTGTTTTTCTCTACTACATTTGATCATGTGGGAATTAACAGATAAC 35186
Db |||||
QY 3000 GGAAGCCGCTGGGTGGTGGCTCAGCGCTGTAATCCCAACTTTGGAGGCCAAGGCA 3059
Db |||||
QY 35187 GGAAGCCGCTGGGTGGTGGCTCAGCGCTGTAATCCCAACTTTGGAGGCCAAGGCA 35246
Db |||||
QY 3060 GCGGATCACTGAGGTGAGGATTCGAGATTAATCTGCGCCAAATGTTGAAACCCCATN 3119
Db |||||
QY 35247 GCGGATCACTGAGGTGAGGATTCGAGATTAATCTGCGCCAAATGTTGAAACCCCATC 35306
Db |||||
QY 3120 TWTACTAAATACGAATTAACGAGGTGTGGTGGCACACATCTCTAGTCCAG 3173
Db |||||
QY 35307 TWTACTAAATACGAATTAACGAGGTGTGGTGGCACACATCTCTAGTCCAG 35360
Db |||||

RESULT 6
US-09-149-476-303
Sequence 303, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 25.6%; Score 813; DB 3; Length 828;
Best Local Similarity 99.2%; Pred. No. 1,1e-243;
Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2146 ACCCTGGCATGCCCAACAAACAGATCACAGCCAGCTTACAGGCAATTAATCTCTCTCA 2205
Db 1 ACCCTGGCATGCCCAACAAACAGATCACAGCCAGCTTACAGGCAATTAATCTCTCTCA 60
QY 2206 ATGAGAGAAGATCATTCACAACTGAGCAAGACATTCATATGATCATTTAAGAGAGTGT 2265
Db 61 ATGAGAGAAGATCATTCACAACTGAGCAAGACATTCATATGATCATTTAAGAGAGTGT 120
QY 2266 CCCTTATGTGTAGCAAGTATTAATCGGCTAACTCCCTAAATCCAAATGATAGTCTTAGGC 2325
Db 121 CCCTTATGTGTAGCAAGTATTAATCGGCTAACTCCCTAAATCCAAATGATAGTCTTAGGC 180
QY 2326 TGGACAGCAATGGCTGCAATTTAGGCAGATAAAGACATCAGTCCCAAGTAAATGATCCAT 2385
Db 181 TGGACAGCAATGGCTGCAATTTAGGCAGATAAAGACATCAGTCCCAAGTAAATGATCCAT 240
QY 2386 AGACTCATCTAGCACCAACTACATAGCACTATGTTAGGAGCTGCAAGCCCAAGTA 2445
Db 241 AGACTCATCTAGCACCAACTACATAGCACTATGTTAGGAGCTGCAAGCCCAAGTA 300
QY 2446 GAAGATGTGCATAATGTCTGTCTTGTGTAGCTCAGGAGACAAATCCAGCACAGACACTA 2505
Db 301 GAAGATGTGCATAATGTCTGTCTTGTGTAGCTCAGGAGACAAATCCAGCACAGACACTA 360
QY 2506 CAGTTAAAGCTGAAGCTGCAAGTAAATAGCAATAGCAAGTAAATGATAGTAAATACCTTATG 2565
Db 361 CAGTTAAAGCTGAAGCTGCAAGTAAATAGCAATAGCAAGTAAATGATAGTAAATACCTTATG 420
QY 2566 AGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGGAATTTGATAGAGAAATGAGGA 2625
Db 421 AGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGGAATTTGATAGAGAAATGAGGA 480
QY 2626 AGACAGAGGCTCCCAAGTGAGAGAAGCATGAAAAATGAGCAGGGGCTGGATCAGTGGG 2685
Db 481 AGACAGAGGCTCCCAAGTGAGAGAAGCATGAAAAATGAGCAGGGGCTGGATCAGTGGG 540
QY 2686 GTGTATTTCAGAGCACTCTCCAGATGCAATGATGCTCAGAGTCCCTTGCCTTGTGTGT 2745
Db 541 GTGTATTTCAGAGCACTCTCCAGATGCAATGATGCTCAGAGTCCCTTGCCTTGTGTGT 600
QY 2746 GGCAGAGTGTCCAGGCGAGATGTGCCCCCCCCCATGTCCTTACATGTCCTTCAAT 2805
Db 601 GGCAGAGTGTCCAGGCGAGATGTGCCCCCCCCCATGTCCTTACATGTCCTTCAAT 660

QY	2806	GCCACCTCAAAGTACCTCTCTGTAAAGCTTTCCCT-CGATACAGGAATCAAAATTA	2864
Db	661	GGCCACCTCAAAGGACCTCTCTGTAAAGCTTTCCCTCGATACAGGAATCAAAATTA	720
QY	2865	ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGGTCTTCTATCACTAAACTCA	2924
Db	721	ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGGTCTTCTATCACTAAACTCA	780
QY	2925	TCTCATTCAGCCTTACAGCATAACTAATTATTGTTTTCCTCACTACA	2972
Db	781	TCTCATTCAGCCTTACAGCATAACTAATTATTGTTTTCCTCACTACA	828
RESULT 7			
US-09-949-016-28971/c			
; Sequence 28971, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 28971			
; LENGTH: 601			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-28971			
Query Match 18.9%; Score 600.6; DB 4; Length 601;			
Best Local Similarity 99.8%; Pred. No. 2.8e-177;			
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1569	TACCTTCGTTGAGGAGATGAGCCCTTCCCGAGTGCATGGCTGGAGAGAGAT	1628
Db	601	TACCTTCGTTGAGGAGATGAGCCCTTCCCGAGTGCATGGCTGGAGAGAGAT	542
QY	1629	GTGGCTGCATATAAGCACACTCATCCCTTTGCTGGGAATCTTTGTGAGGGCATAACA	1688
Db	541	GTGGCTGCATATAAGCACACTCATCCCTTTGCTGGGAATCTTTGTGAGGGCATAACA	482
QY	1689	GGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGAGTGTGGCT	1748
Db	481	GGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGAGTGTGGCT	422
QY	1749	CTAGCCATCTAGACACACTCTCCAAATGAGTGTGGAAATGTTCTTCTGCAGGGTC	1808
Db	421	CTAGCCATCTAGACACACTCTCCAAATGAGTGTGGAAATGTTCTTCTGCAGGGTC	362
QY	1809	TAGAGACTGTGGGACACTTTTCTTGAGTGTCTACTTCAGAACCTTATAGGATTTCTT	1868
Db	361	TAGAGACTGTGGGACACTTTTCTTGAGTGTCTACTTCAGAACCTTATAGGATTTCTT	302
QY	1869	TCTGGCCAGATTCCTTCTGTATCACTCCAGCAGCTCAGCAGAGAGAGCCATGC	1928
Db	301	YCTGGCCAGATTCCTTCTGTATCACTCCAGCAGCTCAGCAGAGAGAGCCATGC	242
QY	1929	CCAGTATTCACACTCTCCAAAGGAAGTGCACAGCTTATATTTCTCACACTTCTGGGAA	1988
Db	241	CCAGTATTCACACTCTCCAAAGGAAGTGCACAGCTTATATTTCTCACACTTCTGGGAA	182
QY	1989	CTGGGTATATCCAAACCATCAAAATAGAGACCTTGAAGACCTTCAAGACAGTCAATCTCCAGA	2048
US-09-949-016-28972/c			
; Sequence 28972, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 28972			
; LENGTH: 601			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-28972			
Query Match 18.9%; Score 600.6; DB 4; Length 601;			
Best Local Similarity 99.8%; Pred. No. 2.8e-177;			
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1906	CTCAGCAGAAAGAACGACGACATGCCCAGTATTTCCCACTCTCCAAAGGAACTGACCACTT	1965
Db	601	CTCAGCAGAAAGAACGACGACATGCCCAGTATTTCCCACTCTCCAAAGGAACTGACCACTT	542
QY	1966	ATATTTCTCACACTTCTGGGGAACCTGGGTATATCCCAACCATCAAAATAGAGACCTTGC	2025
Db	541	ATATTTCTCACACTTCTGGGGAACCTGGGTATATCCCAACCATCAAAATAGAGACCTTGC	482
QY	2026	AAGAGCAGAGCTCATTTCTCCAGAAAGAACTGGGAGATGATGGTGACAGATGATGAAGCTG	2085
Db	481	AAGAGCAGAGCTCATTTCTCCAGAAAGAACTGGGAGATGATGGTGACAGATGATGAAGCTG	422
QY	2086	GGTTTCATCCAGTTTCCAAAGACTCAGAAACTAGAGTTTAAGCTGAGCAGAGTCCGCC	2145
Db	421	GGTTTCATCCAGTTTCCAAAGACTCAGAAACTAGAGTTTAAGCTGAGCAGAGTCCGCC	362
QY	2146	ACCTGGGATGCCCCACAGATCCAGCCAGCTTACACAGCATTAATCTCTCTCA	2205
Db	361	ACCTGGGATGCCCCACAGATCCAGCCAGCTTACACAGCATTAATCTCTCTCA	302
QY	2206	ATGAGCAAGAAATCATTTCAAACTGAGCAAGACATTCATATGATCATTTTAAGAAAGTGT	2265
Db	301	ATGAGCAAGAAATCATTTCAAACTGAGCAAGACATTCATATGATCATTTTAAGAAAGTGT	242
QY	2266	CCCTTATGTTAGCAAGTATATTCGGTAACTCTTAATCCCAATGATAGTCTTAGGC	2325
Db	241	CCCTTATGTTAGCAAGTATATTCGGTAACTCTTAATCCCAATGATAGTCTTAGGC	182
QY	2326	TGGACAGCAATGGGCTGCATTTAGGCAGATAAAGACATCAGTCCCGAGTAAATGATTCAT	2385

Db 181 TGGACAGCAATGGGCTGCAATTAGGCGATGAAGACATCAGTCCCGTAAATGAATCCAT 122
QY 2386 AGACTCATCTAGCACCAACTACCATTTAGCACTATGTTAGAGCTGCAAGGCCCAAGTA 2445
Db 121 AGACTCATCTAGCACCAACTACCATTTAGCACTATGTTAGAGCTGCAAGGCCCAAGTA 62
QY 2446 GAAGATGTCATTAATCTGCTCTTGTGTAGCTCAGGACACAAATCCAGCACACACTA 2505
Db 61 GAAGATGTCATTAATCTGCTCTTGTGTAGCTCAGGACACAAATCCAGCACACACTA 2
QY 2506 C 2506
Db 1 C 1

RESULT 9
US-09-949-016-28973/c
; Sequence 28973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28973
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-28973

Query Match 18.9%; Score 600.6; DB 4; Length 601;
Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2124 TAAGCTGAGCGAGTGCCTGCGCCACCTTGGCATGCCCCCAAAACAGATCACCGCCAGCTT 2183
Db 601 TAAGCTGAGCGAGTGCCTGCGCCACCTTGGCATGCCCCCAAAACAGATCACCGCCAGCTT 542
QY 2184 ACACAGGCATTAATCTCTCAATGAGGAAGAATCTTCACTGAGCAAGACATTCAT 2243
Db 541 ACACAGGCATTAATCTCTCAATGAGGAAGAATCTTCACTGAGCAAGACATTCAT 482
QY 2244 ATGATCATTTAAGGAAGTGTTCCTTATGTTAGCAAGTATAATCGGCTAACTCTAA 2303
Db 481 ATGATCATTTAAGGAAGTGTTCCTTATGTTAGCAAGTATAATCGGCTAACTCTAA 422
QY 2304 ATCCCAATGAATAGTCTTAGCTGGACAGCAATGGCTGCAATTTAGCGCATTAAGACAT 2363
Db 421 ATCCCAATGAATAGTCTTAGCTGGACAGCAATGGCTGCAATTTAGCGCATTAAGACAT 362
QY 2364 CAGTCCCAAGTAATGAATCCATAGACTCATCTAGCACCAACTACCATTTAGCATATGTTA 2423
Db 361 CAGTCCCAAGTAATGAATCCATAGACTCATCTAGCACCAACTACCATTTAGCATATGTTA 302
QY 2424 GGAGCTCAAGGCCCAAGATAGAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGA 2483
Db 301 SGAGCTCAAGGCCCAAGATAGAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGA 242
QY 2484 GACAATTTCCAGCACAGACACTTACAGTTAAGCTGAACTGCGAGCTGCAAGTAATAGCATGA 2543
Db 241 GACAATTTCCAGCACAGACACTTACAGTTAAGCTGAACTGCGAGCTGCAAGTAATAGCATGA 182

QY 2544 ACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGGATG 2603
Db 181 ACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGGATG 122
QY 2604 AAATTTGATAGAGAAATGAGGAAGACAGAGGCTTCAAGTGAAGAGCATGAAGATG 2663
Db 121 AAATTTGATAGAGAAATGAGGAAGACAGAGGCTTCAAGTGAAGAGCATGAAGATG 62
QY 2664 AGCAGGGGCTGATCAGTGGGCTGTATTTCAGAGCACCTCTCCAGATGCACCATGCATGC 2723
Db 61 AGCAGGGGCTGATCAGTGGGCTGTATTTCAGAGCACCTCTCCAGATGCACCATGCATGC 2
QY 2724 T 2724
Db 1 T 1

RESULT 10
US-09-949-016-28974/c
; Sequence 28974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28974
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-28974

Query Match 18.9%; Score 600.6; DB 4; Length 601;
Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2143 GCCACCTTGGCATGCCCCCAAAACAGATCACCGCCAGCTTACACAGGCAATTAACCTCC 2202
Db 601 GCCACCTTGGCATGCCCCCAAAACAGATCACCGCCAGCTTACACAGGCAATTAACCTCC 542
QY 2203 TCAATGAGGAAGAATCATTTCACTGAGCAAGATTCATATGATCATTTAAGGAAGTG 2262
Db 541 TCAATGAGGAAGAATCATTTCACTGAGCAAGATTCATATGATCATTTAAGGAAGTG 482
QY 2263 TTTCCCTTATGTTAGCAAGTATAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTA 2322
Db 481 TTTCCCTTATGTTAGCAAGTATAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTA 422
QY 2323 GGCTGAGCAAGTGGCTGCAATTTAGGAGATAAGACATCAGTCCAGTAATGAATC 2382
Db 421 GGCTGAGCAAGTGGCTGCAATTTAGGAGATAAGACATCAGTCCAGTAATGAATC 362
QY 2383 CATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAA 2442
Db 361 CATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAA 302
QY 2443 GTAGAAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGAGCAATTCAGCACAGACA 2502
Db 301 STAGAAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGAGCAATTCAGCACAGACA 242
QY 2503 CTACAGTTAACGCTGAAGTGCAGCTGCAAGTGAATAGCATGAAGCAAGTAATACCTT 2562
Db 241 CTACAGTTAACGCTGAAGTGCAGCTGCAAGTGAATAGCATGAAGCAAGTAATACCTT 182

Qy	2563	ATGAGGGGCGAGGGCTGAAGCTGGGCGCTTGAAGGATGGATGAAATTTGGATAGAGAAATGA	2622
Db	181	ATGAGGGGCGAGGGCTGAAGCTGGGCGCTTGAAGGATGGATGAAATTTGGATAGAGAAATGA	122
Qy	2623	GGAAAGACAGAGGGGCTCCAACTGAGAGAAGCATGAAAAATCAGCAGGGGCGCTGGATCAGT	2682
Db	121	GGAAAGACAGAGGGGCTCCAACTGAGAGAAGCATGAAAAATCAGCAGGGGCGCTGGATCAGT	62
Qy	2683	GGGCTGTATTGAGAGCACTCTCCAGATGCACCATGCATGCTCAAGTCCCTTGCCTATG	2742
Db	61	GGGCTGTATTGAGAGCACTCTCCAGATGCACCATGCATGCTCAAGTCCCTTGCCTATG	2
Qy	2743	T	2743
Db	1	T	1

```

RESULT 11
US-09-949-016-28975/c
; Sequence 28975, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28975
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-28975

```

Db	241	ATGAAATTTGGATAGAGAAATGAGGAACACAGAGGGCCTCCAACTGTGAGAGAAAGCATGAAA	182
Qy	2661	ATGAGCAGGGGCCTGGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGCACCATGCA	2720
Db	181	ATGAGCAGGGGCCTGGATCAGTGGGGTGTATTTCAGAGCACCTCTCCAGATGCACCATGCA	122
Qy	2721	TGCTCAGATGCCCTTGCTATGTGTGCGCAGAGTGTCCAGCCAGATGTGTGCCCCCACC	2780
Db	121	TGCTCAGATGCCCTTGCTATGTGTGCGCAGAGTGTCCAGCCAGATGTGTGCCCCCACC	62
Qy	2781	CATGTCCATTATCATATGCTTCAATGCCACCTCAAAGGTACCTCTTCTGTAAAGCTTT	2840
Db	61	CATGTCCATTATCATATGCTTCAATGCCACCTCAAAGGTACCTCTTCTGTAAAGCTTT	2
Qy	2841	C 2841	
Db	1	C 1	

RESULT 12

US-09-949-016-49962/c

; Sequence 49962, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49962

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-49962

	Query Match	18.9%;	Score 600.6;	DB 4;	Length 601;	
	Best Local Similarity	99.8%;	Pred. No. 2.8e-177;			
	Matches 600;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1569	TACCCCTTCGCTTGAGGCAGATGACAGCCCTTCCCCGAGTGCATGCTTGGAGAGCAGAAAT	1628			
Db	601	TACCCCTTCGCTTGAGGCAGATGACAGCCCTTCCCCGAGTGCATGCTTGGAGAGCAGAAAT	542			
Qy	1629	GTGGGCTGTCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAGGGCATAACA	1688			
Db	541	GTGGGCTGTCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAGGGCATAACA	482			
Qy	1689	GGCTTTAGTAAGTCCAAACACAGATGACAGTCTGTGTGGGTCTCTGTCTGAGAGTTGTGGCT	1748			
Db	481	GGCTTAGTAAGTCCAAACACAGATGACAGTCTGTGTGGGTCTCTGTCTGAGAGTTGTGGCT	422			
Qy	1749	CTCAGCCATGTAGACACACACTCTCAAATGGAGTGTGGAAAATGTTCTTTCTGCAGGGTC	1808			
Db	421	CTCAGCCATGTAGACACACACTCTCAAATGGAGTGTGGAAAATGTTCTTTCTGCAGGGTC	362			
Qy	1809	TAGAGACTGCTGGGACACTTTTCTTGGAGTCTACTTTCAGAAGCCTTATAGATTTTCTT	1868			
Db	361	TAGAGACTGCTGGGACACTTTTCTTGGAGTCTACTTTCAGAAGCCTTATAGATTTTCTT	302			
Qy	1869	TCTGGCCAGATTTCTTCTGTATCACTCCAGCAGCCTCAGCAGAAAGCAGCCATGC	1928			
Db	301	YCTGGCCAAAGATTTCTTCTGTATCACTCCAAAGCAGCCTCAGCAGAAAGCAGCCATGC	242			
Qy	1929	CCAGTATTTCCCACTCTCCAAAAGGAACCTGACGAGCTTATATTTCTTCACACTTCTCGGGAA	1988			

Db 241 CCAGTAATCCACTCTCCAAAGAACTGACCACTTATATTTCTCACACTTCTGGGAA 182
QY 1989 CTGGGTATATCAACCATCAAAATAGAAGACCTTCAGAGAGCAGTCAATCTCCAGA 2048
Db 181 CTGGGTATATCAACCATCAAAATAGAAGACCTTCAGAGAGCAGTCAATCTCCAGA 122
QY 2049 AGGAACTTGGAGATGATGTGCAGATGATGAACTGGGTTTATCCAGTTCCAAAGACT 2108
Db 121 AGGAACTTGGAGATGATGTGCAGATGATGAACTGGGTTTATCCAGTTCCAAAGACT 62
QY 2109 CAGAGAACTAGATTTAAAGCTGAGGAGAGTGCGCCACCCCTGGCATGCCCAACACAG 2168
Db 61 CAGAGAACTAGATTTAAAGCTGAGGAGAGTGCGCCACCCCTGGCATGCCCAACACAG 2
QY 2169 A 2169
Db 1 A 1

RESULT 13

US-09-949-016-49963/c
; Sequence 49963, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49963
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49963

Query Match 18.9%; Score 600.6; DB 4; Length 601;
Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1906 CTCAGCAGAGAGAGCAGCCATGCCAGTATTCACACTTCCCACTCTCCAAAGGAACTGACCACTT 1965
Db 601 CTCAGCAGAGAGAGCAGCCATGCCAGTATTCACACTTCCCACTCTCCAAAGGAACTGACCACTT 542
QY 1966 ATATTTCTCACACTTCTGGGAACTGGGTATATTCACCACTTCCCACTCTCCAAAGGAACTGACCACTTGC 2025
Db 541 ATATTTCTCACACTTCTGGGAACTGGGTATATTCACCACTTCCCACTCTCCAAAGGAACTGACCACTTGC 482
QY 2026 AAGAGCAGAGTCAATTCACAGAGGAACTTTGGAGATGATGGTGAGATGATGAAGAACTG 2085
Db 481 AAGAGCAGAGTCAATTCACAGAGGAACTTTGGAGATGATGGTGAGATGATGAAGAACTG 422
QY 2086 GGTTCATCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCCGCC 2145
Db 421 GGTTCATCCAGTTCCAAAGACTCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTGCCGCC 362
QY 2146 ACCCTGGCATGCCCAACACAGATCACCACTGAGTTCACAGGCACTTAACTCTCTCTCA 2205
Db 361 ACCCTGGCATGCCCAACACAGATCACCACTGAGTTCACAGGCACTTAACTCTCTCTCA 302
QY 2206 ATGAGGAGAACTCAATTCACAACTGAGGAGAACTTCATATGATCATTTAAGGAAAGTGT 2265
Db 301 RTGAGGAGAACTCAATTCACAACTGAGGAGAACTTCATATGATCATTTAAGGAAAGTGT 242

QY 2266 CCCTTATGTGTAGCAAGTATTAATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGC 2325
Db 241 CCCTTATGTGTAGCAAGTATTAATCGGCTAACTCTTAATCCCAATGAATAGTCTTAGGC 182
QY 2326 TGGACAGCAATGGCTGCAATTTAGGAGATTAAGACATCAGTCCCAAGTAAATGAATCCAT 2385
Db 181 TGGACAGCAATGGCTGCAATTTAGGAGATTAAGACATCAGTCCCAAGTAAATGAATCCAT 122
QY 2386 AGACTCATCTAGCACCAACTAGCATTTAGCACTATGTTAGGAGTGAAGGCCCCCAAGTA 2445
Db 121 AGACTCATCTAGCACCAACTAGCATTTAGCACTATGTTAGGAGTGAAGGCCCCCAAGTA 62
QY 2446 GAAGATGTGCATAATGTCTGCTTCTGTGTAGCTCAGGAGACAAATTCAGCAGACACTA 2505
Db 61 GAAGATGTGCATAATGTCTGCTTCTGTGTAGCTCAGGAGACAAATTCAGCAGACACTA 2
QY 2506 C 2506
Db 1 C 1

RESULT 14

US-09-949-016-49964/c
; Sequence 49964, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49964
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49964

Query Match 18.9%; Score 600.6; DB 4; Length 601;
Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2124 TAAGCTGAGCAGAGTGCGCCACCTGGCATGCCCAACAGATCACCAGCCAGCTT 2183
Db 601 TAAGCTGAGCAGAGTGCGCCACCTGGCATGCCCAACAGATCACCAGCCAGCTT 542
QY 2184 ACACAGCATTAATCTCTCTCAATGAGGAAGAAATATTCAACTGAGCAAGACATTCAT 2243
Db 541 ACACAGCATTAATCTCTCTCAATGAGGAAGAAATATTCAACTGAGCAAGACATTCAT 482
QY 2244 ATGATCATTTAAGGAAGTGTTCCTTATGTTAGCAAGTATTAATCGGCTTAATCTCTAA 2303
Db 481 ATGATCATTTAAGGAAGTGTTCCTTATGTTAGCAAGTATTAATCGGCTTAATCTCTAA 422
QY 2304 ATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAATTTAGGAGATAAGACAT 2363
Db 421 ATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGCTGCAATTTAGGAGATAAGACAT 362
QY 2364 CAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTA 2423
Db 361 CAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTA 302
QY 2424 GAGAGTGCAGAGGCCCAAGATGAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGA 2483
Db 301 SGAGCTGCAAGGCCCAAGATGAGATGTCATAATGTCTGCTCTTGTGTAGCTCAGGA 242

QY 2484 GACAAATCCAGACAGACACTACAGTTAAAGCTGAACTGCAGCTGCAGTGAATAGCATGA 2543
DB 241 GACAATCCAGACAGACACTACAGTTAAAGCTGAACTGCAGCTGCAGTGAATAGCATGA 182
QY 2544 ACAGTCAGAAAAATACCTTATGAGGGGGGAGGGCTGAAAGCTGGGCTTGAAGGATGGATG 2603
DB 181 ACAGTCAGAAAAATACCTTATGAGGGGGGAGGGCTGAAAGCTGGGCTTGAAGGATGGATG 122
QY 2604 AAATTTGGATAGAGAAATAGGAAGACAGAGAGGGCTTCCAAAGTCAGAGAGCATGAAAAATG 2663
DB 121 AAATTTGGATAGAGAAATAGGAAGACAGAGAGGGCTTCCAAAGTCAGAGAGCATGAAAAATG 62
QY 2664 ACAGGGGGCTGGATCAGTGGGGTGTATTACAGAGCACCTCTCCAGATGCACCATGCATGC 2723
DB 61 AGAGGGGGCTGGATCAGTGGGGTGTATTACAGAGCACCTCTCCAGATGCACCATGCATGC 2
QY 2724 T 2724
DB 1 T 1

RESULT 15
US-09-949-016-49965/c
; Sequence 49965; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49965
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49965

Query Match 18.9%; Score 600.6; DB 4; Length 601;
Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2143 GCCACCTGGATGCCCAACACAGATCACAGGCAGCTTACAGGGCATTAACTCTCC 2202
DB 601 GCCACCTGGATGCCCAACACAGATCACAGGCAGCTTACAGGGCATTAACTCTCC 542
QY 2203 TCAATGAGGAAGAAATCATTCACAACTGACAGACATTCATATGATCATTTAAGGAAGTG 2262
DB 541 TCAATGAGGAAGAAATCATTCACAACTGACAGACATTCATATGATCATTTAAGGAAGTG 482
QY 2263 TTTCCCTTATGTTAGCAAGTATATCGGCTAACTCTTAAATCCCAATGAATAGTCCTA 2322
DB 481 TTTCCCTTATGTTAGCAAGTATATCGGCTAACTCTTAAATCCCAATGAATAGTCCTA 422
QY 2323 GCGTGACAGCAATGGCTGCAATTAGGAGATTAAGACATCAGTCCCGAATGAATC 2382
DB 421 GCGTGACAGCAATGGCTGCAATTAGGAGATTAAGACATCAGTCCCGAATGAATC 362
QY 2383 CATAGACTCATCTAGCACCAACTTACCATTAGCACTATGTTAGAGCTGCAAGGCCCAA 2442
DB 361 CATAGACTCATCTAGCACCAACTTACCATTAGCACTATGTTAGAGCTGCAAGGCCCAA 302
QY 2443 GTAGAGATGTGCATATCTCTGCTCTGTAGCTCAGGAGACAATTCAGACAGACA 2502

DB 301 STAGAGATGTGCATATATGTCTGCTCTTGTGTAGCTCAGGAGACAATTCAGACAGACA 242
QY 2503 CTACAGTTTAAAGCTGAACTGCAGCTGCAAGTAAATAGCATGAACAGTCAAGAAAATACCTT 2562
DB 241 CTACAGTTTAAAGCTGAACTGCAGCTGCAAGTAAATAGCATGAACAGTCAAGAAAATACCTT 182
QY 2563 ATGAGGGGGCAGGGCTGAAAGCTGGGCTTGAAGGATGGATGAAAATTTGGATAGAGAATGA 2622
DB 181 ATGAGGGGGCAGGGCTGAAAGCTGGGCTTGAAGGATGGATGAAAATTTGGATAGAGAATGA 122
QY 2623 GGAAGACAGAGGGGGCTTCCAAAGTCAGAGAGCATGAAAAATGACGAGGGGGCTTGGATCAGT 2682
DB 121 GGAAGACAGAGGGGGCTTCCAAAGTCAGAGAGCATGAAAAATGACGAGGGGGCTTGGATCAGT 62
QY 2683 GGGGTGTATTACAGAGCACCTCTCCAGATGCACCATGCATGCTCCAGTCCCTTGGCTATG 2742
DB 61 GGGGTGTATTACAGAGCACCTCTCCAGATGCACCATGCATGCTCCAGTCCCTTGGCTATG 2
QY 2743 T 2743
DB 1 T 1

Search completed: February 6, 2005, 00:26:49
Job time : 507 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: February 5, 2005, 18:18:04 ; Search time 1606 Seconds
(without alignments)
11371.712 Million cell updates/sec

Title: US-09-882-171-174
Perfect score: 3173
Sequence: 1 tcgacccasgcgtccgtgc.....gcacacatctgtagctccag 3173

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues
Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:
11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/2/pubpna/US09C_NEW_PUB.seq:
13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/prodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/prodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3169.4	99.9	3173	10	US-09-809-391-174
2	3169.4	99.9	3173	10	US-09-882-171-174
3	3169.4	99.9	3173	17	US-10-164-861-174
4	3159.8	99.6	3687	14	US-10-198-846-13255
5	3142.2	99.0	3326	18	US-10-723-860-6219
6	1034	32.6	1067	18	US-10-723-860-1885
7	1033.4	32.6	1040	16	US-10-436-523-29
8	813	25.6	828	10	US-09-809-391-303
9	813	25.6	828	10	US-09-882-171-303
10	813	25.6	828	17	US-10-164-861-303
11	414.2	-13.1	420	10	US-09-918-995-36774

12	217.6	6.9	502	9	US-09-783-590-5649	Sequence 5649, Ap
13	212.4	6.7	820	14	US-10-198-846-6370	Sequence 6370, Ap
14	141.2	4.5	16815	15	US-10-017-161-1579	Sequence 1579, Ap
15	140	4.4	96592	17	US-10-052-482-184	Sequence 184, App
16	138.4	4.4	845	13	US-10-027-632-166284	Sequence 166284,
17	138.4	4.4	845	13	US-10-027-632-166285	Sequence 166285,
18	138.4	4.4	845	13	US-10-027-632-166286	Sequence 166286,
19	138.4	4.4	845	13	US-10-027-632-166284	Sequence 166284,
20	138.4	4.4	845	17	US-10-027-632-166285	Sequence 166285,
21	138.4	4.4	845	17	US-10-027-632-166286	Sequence 166286,
22	137.8	4.4	17321	17	US-10-376-344-3	Sequence 3, Appli
23	136.8	4.3	25899	18	US-10-322-696-10	Sequence 10, Appli
24	136	4.3	131576	13	US-10-087-192-1564	Sequence 1564, Ap
25	135.8	4.3	126990	18	US-10-717-597-68	Sequence 68, Appli
26	135	4.3	17996	9	US-09-764-877-2695	Sequence 2695, Ap
27	135	4.3	17996	17	US-10-242-515-2695	Sequence 2695, Ap
28	135	4.3	60057	13	US-10-087-192-700	Sequence 700, App
29	135	4.3	112241	18	US-10-322-281-656	Sequence 656, App
30	134.8	4.2	3347	13	US-10-027-632-114894	Sequence 114894,
31	134.8	4.2	3347	17	US-10-027-632-114894	Sequence 114894,
32	134.8	4.2	8158	10	US-09-832-292-30	Sequence 30, Appli
33	134.6	4.2	2625	9	US-09-764-891-8802	Sequence 8802, Ap
34	134.6	4.2	9519	9	US-09-764-847-1056	Sequence 1056, Ap
35	134.6	4.2	9519	9	US-09-764-877-3534	Sequence 3534, Ap
36	134.6	4.2	9519	14	US-10-092-154-1056	Sequence 1056, Ap
37	134.6	4.2	9519	17	US-10-242-515-3534	Sequence 3534, Ap
38	134.6	4.2	39729	17	US-10-292-798-1285	Sequence 1285, Ap
39	134.4	4.2	9474	9	US-09-764-878-372	Sequence 372, App
40	134.4	4.2	9474	14	US-10-079-854-372	Sequence 372, App
41	134.4	4.2	50000	17	US-10-364-505-8	Sequence 8, Appli
42	134.4	4.2	50000	18	US-10-681-199-8	Sequence 8, Appli
43	134.2	4.2	633	13	US-10-027-632-5668	Sequence 5668, Ap
44	134.2	4.2	633	13	US-10-027-632-5669	Sequence 5669, Ap
45	134.2	4.2	633	17	US-10-027-632-5668	Sequence 5668, Ap

ALIGNMENTS

RESULT 1
US-09-809-391-174
; Sequence 174, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 3173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3119)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (3121)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-174

Query Match 99.9%; Score 3169.4; DB 10; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCACACCCASGCGTCGCTGCTTTTCCACACAGGTAGACCTGAAAGAGATGGCTCAGC 60
Db 1 TCACACCCASGCGTCGCTGCTTTTCCACACAGGTAGACCTGAAAGAGATGGCTCAGC 60

QY 61 ACCACCTATGGATCTTGCTCCCTTTCCTGCGGCGGAGCAGCTGGAAAAAGACT 120
DB 61 ACCACCTATGGATCTTGCTCCCTTTCCTGCGGCGGAGCAGCTGGAAAAAGACT 120
QY 121 CAGAAATCTTACAGTGAATGGATCTGGGAGAGTCACTTCCCTCTGAATATCC 180
DB 121 CAGAAATCTTACAGTGAATGGATCTGGGAGAGTCACTTCCCTCTGAATATCC 180
QY 181 AAGAACCAAGCAAGTAAATCAATCTTGAGCTTCTAAACATCTCTGCTGATGTA 240
DB 181 AAGAACCAAGCAAGTAAATCAATCTTGAGCTTCTAAACATCTCTGCTGATGTA 240
QY 241 CACAGGAGACTCAGAAACAGCACCCGCTAGTTATCTGTGACCCACAGAAATTAATGAAC 300
DB 241 CACAGGAGACTCAGAAACAGCACCCGCTAGTTATCTGTGACCCACAGAAATTAATGAAC 300
QY 301 GGATACATGCTTAGTCCGAATCAATCTGCTATAGCGATCTGAGGATGGAGAGC 360
DB 301 GGATACATGCTTAGTCCGAATCAATCTGCTATAGCGATCTGAGGATGGAGAGC 360
QY 361 CAGGAGACTCAGAAACAGACATAAATACACAGGCTGATCCCTACACACCACCAAGCGCT 420
DB 361 CAGGAGACTCAGAAACAGACATAAATACACAGGCTGATCCCTACACACCACCAAGCGCT 420
QY 421 ACAACCTGCAATCTATGCTGGCTGGGAAACCAAAAATTAACAGAGTTTAATGGCAT 480
DB 421 ACAACCTGCAATCTATGCTGGCTGGGAAACCAAAAATTAACAGAGTTTAATGGCAT 480
QY 481 CTGTGAACAGCACTGTAATGTCACACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540
DB 481 CTGTGAACAGCACTGTAATGTCACACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540
QY 541 TGACATACAAATCTGCTGGCTGGGAAAGAGGTAATGCTCCTCAAAATCTTCCAGACTC 600
DB 541 TGACATACAAATCTGCTGGCTGGGAAAGAGGTAATGCTCCTCAAAATCTTCCAGACTC 600
QY 601 CTGAGAACCAAGAGCTGATTAACAGTGTACAGCCAGAACCTGTGAGCAACAAATCTG 660
DB 601 CTGAGAACCAAGAGCTGATTAACAGTGTACAGCCAGAACCTGTGAGCAACAAATCTG 660
QY 661 ACTCCATCTGCGCGGAGCTCTGTGAGACATCGCAATGGCTTCCGTAATCCACCA 720
DB 661 ACTCCATCTGCGCGGAGCTCTGTGAGACATCGCAATGGCTTCCGTAATCCACCA 720
QY 721 CCGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTGTTCTCAATCTGCTCAGTGT 780
DB 721 CCGGTTGCTGAGCGTCTGGCTATGTTCTTCTGCTGTTCTCAATCTGCTCAGTGT 780
QY 781 TTTTGTTCGTTGTTCAAGAGNAGACAGATGCTGCTCAAGAAAAACATATACAT 840
DB 781 TTTTGTTCGTTGTTCAAGAGNAGACAGATGCTGCTCAAGAAAAACATATACAT 840
QY 841 ATATCATGGCTTCAAGAAACACCCAGCAGCAGTCCAGAAATCTATGATGAAATCCTGC 900
DB 841 ATATCATGGCTTCAAGAAACACCCAGCAGCAGTCCAGAAATCTATGATGAAATCCTGC 900
QY 901 AGTCCAAGTGTCTCCCTCAAGGAAAGCCAGTGAACACAGTTTATCCGAAGTGCAGT 960
DB 901 AGTCCAAGTGTCTCCCTCAAGGAAAGCCAGTGAACACAGTTTATCCGAAGTGCAGT 960
QY 961 TTGCTGATAGTGGGAAAGCCAGCACAGACAGTAAACCTCTGGGACTTCAAGCT 1020
DB 961 TTGCTGATAGTGGGAAAGCCAGCACAGACAGTAAACCTCTGGGACTTCAAGCT 1020
QY 1021 ATGAAATGTGATCTAGGCTGCTGGCTGAATTTCTCCCTCTGGAATCTGAGTTTACAA 1080
DB 1021 ATGAAATGTGATCTAGGCTGCTGGCTGAATTTCTCCCTCTGGAATCTGAGTTTACAA 1080
QY 1081 CCAATCTGGCAGTTCCCTGGATCCAGATCTTCTGCGCAACTCTTACTGGGAGATTG 1140
DB 1081 CCAATCTGGCAGTTCCCTGGATCCAGATCTTCTGCGCAACTCTTACTGGGAGATTG 1140
QY 1141 CAAACTGCCACATCTCAGCGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGT 1200

DB 1141 CAAACTGCCACATCTCAGCGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGT 1200
QY 1201 GCCTAAATGGACAAATGGATGCATACCTTCTCTGAAATGATCCCTTCTGAATGAATGAC 1260
DB 1201 GCCTAAATGGACAAATGGATGCATACCTTCTCTGAAATGATCCCTTCTGAATGAATGAC 1260
QY 1261 AAGCAGGTTACCTAGTATAGTTTTCCTAAACTTCTTCCCATCATAGCACATGTAGAAA 1320
DB 1261 AAGCAGGTTACCTAGTATAGTTTTCCTAAACTTCTTCCCATCATAGCACATGTAGAAA 1320
QY 1321 TAAATATTTTATGGCACACCTGGGATAAACAAGCAAGATTTGCTCACTTCTGGAAGCTGCAT 1380
DB 1321 TAAATATTTTATGGCACACCTGGGATAAACAAGCAAGATTTGCTCACTTCTGGAAGCTGCAT 1380
QY 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
DB 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACAACCTGCCAGTAACTGTGGGAGAGG 1440
QY 1441 GGATCAATATTTGACACACCTGTAATAGGCCATGGCACACGAGCAAGATGCTCTGCTCA 1500
DB 1441 GGATCAATATTTGACACACCTGTAATAGGCCATGGCACACGAGCAAGATGCTCTGCTCA 1500
QY 1501 CAGTCAGTATCTGTGAAGATCCCTGCTGGTGGCTTTCACACGCATCTTCTGAGCAAAATTA 1560
DB 1501 CAGTCAGTATCTGTGAAGATCCCTGCTGGTGGCTTTCACACGCATCTTCTGAGCAAAATTA 1560
QY 1561 GGAAAAATGTACCTTTCGCTGAGGAGATGAGGAGGCTTCCCGAGTGCATGGCTGGAG 1620
DB 1561 GGAAAAATGTACCTTTCGCTGAGGAGATGAGGAGGCTTCCCGAGTGCATGGCTGGAG 1620
QY 1621 AGCAGAAATGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGCAAG 1680
DB 1621 AGCAGAAATGGGCTGCATATAAGCACACTCATCCCTTGTCTGGGAATCTTGTGCAAG 1680
QY 1681 GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGCTCTCTGTCAAG 1740
DB 1681 GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGCTCTCTGTCAAG 1740
QY 1741 TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTCT 1800
DB 1741 TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTCT 1800
QY 1801 GCAGGCTCTAGAGACTGCTGGGACACTTCTTGGAGTGTCTTCAAGAGCCTTATAGG 1860
DB 1801 GCAGGCTCTAGAGACTGCTGGGACACTTCTTGGAGTGTCTTCAAGAGCCTTATAGG 1860
QY 1861 ATTTTCTTCTGGCCCAAGATTTCCCTCTGTATCACTCCAAAGCAGCCTCAGCAGAAAGC 1920
DB 1861 ATTTTCTTCTGGCCCAAGATTTCCCTCTGTATCACTCCAAAGCAGCCTCAGCAGAAAGC 1920
QY 1921 AGCAGTCCAGTATTTCCACTCTCCAAAGAGAACTGACAGCTTATATTTCTCACAT 1980
DB 1921 AGCAGTCCAGTATTTCCACTCTCCAAAGAGAACTGACAGCTTATATTTCTCACAT 1980
QY 1981 CTGGGAACTGGGATAATCAAAACATCAAGACCTTTCAGAAAGCAGAGTGCAT 2040
DB 1981 CTGGGAACTGGGATAATCAAAACATCAAGACCTTTCAGAAAGCAGAGTGCAT 2040
QY 2041 TCTCCAGAAAGAACTTGGGAGATGATGTGAGATGATGAAACTGGGTTTATCCAGTTT 2100
DB 2041 TCTCCAGAAAGAACTTGGGAGATGATGTGAGATGATGAAACTGGGTTTATCCAGTTT 2100
QY 2101 CAAAGACTCAGAGAACTAGATTTAAGCTGAGGAGAGTGGCCACCTGCGATGCC 2160
DB 2101 CAAAGACTCAGAGAACTAGATTTAAGCTGAGGAGAGTGGCCACCTGCGATGCC 2160
QY 2161 ACAACAGATCAACAGCAGCTTACAGAGGCAATTAACCTCTCAATGAGGAAATCAT 2220
DB 2161 ACAACAGATCAACAGCAGCTTACAGAGGCAATTAACCTCTCAATGAGGAAATCAT 2220
QY 2221 TCACAACTGAGAGAAACATTTATATGATCATTTAAGGAAGTGTTCCTCTATGCTTAGC 2280

Db	2221	TCACAACTGACGACGACATTCATATGATCATTTAAAGGAAGTGTTTCCCTCTATGTGTAGC	2280	;	PRIOR APPLICATION NUMBER: 09/809,391
Qy	2281	AAGTATAATCGGCTAACTCTTAATCCCAATAGTCTAGGCTGGACGACGATGGC	2340	;	PRIOR FILING DATE: 2001-03-16
Db	2281	AAGTATAATCGGCTAACTCTTAATCCCAATAGTCTAGGCTGGACGACGATGGC	2340	;	PRIOR APPLICATION NUMBER: 09/149,476
Qy	2341	TGCAATATAGGAGATTAAGACATAGTCCAGTAAATGAATCCATAGACTCATCTAGCAC	2400	;	PRIOR FILING DATE: 1998-09-08
Db	2341	TGCAATATAGGAGATTAAGACATAGTCCAGTAAATGAATCCATAGACTCATCTAGCAC	2400	;	PRIOR APPLICATION NUMBER: PCT/US98/04493
Qy	2401	CAACTACCAATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGATTAAT	2460	;	PRIOR FILING DATE: 1998-03-06
Db	2401	CAACTACCAATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGATTAAT	2460	;	PRIOR APPLICATION NUMBER: 60/040,162
Qy	2461	GTCTGCTCTTGTGTAGTCAGAGACAATTCAGACAGACACTACAGTTAAGCTGAC	2520	;	PRIOR FILING DATE: 1997-03-07
Db	2461	GTCTGCTCTTGTGTAGTCAGAGACAATTCAGACAGACACTACAGTTAAGCTGAC	2520	;	PRIOR APPLICATION NUMBER: 60/040,333
Qy	2521	TGCAGCTGCAAGTAAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGA	2580	;	PRIOR FILING DATE: 1997-03-07
Db	2521	TGCAGCTGCAAGTAAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGCGAGGCTGA	2580	;	PRIOR APPLICATION NUMBER: 60/040,334
Qy	2581	AGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCC	2640	;	PRIOR FILING DATE: 1997-03-07
Db	2581	AGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCC	2640	;	PRIOR APPLICATION NUMBER: 60/040,336
Qy	2641	AAGTGAGAGACATGAAAAATGAGCAGGGGCTGATCAGTGGGGTGATTCAGAGCAC	2700	;	PRIOR FILING DATE: 1997-03-07
Db	2641	AAGTGAGAGACATGAAAAATGAGCAGGGGCTGATCAGTGGGGTGATTCAGAGCAC	2700	;	PRIOR APPLICATION NUMBER: 60/040,163
Qy	2701	CTCTCAGATGCAACCATGATGCTCAGTCCCTTGCCTATGTGGCAGAGTGTCCAG	2760	;	PRIOR FILING DATE: 1997-03-07
Db	2701	CTCTCAGATGCAACCATGATGCTCAGTCCCTTGCCTATGTGGCAGAGTGTCCAG	2760	;	PRIOR APPLICATION NUMBER: 60/047,600
Qy	2761	CCAGATGTGTGCCCCCACCACCCCATGTCCATTTACATGTCCTTCAATGCCACCTCAAAAGG	2820	;	PRIOR FILING DATE: 1997-05-23
Db	2761	CCAGATGTGTGCCCCCACCACCCCATGTCCATTTACATGTCCTTCAATGCCACCTCAAAAGG	2820	;	PRIOR APPLICATION NUMBER: 60/047,615
Qy	2821	TACCTCTTGTAAAGCTTCCCTGATCAGGAATCAAAATTAATCAGGGATCTTTTCA	2880	;	PRIOR FILING DATE: 1997-05-23
Db	2821	TACCTCTTGTAAAGCTTCCCTGATCAGGAATCAAAATTAATCAGGGATCTTTTCA	2880	;	PRIOR APPLICATION NUMBER: 60/047,502
Qy	2881	CAGTGTGTTTTTCTTTGTCCTTCTATCACTAAACTCATCTCATTCAGCCTTAC	2940	;	PRIOR FILING DATE: 1997-05-23
Db	2881	CAGTGTGTTTTTCTTTGTCCTTCTATCACTAAACTCATCTCATTCAGCCTTAC	2940	;	PRIOR APPLICATION NUMBER: 60/047,503
Qy	2941	AGCAATAAATAATTTGTTTTCTCACTACATTTGTACATGTGGGAATTACAGATAAACG	3000	;	PRIOR FILING DATE: 1997-05-23
Db	2941	AGCAATAAATAATTTGTTTTCTCACTACATTTGTACATGTGGGAATTACAGATAAACG	3000	;	PRIOR APPLICATION NUMBER: 60/047,581
Qy	3001	GAAGCKGCTGGGGTGTGCTACGCTGTATCCCAACACTTTGGGAGGCCAAGGCAG	3060	;	PRIOR FILING DATE: 1997-05-23
Db	3001	GAAGCKGCTGGGGTGTGCTACGCTGTATCCCAACACTTTGGGAGGCCAAGGCAG	3060	;	PRIOR APPLICATION NUMBER: 60/047,584
Qy	3061	GGCGATCACCTGAGTTCAGGARTTCGAGATTARTCTGCCCAACATGGTGAACCCCATNT	3120	;	PRIOR FILING DATE: 1997-05-23
Db	3061	GGCGATCACCTGAGTTCGAGARTTCGAGATTARTCTGGCCCAACATGGTGAACCCCATNT	3120	;	PRIOR APPLICATION NUMBER: 60/047,492
Qy	3121	NTACTAAAAATACGAAATTAGCCAGGTGTGGTGCCACACATCTGTAGTCCAG	3173	;	PRIOR FILING DATE: 1997-05-23
Db	3121	NTACTAAAAATACGAAATTAGCCAGGTGTGGTGCCACACATCTGTAGTCCAG	3173	;	PRIOR APPLICATION NUMBER: 60/047,598

RESULT 2
US-09-882-171-174
; Sequence 174, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18

1	PRIOR APPLICATION NUMBER: 60/047,586
2	PRIOR FILING DATE: 1997-05-23
3	PRIOR APPLICATION NUMBER: 60/047,590
4	PRIOR FILING DATE: 1997-05-23
5	PRIOR APPLICATION NUMBER: 60/047,594
6	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,589
8	PRIOR FILING DATE: 1997-05-23
9	PRIOR APPLICATION NUMBER: 60/047,593
10	PRIOR FILING DATE: 1997-05-23
11	PRIOR APPLICATION NUMBER: 60/047,614
12	PRIOR FILING DATE: 1997-05-23
13	PRIOR APPLICATION NUMBER: 60/043,578
14	PRIOR FILING DATE: 1997-04-11
15	PRIOR APPLICATION NUMBER: 60/043,576
16	PRIOR FILING DATE: 1997-04-11
17	PRIOR APPLICATION NUMBER: 60/047,501
18	PRIOR FILING DATE: 1997-05-23
19	PRIOR APPLICATION NUMBER: 60/043,670
20	PRIOR FILING DATE: 1997-04-11
21	PRIOR APPLICATION NUMBER: 60/056,632
22	PRIOR FILING DATE: 1997-08-22
23	PRIOR APPLICATION NUMBER: 60/056,664
24	PRIOR FILING DATE: 1997-08-22
25	PRIOR APPLICATION NUMBER: 60/056,876
26	PRIOR FILING DATE: 1997-08-22
27	PRIOR APPLICATION NUMBER: 60/056,881
28	PRIOR FILING DATE: 1997-08-22
29	PRIOR APPLICATION NUMBER: 60/056,909
30	PRIOR FILING DATE: 1997-08-22
31	PRIOR APPLICATION NUMBER: 60/056,875
32	PRIOR FILING DATE: 1997-08-22
33	PRIOR APPLICATION NUMBER: 60/056,862
34	PRIOR FILING DATE: 1997-08-22
35	PRIOR APPLICATION NUMBER: 60/056,887
36	PRIOR FILING DATE: 1997-08-22
37	PRIOR APPLICATION NUMBER: 60/056,908
38	PRIOR FILING DATE: 1997-08-22
39	PRIOR APPLICATION NUMBER: 60/048,964
40	PRIOR FILING DATE: 1997-06-06
41	PRIOR APPLICATION NUMBER: 60/057,650
42	PRIOR FILING DATE: 1997-09-05
43	PRIOR APPLICATION NUMBER: 60/056,884
44	PRIOR FILING DATE: 1997-08-22
45	PRIOR APPLICATION NUMBER: 60/057,669
46	PRIOR FILING DATE: 1997-09-05

Query Match	99.9%;	Score	3169.4;	DB	10;	Length	3173;	
Best Local Similarity	100.0%;	Pred. No.	0;					
Matches 3173;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TCGACCCCSAGCGTCGCTGCTTTTCCACAGAAGTTAGACCCCTGAAAGAGATGGCTCAGC	60					
Db	1	TCGACCCCSAGCGTCGCTGCTTTTCCACAGAAGTTAGACCCCTGAAAGAGATGGCTCAGC	60					
Qy	61	ACCACCTATGGATCTTGGCTCTCTTGGCTGCAAAACCTGCCCGGAAGCAGCTGGAAGAAGACT	120					
Db	61	ACCACCTATGGATCTTGGCTCTCTTGGCTGCAAAACCTGCCCGGAAGCAGCTGGAAGAAGACT	120					
Qy	121	CAGAAATCTTCACAGTGAATGGATCTGGGAGAGTCAGTCACCTTCCCTGCTAAATATCC	180					
Db	121	CAGAAATCTTCACAGTGAATGGGATCTGGGAGAGTCAGTCACCTTCCCTGCTAAATATCC	180					
Qy	181	AAGAACCACGGCAAGTTAAAAATCATTTGCTTGGACTTCTAAAAACATCTGTTGCTTATGTAA	240					
Db	181	AAGAACCACGGCAAGTTAAAAATCATTTGCTTGGACTTCTAAAAACATCTGTTGCTTATGTAA	240					
Qy	241	CACCAGGAGACTCAGAAACAGCACCCGTAATTACTGTGACCCACAGAAATTTATTATGAAC	300					
Db	241	CACCAGGAGACTCAGAAACAGCACCCGTAATTACTGTGACCCACAGAAATTTATTATGAAC	300					
Qy	301	GGATACATGCTTGGTGCAGAACTACAATCTGGTCAATTAGCGATCTCAGAGATGGAAGACG	360					

301 GGATACATGCCCTTAGGTCGGAACCTACAACTCTGGTCATTAGCGATCTGAGGATGGAAGCG 360 Db
361 CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCAAGCGCT 420 QY
361 CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCAAGCGCT 420 Db
421 ACAACCTGCAAACTCTATCTCGGCTTGGGAACCAAAAATACACAGAGTTTAAATGGCAT 480 QY
421 ACAACCTGCAAACTCTATCTCGGCTTGGGAACCAAAAATACACAGAGTTTAAATGGCAT 480 Db
481 CTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540 QY
481 CTGTGAACAGCACCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540 Db
541 TGACATACAAATGGAGTCCCTGGGAGAGAGGTAATGTCTTCAAACTCTCCAGACTC 600 QY
541 TGACATACAAATGGAGTCCCTGGGAGAGAGGTAATGTCTTCAAACTCTCCAGACTC 600 Db
601 CTGAGGACCAAGAGCTGACTTACACGTGTACGCCAGAACCCCTGTGAGCAACAAATCTG 660 QY
601 CTGAGGACCAAGAGCTGACTTACACGTGTACGCCAGAACCCCTGTGAGCAACAAATCTG 660 Db
661 ACTCCATCTCTGCCCCGCGAGCTCTGTGCGAGACATCGCAATGGGCTTCCGTAATCACACA 720 QY
661 ACTCCATCTCTGCCCCGCGAGCTCTGTGCGAGACATCGCAATGGGCTTCCGTAATCACACA 720 Db
721 CCGGGTTGCTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCAATCTGCTCTCAAGTGT 780 QY
721 CCGGGTTGCTGAGCGTGTGGCTATGTTCTTTCTGCTTGTCTCAATCTGCTCTCAAGTGT 780 Db
781 TTTTGTTCGGTTTTCAGAGAGACAGATCTGCTCAAGAGAAACCATATACACAT 840 QY
781 TTTTGTTCGGTTTTCAGAGAGACAGATCTGCTCAAGAGAAACCATATACACAT 840 Db
841 ATATCATGGCTTCAAGGAAACACCCAGCCAGCAGTCCAGAACTATGATGAAATCCTGC 900 QY
841 ATATCATGGCTTCAAGGAAACACCCAGCCAGCAGTCCAGAACTATGATGAAATCCTGC 900 Db
901 AGTCCAAAGTGTCTCCCTCAAGAGAGCAGTGAACACAGTTTATTCGGAAGTGCAGT 960 QY
901 AGTCCAAAGTGTCTCCCTCAAGAGAGCAGTGAACACAGTTTATTCGGAAGTGCAGT 960 Db
961 TTGCTGATAGATGGGAAAGCCAGACACAGGACAGTAAACCTCTCGGACCTTCAAGCT 1020 QY
961 TTGCTGATAGATGGGAAAGCCAGACACAGGACAGTAAACCTCTCGGACCTTCAAGCT 1020 Db
1021 ATGAAATTTGATCTAGGCTGCTGGGCTGAATCTCCCTCTGGAACCTGAGTTACACCA 1080 QY
1021 ATGAAATTTGATCTAGGCTGCTGGGCTGAATCTCCCTCTGGAACCTGAGTTACACCA 1080 Db
1081 CCAATACCTGGCAGGTTCCCTGGATCCAGATCTTCTGCGCAACTCTTACTGGGAGATTG 1140 QY
1081 CCAATACCTGGCAGGTTCCCTGGATCCAGATCTTCTGCGCAACTCTTACTGGGAGATTG 1140 Db
1141 CAAACTGCCACATCTCAGCTGTAAAGCAAGCAGAAACCTTCTGCTGGCAGTACGTTGT 1200 QY
1141 CAAACTGCCACATCTCAGCTGTAAAGCAAGCAGAAACCTTCTGCTGGCAGTACGTTGT 1200 Db
1201 GCCTAAATGGACAAATGGATGCATACCTTCTGAAATGACTCCCTCTGAAATGAATGAC 1260 QY
1201 GCCTAAATGGACAAATGGATGCATACCTTCTGAAATGACTCCCTCTGAAATGAATGAC 1260 Db
1261 AAAGCAGGTTACCTAGTATAGTTTCCCAAACCTTCTCCCAATCATAGACATGTAGAAAA 1320 QY
1261 AAAGCAGGTTACCTAGTATAGTTTCCCAAACCTTCTCCCAATCATAGACATGTAGAAAA 1320 Db
1321 TAATATTTTATGGCAGACTGGGATTAACAGAGAGATGCTCACTTCTGGAAGCTGCAT 1380 QY
1321 TAATATTTTATGGCAGACTGGGATTAACAGAGAGATGCTCACTTCTGGAAGCTGCAT 1380 Db
1381 ATGACTAGAGGCTCTTGTGACTGGAGGTAAACACCTTCCCAAGTAACTGTGGGAGAGG 1440 QY
1381 ATGACTAGAGGCTCTTGTGACTGGAGGTAAACACCTTCCCAAGTAACTGTGGGAGAGG 1440 Db

1441 GGATCAATATTTTGCACACCTGTAAATAGGCCATGCGACACCCAGCCAAAGATGCTCTGCTCA 1500 QY
1441 GGATCAATATTTTGCACACCTGTAAATAGGCCATGCGACACCCAGCCAAAGATGCTCTGCTCA 1500 Db
1501 CAGTCAGTATGTGTGAAGATCCCTGGTGGTGGCTTCCACACGATCTTTGAGCAAAATTA 1560 QY
1501 CAGTCAGTATGTGTGAAGATCCCTGGTGGTGGCTTCCACACGATCTTTGAGCAAAATTA 1560 Db
1561 GGAAAAATGTPACCCCTTTCGCTTGGAGGAGATGACAGCCCTTCCCGGAGTGCATGGCTGGAG 1620 QY
1561 GGAAAAATGTPACCCCTTTCGCTTGGAGGAGATGACAGCCCTTCCCGGAGTGCATGGCTGGAG 1620 Db
1621 AGCAGAAATGTGGGCTGTCATATAAGCACACTCATCCCTTGTCTGGGAAATCTTTGTGCAGG 1680 QY
1621 AGCAGAAATGTGGGCTGTCATATAAGCACACTCATCCCTTGTCTGGGAAATCTTTGTGCAGG 1680 Db
1681 GCATTAACAGGCTTAGTAAGTCCAAAACACAGATGACAGTCTGTGGGCTCTCTGTGCAGAG 1740 QY
1681 GCATTAACAGGCTTAGTAAGTCCAAAACACAGATGACAGTCTGTGGGCTCTCTGTGCAGAG 1740 Db
1741 TTTGTGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTCT 1800 QY
1741 TTTGTGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAAAATGTTCTTTCT 1800 Db
1801 GCAGGCTCTAGAGACTGCTGGGACACTTTTCTTTGGAGTGTCTTCCAGAGCCTTATAGG 1860 QY
1801 GCAGGCTCTAGAGACTGCTGGGACACTTTTCTTTGGAGTGTCTTCCAGAGCCTTATAGG 1860 Db
1861 ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCATTCCAGAGCCTCAGCAGAAAGC 1920 QY
1861 ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCATTCCAGAGCCTCAGCAGAAAGC 1920 Db
1921 AGCCATGCCAGTATTTCCCACTCTCCAAAAGGAACTGACAGCTTATATTTCTCACACTT 1980 QY
1921 AGCCATGCCAGTATTTCCCACTCTCCAAAAGGAACTGACAGCTTATATTTCTCACACTT 1980 Db
1981 CTGGGGAACTGGGTATAATCCAAACCATCAAAATAGAAAGACCTTTGCAAGAGCAGAGTCAT 2040 QY
1981 CTGGGGAACTGGGTATAATCCAAACCATCAAAATAGAAAGACCTTTGCAAGAGCAGAGTCAT 2040 Db
2041 TCTCCAGAGAGAACTTTGGGAGATGATGTTGAGTGAATGAACTGGGTTTCTCCAGTTC 2100 QY
2041 TCTCCAGAGAGAACTTTGGGAGATGATGTTGAGTGAATGAACTGGGTTTCTCCAGTTC 2100 Db
2101 CAAAGACTCAGAGAACTTAGAGTTTAAAGTGGAGTGCAGATGATGAACTGGGTTTCTCCAGTTC 2160 QY
2101 CAAAGACTCAGAGAACTTAGAGTTTAAAGTGGAGTGCAGATGATGAACTGGGTTTCTCCAGTTC 2160 Db
2161 ACAACAGATCACAGCCAGCTTTACACAGGCAATTAACCTCTCAATGAGGAAAGAAATCAT 2220 QY
2161 ACAACAGATCACAGCCAGCTTTACACAGGCAATTAACCTCTCAATGAGGAAAGAAATCAT 2220 Db
2221 TCACAACTGAGCAGAACTTATGATGATTAAGGAAAGTGTTCCTTATGTTGAGC 2280 QY
2221 TCACAACTGAGCAGAACTTATGATGATTAAGGAAAGTGTTCCTTATGTTGAGC 2280 Db
2281 AAGTATAATCGGCTTAACCTTAATCCCAATGATAGTCTTAGCTGAGCAGCAATGGGC 2340 QY
2281 AAGTATAATCGGCTTAACCTTAATCCCAATGATAGTCTTAGCTGAGCAGCAATGGGC 2340 Db
2341 TGCAATTTAGGCGAGATAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCAC 2400 QY
2341 TGCAATTTAGGCGAGATAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCAC 2400 Db
2401 CAACTACCAATTAGCACTATGTTAGGAGCTGCAAGGCCCCCAAGATGTCATTAAT 2460 QY
2401 CAACTACCAATTAGCACTATGTTAGGAGCTGCAAGGCCCCCAAGATGTCATTAAT 2460 Db
2461 GTCTGCTCTTGTGTAGCTCAGGAGACAAATTCACAGCAGACACTTACAGTTAAACCTGAAC 2520 QY
2461 GTCTGCTCTTGTGTAGCTCAGGAGACAAATTCACAGCAGACACTTACAGTTAAACCTGAAC 2520 Db

2521 TGCAGTCAAGTAATAGCATGAACAGTCAAGAAATACCTTATCAGGGGCGAGGCTGA 2580
2521 TGCAGTCAAGTAATAGCATGAACAGTCAAGAAATACCTTATCAGGGGCGAGGCTGA 2580
2581 AGCTGGGCTTGAAGATGATGAATTTGGATAGAGAATAGGAAGACAGAGGCGCTCC 2640
2581 AGCTGGGCTTGAAGATGATGAATTTGGATAGAGAATAGGAAGACAGAGGCGCTCC 2640
2641 AAGTCAGAGAAGCATGAATAATGACAGGGGCTGGATCAGTGGGGTGTATTACAGGAC 2700
2641 AAGTCAGAGAAGCATGAATAATGACAGGGGCTGGATCAGTGGGGTGTATTACAGGAC 2700
2701 CTCTCAGATGACCATGATGCTCAAGTCCCTTGCCTTATGTGGGAGAGTGTCCAG 2760
2701 CTCTCAGATGACCATGATGCTCAAGTCCCTTGCCTTATGTGGGAGAGTGTCCAG 2760
2761 CAGATGTGTGCCCCACACCCATGTCATTTACATGTCCTTCAATGCCCCACCTCAAAAGG 2820
2761 CAGATGTGTGCCCCACACCCATGTCATTTACATGTCCTTCAATGCCCCACCTCAAAAGG 2820
2821 TACCTCTCTGTAAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTCA 2880
2821 TACCTCTCTGTAAAGCTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTCA 2880
2881 CACTGCTGTTTTTCTCTTTGGTCTTCTATCACTAAACCTCATCTCAATCAGGCTTAC 2940
2881 CACTGCTGTTTTTCTCTTTGGTCTTCTATCACTAAACCTCATCTCAATCAGGCTTAC 2940
2941 AGCATAACTAAATTTATTTGTTTTCCTCACTACATGTTGAGTGGGAAATACAGATAAACG 3000
2941 AGCATAACTAAATTTATTTGTTTTCCTCACTACATGTTGAGTGGGAAATACAGATAAACG 3000
3001 GAAGCKGTGGGGTGGGCTCAGCCCTGTAATCCCAACCTTTGGGGGCCAAGGCGAG 3060
3001 GAAGCKGTGGGGTGGGCTCAGCCCTGTAATCCCAACCTTTGGGGGCCAAGGCGAG 3060
3061 GCGGATCACCTCAGGTCAGGARTTCGAGATTARTCTGGCCAAACATGGTGAAACCCCATNT 3120
3061 GCGGATCACCTCAGGTCAGGARTTCGAGATTARTCTGGCCAAACATGGTGAAACCCCATNT 3120
3121 NTACTAAATAACGAAATTAGCCAGGTGTGGGACACATCTGTAGTCCGAG 3173
3121 NTACTAAATAACGAAATTAGCCAGGTGTGGGACACATCTGTAGTCCGAG 3173

RESULT 3

US-10-164-861-174
; Sequence 174, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 3173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3119)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3121)
; OTHER INFORMATION: n equals a,t,g, or c

US-10-164-861-174
Query Match 99.9%; Score 3169.4; DB 17; Length 3173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGACCCCCASCGTCGTCCTTTTCCACAGAAAGGTTAGACCCCTGAAAGAGATGGCTCAGC 60
DB 1 TCGACCCCCASCGTCGTCCTTTTCCACAGAAAGGTTAGACCCCTGAAAGAGATGGCTCAGC 60
QY 61 ACCACCTATGATCTTGTCTCTCTTTGCTCGTGAACCTGCGCCGAGAGCAGCTGGAAGACT 120
DB 61 ACCACCTATGATCTTGTCTCTCTTTGCTCGTGAACCTGCGCCGAGAGCAGCTGGAAGACT 120
QY 121 CAGAAATCTTCCACAGTGAATGGGATTTCTGGCAGAGTCACTTTCCTCTGTAATATACC 180
DB 121 CAGAAATCTTCCACAGTGAATGGGATTTCTGGCAGAGTCACTTTCCTCTGTAATATACC 180
QY 181 AAGAACCCAGCGCAAGTTAAATCATTTGCTTGGACTTCTTAAACATCTCTTGTCTATGTAA 240
DB 181 AAGAACCCAGCGCAAGTTAAATCATTTGCTTGGACTTCTTAAACATCTCTTGTCTATGTAA 240
QY 241 CACAGGAGACTCAGAAACAGCACCCGCTAGTCTCTGTGACCCACAGAAATTTATATGAC 300
DB 241 CACAGGAGACTCAGAAACAGCACCCGCTAGTCTCTGTGACCCACAGAAATTTATATGAC 300
QY 301 GGATACATGCTTAGGTCGGAACCTACATCTGCTCATTTAGCGATCTGAGGATGGAAGACG 360
DB 301 GGATACATGCTTAGGTCGGAACCTACATCTGCTCATTTAGCGATCTGAGGATGGAAGACG 360
QY 361 CAGGAGACTCAAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACCAAGCGCT 420
DB 361 CAGGAGACTCAAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACCAAGCGCT 420
QY 421 ACAACCTGCAATCTATCTGCTCGCTTGGGAAAACAAAATTTACACAGAGTTTAAATGGAT 480
DB 421 ACAACCTGCAATCTATCTGCTCGCTTGGGAAAACAAAATTTACACAGAGTTTAAATGGAT 480
QY 481 CTGTGAACAGACACCTGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540
DB 481 CTGTGAACAGACACCTGTAATGTCACTGACATGCTCTGTAGAGAAAGAAAGAAATG 540
QY 541 TGACATACAAATTTGGAGTCCCTCGGAGAAAGGGTAAATGTCTTCAAAATCTTCCAGACTC 600
DB 541 TGACATACAAATTTGGAGTCCCTCGGAGAAAGGGTAAATGTCTTCAAAATCTTCCAGACTC 600
QY 601 CTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGAACCCCTGTACGACCAATTTCTG 660
DB 601 CTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGAACCCCTGTACGACCAATTTCTG 660
QY 661 ACTCCATCTCTGCCGCGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACACCA 720
DB 661 ACTCCATCTCTGCCGCGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACACCA 720
QY 721 CCGGGTGTCTGAGCGTGTGGCTATGTTTCTTCTGTTTCTCAATCTGCTTCAAGTGT 780
DB 721 CCGGGTGTCTGAGCGTGTGGCTATGTTTCTTCTGTTTCTCAATCTGCTTCAAGTGT 780
QY 781 TTTTGTTCGGTGTGTTCAAGAGACAGAGATGTGCTCTCAAGAAACCATATACAT 840
DB 781 TTTTGTTCGGTGTGTTCAAGAGACAGAGATGTGCTCTCAAGAAACCATATATACAT 840
QY 841 ATATCATGGCTTCAAGGAACACCCAGCCAGAGTCCAGAAATCTATGATGAAATCTCTGC 900
DB 841 ATATCATGGCTTCAAGGAACACCCAGCCAGAGTCCAGAAATCTATGATGAAATCTCTGC 900
QY 901 AGTCCAAGGTGCTTCCCTTCCAGGAGAGCCAGTGAAACAGATTTATTTCCGAAGTGCAGT 960
DB 901 AGTCCAAGGTGCTTCCCTTCCAGGAGAGCCAGTGAAACAGATTTATTTCCGAAGTGCAGT 960
QY 961 TTGCTGATAAGATGGGGAAGCCAGACACAGGACAGTAAACCTCTGGGACTTCAAGCT 1020
DB 961 TTGCTGATAAGATGGGGAAGCCAGACACAGGACAGTAAACCTCTGGGACTTCAAGCT 1020

QY 1021 ATGAAATTGTGATCTAGGCTGCTGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACA 1080
DB |||||
DB 1021 ATGAAATTGTGATCTAGGCTGCTGGCTGAATTTCTCCCTCTGGAACCTGAGTTACAACA 1080
QY 1081 CCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAAACCTTTACTGGGAGATTG 1140
DB |||||
DB 1081 CCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAAACCTTTACTGGGAGATTG 1140
QY 1141 CAAACTGACATCTCAGCCTGTAAAGCAAGCAGGAACCTTCTGCTGGGCATAGCTTGT 1200
DB |||||
DB 1141 CAAACTGACATCTCAGCCTGTAAAGCAAGCAGGAACCTTCTGCTGGGCATAGCTTGT 1200
QY 1201 GCCTAAATGGAACAATGGATGATACCTCTCTCTGAAATGACTCCCTCTCTGAAATGAATGAC 1260
DB |||||
DB 1201 GCCTAAATGGAACAATGGATGATACCTCTCTCTGAAATGACTCCCTCTCTGAAATGAATGAC 1260
QY 1261 AAAGCAGGTTACTAGTAGTATGTTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAA 1320
DB |||||
DB 1261 AAAGCAGGTTACTAGTAGTATGTTTTCCCAAACCTTCTCCCATCATAGCACATGTAGAAA 1320
QY 1321 TAATATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCATCTTCTGGAAGCTGCAT 1380
DB |||||
DB 1321 TAATATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCATCTTCTGGAAGCTGCAT 1380
QY 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACAACCTGCCAGTAACTGTGGAGAGG 1440
DB |||||
DB 1381 ATGACTAGAGGCTCTTGTGACTGGAGTAAACAACCTGCCAGTAACTGTGGAGAGG 1440
QY 1441 GGATCAATATTTTGCACACTGTAAATAGCCATGGCACACACAGCCAAAGATGCTCTGCTCA 1500
DB |||||
DB 1441 GGATCAATATTTTGCACACTGTAAATAGCCATGGCACACACAGCCAAAGATGCTCTGCTCA 1500
QY 1501 CAGTCAAGTATGTGAAGATCCCTGTGTGGTCCCTTACCAGCATCTTTGAGCAAAATTA 1560
DB |||||
DB 1501 CAGTCAAGTATGTGAAGATCCCTGTGTGGTCCCTTACCAGCATCTTTGAGCAAAATTA 1560
QY 1561 GGAAATGTACCTTCTGCTTGGAGATGACAGCCCTTCCCGAGTGATGCTGGAG 1620
DB |||||
DB 1561 GGAAATGTACCTTCTGCTTGGAGATGACAGCCCTTCCCGAGTGATGCTGGAG 1620
QY 1621 AGCAGAAATGGGCTGCATATAGCACACTCATCTCTTGTCTGGGAATCTTTGTGCAGG 1680
DB |||||
DB 1621 AGCAGAAATGGGCTGCATATAGCACACTCATCTCTTGTCTGGGAATCTTTGTGCAGG 1680
QY 1681 GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGCAGAG 1740
DB |||||
DB 1681 GCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGGTCTCTGTGCAGAG 1740
QY 1741 TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTCT 1800
DB |||||
DB 1741 TTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTCT 1800
QY 1801 GCAGGCTTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTTCAGAGCCCTTATAGG 1860
DB |||||
DB 1801 GCAGGCTTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTTCAGAGCCCTTATAGG 1860
QY 1861 ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCATCTCCAAAGCCTTCAGCAGAGAGC 1920
DB |||||
DB 1861 ATTTTCTTTCTGGCCAAAGATTTCTTCTGTATCATCTCCAAAGCCTTCAGCAGAGAGC 1920
QY 1921 AGCCATGCCAGATTTCCCACTCTCCAAAGGAACTGACCCAGCTTATATTTCTCACACTT 1980
DB |||||
DB 1921 AGCCATGCCAGATTTCCCACTCTCCAAAGGAACTGACCCAGCTTATATTTCTCACACTT 1980
QY 1981 CTGGGAACTGGGTATTAATCCAACTCAAAATAGAGACCTTGCAAGAGCAGAGTCAAT 2040
DB |||||
DB 1981 CTGGGAACTGGGTATTAATCCAACTCAAAATAGAGACCTTGCAAGAGCAGAGTCAAT 2040
QY 2041 TCTCCAGAGGAACTTGGGAGATGATGGTGAGATGATGAATGAATGAGTTCATCCAGTTC 2100
DB |||||
DB 2041 TCTCCAGAGGAACTTGGGAGATGATGGTGAGATGATGAATGAATGAGTTCATCCAGTTC 2100

QY 2101 CAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCGAGAGTGCGGCACACCTTGGCATGCCCC 2160
DB |||||
DB 2101 CAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCGAGAGTGCGGCACACCTTGGCATGCCCC 2160
QY 2161 ACAAACAGATCACCAGCCAGCTTACAGAGGCAATTAACCTCTCTCAATGAGGAAGAAATCAT 2220
DB |||||
DB 2161 ACAAACAGATCACCAGCCAGCTTACAGAGGCAATTAACCTCTCTCAATGAGGAAGAAATCAT 2220
QY 2221 TCACAACCTGAGCAGACATTCATATGATCATTTTAAGGAAGTGTTCCTTATGTGTAGC 2280
DB |||||
DB 2221 TCACAACCTGAGCAGACATTCATATGATCATTTTAAGGAAGTGTTCCTTATGTGTAGC 2280
QY 2281 AAGTATAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGC 2340
DB |||||
DB 2281 AAGTATAATCGGCTAACTCTTAAATCCCAATGAATAGTCTTAGGCTGGACAGCAATGGGC 2340
QY 2341 TGCAATTAGGCGAGATAAGACATCAGTCCCAATGAATGAATCCATAGACTCATCTAGCAC 2400
DB |||||
DB 2341 TGCAATTAGGCGAGATAAGACATCAGTCCCAATGAATGAATCCATAGACTCATCTAGCAC 2400
QY 2401 CAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGCATAAT 2460
DB |||||
DB 2401 CAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTGAAGATGTGCATAAT 2460
QY 2461 GTCTGCTCTTGTGTAGCTCAGAGACAATTCAGACAGACACTACAGTTAACGCTGAAC 2520
DB |||||
DB 2461 GTCTGCTCTTGTGTAGCTCAGAGACAATTCAGACAGACACTACAGTTAACGCTGAAC 2520
QY 2521 TGCACTGCAAGTATAGCATGAAACAGTCAGAAATAACCTTATGAGGGGCGAGGCTCA 2580
DB |||||
DB 2521 TGCACTGCAAGTATAGCATGAAACAGTCAGAAATAACCTTATGAGGGGCGAGGCTCA 2580
QY 2581 AGCTGGGCTTCAAGGATGGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCC 2640
DB |||||
DB 2581 AGCTGGGCTTCAAGGATGGATGAAATTTGGATAGAGATGAGGAAGACAGAGGGGCTCC 2640
QY 2641 AAGTGAGAGAACATGAAATAAGCAGGGGCTGGATCAGTGGGGTGTATTTCAGAGCAC 2700
DB |||||
DB 2641 AAGTGAGAGAACATGAAATAAGCAGGGGCTGGATCAGTGGGGTGTATTTCAGAGCAC 2700
QY 2701 CTCTCCAGATGACCATGCTCAGTCCCTTGCCTTATGTTGGCAGAGTGTCCCAG 2760
DB |||||
DB 2701 CTCTCCAGATGACCATGCTCAGTCCCTTGCCTTATGTTGGCAGAGTGTCCCAG 2760
QY 2761 CCAGATGTGTGCCCCCACCACCTCATGTCATTTACATGTCCTTCAATGCCACCTCAAAAGG 2820
DB |||||
DB 2761 CCAGATGTGTGCCCCCACCACCTCATGTCATTTACATGTCCTTCAATGCCACCTCAAAAGG 2820
QY 2821 TACCTCTCTGTAAAGCTTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
DB |||||
DB 2821 TACCTCTCTGTAAAGCTTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA 2880
QY 2881 CACTGTCTTTTTTCTCTTGTGCTTCTATCCTTAAACCTCATCTTACAGCCTTAC 2940
DB |||||
DB 2881 CACTGTCTTTTTTCTCTTGTGCTTCTATCCTTAAACCTCATCTTACAGCCTTAC 2940
QY 2941 AGCATAAATAATTTATTTGTTTCTCTCATCATTTGATGATGAGGAATTTACAGATAAAG 3000
DB |||||
DB 2941 AGCATAAATAATTTATTTGTTTCTCTCATCATTTGATGATGAGGAATTTACAGATAAAG 3000
QY 3001 GAAGCCGCTGGGGTGGTGGCTCAGCCTGTAAATCCCAACACTTTGGGAGGCCAAGGCAG 3060
DB |||||
DB 3001 GAAGCCGCTGGGGTGGTGGCTCAGCCTGTAAATCCCAACACTTTGGGAGGCCAAGGCAG 3060
QY 3061 GCGGATCACTGAGGTCAGGARTTCAGATTATCTGGCCAAACATCTGTGGAACCCCATNT 3120
DB |||||
DB 3061 GCGGATCACTGAGGTCAGGARTTCAGATTATCTGGCCAAACATCTGTGGAACCCCATNT 3120
QY 3121 NTACTAAATAACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG 3173
DB |||||
DB 3121 NTACTAAATAACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG 3173

RESULT 4

US-10-198-846-13255
; Sequence 13255, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13255
; LENGTH: 3687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677,
; LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687,
; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-13255

Query Match 99.6%; Score 3159.8; DB 14; Length 3687;
Best Local Similarity 99.8%; Pred No. 0;
Matches 3158; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY	9	ASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCCTGAAAGAGATGGCTCAGCACACCTA	68
DB	391	ACGCGTCGCTGCTTTTCCACAGAAGGTTAGACCCCTGAAAGAGATGGCTCAGCACACCTA	450
QY	69	TGGATCTTGCTCTTTTGGCTGCAACCTGGCGGAGCAGCTGGAAGACTCAGAAATC	128
DB	451	TGGATCTTGCTCTTTTGGCTGCAACCTGGCGGAGCAGCTGGAAGACTCAGAAATC	510
QY	129	TTCCAGATGAATGGGATCTGGGAGAGTCAGTCATCTTCCCTGTAAATATCCAGAACCA	188
DB	511	TTCCAGATGAATGGGATCTGGGAGAGTCAGTCATCTTCCCTGTAAATATCCAGAACCA	570
QY	189	CGGCAAGTAAATCATGCTTGGACTTCTAAACCATCTGTTGCTTATGTAACACAGGA	248
DB	571	CGGCAAGTAAATCATGCTTGGACTTCTAAACCATCTGTTGCTTATGTAACACAGGA	630
QY	249	GACTCAGAACAGCACCCGTAGTTACTGTGACCCACAGAAATATATGAACGGATACAT	308
DB	631	GACTCAGAACAGCACCCGTAGTTACTGTGACCCACAGAAATATATGAACGGATACAT	690
QY	309	GGCTTAGGTCGAACTACAACTCTGCTCATTTAGCGATCTGAGGATGGAAGACGACGAGAC	368
DB	691	GGCTTAGGTCGAACTACAACTCTGCTCATTTAGCGATCTGAGGATGGAAGACGACGAGAC	750
QY	369	TACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCAACCAACGCGCTACAACTG	428
DB	751	TACAAAGCAGACATAAATACACAGGCTGATCCCTACACACCAACCAACGCGCTACAACTG	810
QY	429	CAAAATCTATCGTCGCTGGGAAACCAAAATTTACACAGATTTAATGGCATCTGTGAAC	488
DB	811	CAAAATCTATCGTCGCTGGGAAACCAAAATTTACACAGATTTAATGGCATCTGTGAAC	870
QY	489	AGCAGCTGTAAATGTACACACTGATCTCTGTAGAGAAAGAGAAAGATGTGACATAC	548
DB	871	AGCAGCTGTAAATGTACACACTGATCTCTGTAGAGAAAGAGAAAGATGTGACATAC	930
QY	549	AATTGAGTCCCTGGGAGAGAGGGTAAATGTCCTTCAAATCTTCCAGACTCCTGAGGAC	608
DB	931	AATTGAGTCCCTGGGAGAGAGGGTAAATGTCCTTCAAATCTTCCAGACTCCTGAGGAC	990

QY	609	CAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAACAAATTTCTGACTCCATC	668
DB	991	CAAGAGCTGACTTACACGTGTACAGCCAGAACCCCTGTGAGCAACAAATTTCTGACTCCATC	1050
QY	669	TCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGGTTG	728
DB	1051	TCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGGTTG	1110
QY	729	CTGAGCGTGGCTATGTTCTTTCTGCTTGTCTCATCTCTGCTTCTAGTGTCTTGTCTC	788
DB	1111	CTGAGCGTGGCTATGTTCTTTCTGCTTGTCTCATCTCTGCTTCTAGTGTCTTGTCTC	1170
QY	789	CGTTTGTTCAGAGAAGACAGAGTCTGCCCTCAAGAAACCATATACATATATCATG	848
DB	1171	CGTTTGTTCAGAGAAGACAGAGTCTGCCCTCAAGAAACCATATACATATATCATG	1230
QY	849	GCTTCAAGGAACACCCAGCAGAGTCCAGAAATCTATGATGAATCCTGCAAGTCCAAG	908
DB	1231	GCTTCAAGGAACACCCAGCAGAGTCCAGAAATCTATGATGAATCCTGCAAGTCCAAG	1290
QY	909	GTGCTTCCCTCAAAGGAAGCCAGTGAACACAGTTTATTCGGAAGTGCAGTTTCTGCTGAT	968
DB	1291	GTGCTTCCCTCAAAGGAAGCCAGTGAACACAGTTTATTCGGAAGTGCAGTTTCTGCTGAT	1350
QY	969	AAGATGGGGAAGCCAGCAGACAGAGTAAACCTCCTGGGACTTCAAGCTATGAAAT	1028
DB	1351	AAGATGGGGAAGCCAGCAGACAGAGTAAACCTCCTGGGACTTCAAGCTATGAAAT	1410
QY	1029	GTGATCTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTTACCAACCAATACT	1088
DB	1411	GTGATCTAGGCTGCTGGGCTGAATTTCTCCCTCTGGAACCTGAGTTTACCAACCAATACT	1470
QY	1089	GGCAGGTTCCCTGAGTCCAGATCTTCTGCTGCCAACTCTTACTGGGAGATGCAAACTGC	1148
DB	1471	GGCAGGTTCCCTGAGTCCAGATCTTCTGCTGCCAACTCTTACTGGGAGATGCAAACTGC	1530
QY	1149	CACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGTGCTTAAT	1208
DB	1531	CACATCTCAGCTGTGAAGCAAGCAGGAAACCTTCTGCTGGGCATAGCTTGTGCTTAAT	1590
QY	1209	GGACAAATGGATGATACCTTCTGGAATGACTCCCTTCTGGAATGAATGAACGAGG	1268
DB	1591	GGACAAATGGATGATACCTTCTGGAATGACTCCCTTCTGGAATGAATGAACGAGG	1650
QY	1269	TTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCATGTAGAAATATATATTT	1328
DB	1651	TTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCATGTAGAAATATATATTT	1710
QY	1329	TTATGGCACACTGGGATAAACAAAGCAAGATTTGCTCACTTCTGGAAGCTGCATATGACTAG	1388
DB	1711	TTATGGCACACTGGGATAAACAAAGCAAGATTTGCTCACTTCTGGAAGCTGCATATGACTAG	1770
QY	1389	AGGCTCTTGTGACTGGAGGTAAACAAACCTGCCAGTAACTGTGGGAGAGGGGATCAAT	1448
DB	1771	AGGCTCTTGTGACTGGAGGTAAACAAACCTGCCAGTAACTGTGGGAGAGGGGATCAAT	1830
QY	1449	ATTTTGCACACTGTAATAGCCATGGCACACGAGCCAGATGCTCTGCTCACAGTCAAT	1508
DB	1831	ATTTTGCACACTGTAATAGCCATGGCACACGAGCCAGATGCTCTGCTCACAGTCAAT	1890
QY	1509	ATGTTGTAAGATCCCTGCTGGTGGCTTCCACAGCATCTTGAGCAATTAGGAAATG	1568
DB	1891	ATGTTGTAAGATCCCTGCTGGTGGCTTCCACAGCATCTTGAGCAATTAGGAAATG	1950
QY	1569	TACCTTCCCTTGAGGAGATGCAAGCTTCCCGAGTGCATGCTGCTGGAGAGAGCAAT	1628
DB	1951	TACCTTCCCTTGAGGAGATGCAAGCTTCCCGAGTGCATGCTGCTGGAGAGAGCAAT	2010
QY	1629	GTGGCTGCATATAGCACACTCATCTCTGCTGGAAATCTTGTGAGGAGGATACA	1688
DB	2011	GTGGCTGCATATAGCACACTCATCTCTGCTGGAAATCTTGTGAGGAGGATACA	2070

1689 QY GGCCTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGTGAGTGTGGCT 1748
1690 DB |||||
2071 DB GGCCTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGTGAGTGTGGCT 2130
1749 QY CTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTTCTGCGGGTC 1808
1750 DB |||||
2131 DB CTCAGCCATGTAGACACACTCTCCAAATGGAGTGTGGAAATGTTCTTTCTGCGAGGTC 2190
1809 QY TAGAGACTGCTGGGACACTTTCTGGAGTGTACTTTAGAGCCCTTATAGATTTCTT 1868
1810 DB |||||
2191 DB TAGAGACTGCTGGGACACTTTCTGGAGTGTACTTTAGAGCCCTTATAGATTTCTT 2250
1869 QY TCTGGCCAAAGATTTCTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGCAGCCATGC 1928
1870 DB |||||
2251 DB TCTGGCCAAAGATTTCTCTGTATCACTCCAAAGCAGCTCAGCAGAAAGCAGCCATGC 2310
1929 QY CCAGTATTTCCCACTCTCCAAAGGAACTGACACAGCTTATTTCTCACACTTCTGGGAA 1988
1930 DB |||||
2311 DB CCAGTATTTCCCACTCTCCAAAGGAACTGACACAGCTTATTTCTCACACTTCTGGGAA 2370
1989 QY CTGGGTATTAATCCAAACCATCAAAATAGAGACTTGCAGAGGAGCAGAGTCAATCTCCAGA 2048
1990 DB |||||
2371 DB CTGGGTATTAATCCAAACCATCAAAATAGAGACTTGCAGAGGAGCAGAGTCAATCTCCAGA 2430
2049 QY AGGAACCTTGGGAGATGATGTGAGATGATGAACTGGGTTCATCCAGTTCCAAAGACT 2108
2050 DB |||||
2431 DB AGGAACCTTGGGAGATGATGTGAGATGATGAACTGGGTTCATCCAGTTCCAAAGACT 2490
2109 QY CAGAGAACTAGAGTTAAGCTGAGGAGAGTGCGCCACCTCGGCATGCCCCACAAACAG 2168
2110 DB |||||
2491 DB CAGAGAACTAGAGTTAAGCTGAGGAGAGTGCGCCACCTCGGCATGCCCCACAAACAG 2550
2169 QY ATCACCAGCAGCTTACAGAGGATTAACCTCTCAATGAGGAGAAATCATTCACAACT 2228
2170 DB |||||
2551 DB ATCACCAGCAGCTTACAGAGGATTAACCTCTCAATGAGGAGAAATCATTCACAACT 2610
2229 QY GAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTAGCAAGTATAA 2288
2230 DB |||||
2611 DB GAGCAAGACATTCATATGATCAATTAAGGAAGTGTTCCTTATGTGTAGCAAGTATAA 2670
2289 QY TCGGCTAACTCTTAATCCCAATGAATAGTCTTAGCTGGACAGCAATGGCTGCAATTA 2348
2290 DB |||||
2671 DB TCGGCTAACTCTTAATCCCAATGAATAGTCTTAGCTGGACAGCAATGGCTGCAATTA 2730
2349 QY GGCAATAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCAATACC 2408
2350 DB |||||
2731 DB GGCAATAAAGACATCAGTCCCAAGTAAATGAATCCATAGACTCATCTAGCACCAATACC 2790
2409 QY ATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATAATGCTGTCTC 2468
2410 DB |||||
2791 DB ATTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGCATAATGCTGTCTC 2850
2469 QY TTGTGTAGCTCAGGAGCAATTCAGCAGACAGACACTACAGTTAAACGCTGAACCTGCAGCTG 2528
2470 DB |||||
2851 DB TTGTGTAGCTCAGGAGCAATTCAGCAGACAGACACTACAGTTAAACGCTGAACCTGCAGCTG 2910
2529 QY CAAGTAATAGCAATGAGTCCAGAAATACCTTATGAGGGGCGAGGCTGAGCTGGGC 2588
2530 DB |||||
2911 DB CAAGTAATAGCAATGAGTCCAGAAATACCTTATGAGGGGCGAGGCTGAGCTGGGC 2970
2589 QY CTTGAGGATGGATGAAATTTGGATAGAGATGAGGAAGCAGAGGGGCTCCAAAGTGAGA 2648
2590 DB |||||
2971 DB CTTGAGGATGGATGAAATTTGGATAGAGATGAGGAAGCAGAGGGGCTCCAAAGTGAGA 3030
2649 QY GAAGCATGAAAAATGAGCAGGGGCTGGATCAGTGGGGTGTATTCAGAGCACTCTCCAG 2708
2650 DB |||||
3031 DB GAAGCATGAAAAATGAGCAGGGGCTGGATCAGTGGGGTGTATTCAGAGCACTCTCCAG 3090
2709 QY ATGCACCATGATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCAGCCAGATGT 2768
2710 DB |||||
3091 DB ATGCACCATGATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCAGCCAGATGT 3150
2769 QY GTGCCCCACCCCATGTCCATTTACATGTCTTTCAATGCCACCTCAAAAGGTACCTCTT 2828

3151 DB GTGCCCCACCCCATGTCCAATTTACATGTCTTCAATGCCACCTCAAAAGGTACCTCTT 3210
2829 QY CTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTTCACACTGCTG 2888
3211 DB CTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGATCTTTTTCACACTGCTG 3270
2889 QY TTTTTCCTCTTTGTGCTCTCTATCACTAAACTCATCTCATTAGCCCTTACAGCATAAC 2948
2890 DB |||||
3271 DB TTTTTCCTCTTTGTGCTCTCTATCACTAAACTCATCTCATTAGCCCTTACAGCATAAC 3330
2949 QY TAATTAATTTGTTTCTCTCACTACATGTATGATGGGAATTAACAGATAAACGGAAGCCG 3008
3331 DB TAATTAATTTGTTTCTCTCACTACATGTATGATGGGAATTAACAGATAAACGGAAGCCG 3390
3009 QY CTGGGGTGGTGGCTCAGCCCTGTAATCCCAACACTTTGGGAGCCCAAGCAGCGGATCA 3068
3391 DB CTGGGGTGGTGGCTCAGCCCTGTAATCCCAACACTTTGGGAGCCCAAGCAGCGGATCA 3450
3069 QY CCTGAGGTCAGGATTCGAGATTAATCTGGCCCAACATGTTGAAACCCCATTTNTACTAAA 3128
3451 DB CCTGAGGTCAGGATTCGAGATTAATCTGGCCCAACATGTTGAAACCCCATTTCTACTAAA 3510
3129 QY AATACGAATTAAGCAGGTGTGGTGCCACACATCTGTAGTCCAG 3173
3511 DB AATACGAATTAAGCAGGTGTGGTGCCACACATCTGTAGTCCAG 3555

RESULT 5
US-10-723-860-6219
; Sequence 6219, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6219
; LENGTH: 3326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (253)..(2547)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6219

Query Match 99.0%; Score 3142.2; DB 18; Length 3326;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 3141; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 8 CAGCGCTCGTGTCTTTTCCACAGAGGTTAGACCTTGAAGAGATGGCTCAGCACCACT 67
DB 29 CAGCGTCCGTGTCTTTTCCACAGAGGTTAGACCTTGAAGAGATGGCTCAGCACCACT 88
QY 68 ATGGATCTTGTCTCTTTGCTGCAAACTGGCGGAGCAGCTGGAAAGACTCAGAAAT 127
DB 89 ATGGATCTTGTCTCTTTGCTGCAAACTGGCGGAGCAGCTGGAAAGACTCAGAAAT 148
QY 128 CTTTACAGTGAATGGATTTCTGGGAGAGTCAGTCACTTTCCCTGTAAATATCCAAGAAC 187
DB 149 CTTTACAGTGAATGGATTTCTGGGAGAGTCAGTCACTTTCCCTGTAAATATCCAAGAAC 208
QY 188 ACGGCAAGTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCTTATGTAAACACG 247

Db 209 ACGGCAAGTTAAATCAITGCTTGGACTTCTAAACAATCTGTTGCTTATGTAAACACGAG 268
Qy 248 AGACTCAGAAACAGCAACCGTAGTTACTGTGACCCACAGAAATATATATGAACGGATACA 307
Db 269 AGACTCAGAAACAGCAACCGTAGTTACTGTGACCCACAGAAATATATATGAACGGATACA 328
Qy 308 TGCCCTTAGTCCGAATACAACTGTGTCATTAAGCGATCTGAGGATGGAAGAGCGAGGAGA 367
Db 329 TGCCCTTAGTCCGAATCAATCTGGTCAATTAAGCGATCTGAGGATGGAAGAGCGAGGAGA 388
Qy 368 CTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACACACCGACGCTACAACT 427
Db 389 CTACAAAGCAGACATAAATACACAGGCTGATCCCTACACACACCGACGCTACAACT 448
Qy 428 GCAATCTATCGTGGCTTGGGAAACCAAAATTAACACAGAGTTTAATGGCATCTGTGAA 487
Db 449 GCAATCTATCGTGGCTTGGGAAACCAAAATTAACACAGAGTTTAATGGCATCTGTGAA 508
Qy 488 CAGCACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAAGTGCACATA 547
Db 509 CAGCACCTGTAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAAGAAAGTGCACATA 568
Qy 548 CAATTGGAGTCCCTCGGAGAGAGGGTAATGTCTTCAAATCTTCCAGACTCCTGAGGA 607
Db 569 CAATTGGAGTCCCTCGGAGAGAGGGTAATGTCTTCAAATCTTCCAGACTCCTGAGGA 628
Qy 608 CCAAGAGCTGACTTACACGTGTACAGCCAGAAACCTGTACAGAACAAATCTGACTCCAT 667
Db 629 CCAAGAGCTGACTTACACGTGTACAGCCAGAAACCTGTACAGAACAAATCTGACTCCAT 688
Qy 668 CTCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGTT 727
Db 689 CTCTGCCCGGAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGTT 748
Qy 728 GCTGAGCGTCTGGCTATGTTCTTTCTGCTTGTCTCAATCTGCTCTCAGTGTCTTTTGT 787
Db 749 GCTGAGCGTCTGGCTATGTTCTTTCTGCTTGTCTCAATCTGCTCTCAGTGTCTTTTGT 808
Qy 788 CGGTTTGTTCAGAGNAGNAGATGCTGCTTCAAGAAACCATATACACATATATCAT 847
Db 809 CGGTTTGTTCAGAGNAGNAGATGCTGCTTCAAGAAACCATATACACATATATCAT 868
Qy 848 GGCCTTCAAGGAACACCCAGCAGAGTCCAGAAATCTATGATGAAATCCTCGACTCCAA 907
Db 869 GGCCTTCAAGGAACACCCAGCAGAGTCCAGAAATCTATGATGAAATCCTCGACTCCAA 928
Qy 908 GGTGCTTCCCTCAAGGAAGAGCAGTGAAACACAGTTTATTCGGAAGTGCAGTTTGTGA 967
Db 929 GGTGCTTCCCTCAAGGAAGAGCAGTGAAACACAGTTTATTCGGAAGTGCAGTTTGTGA 988
Qy 968 TAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTGGGACTTCAAGCTATGAAAT 1027
Db 989 TAAGATGGGAAAGCCAGCACAGGACAGTAAACCTCTGGGACTTCAAGCTATGAAAT 1048
Qy 1028 TGTGATCTAGGCTGTGGGCTGAAATCTCCTCTGGAAACTGAGTTACAAACCAATAC 1087
Db 1049 TGTGATCTAGGCTGTGGGCTGAAATCTCCTCTGGAAACTGAGTTACAAACCAATAC 1108
Qy 1088 TGGCAGGTTCCCTGATCCAGATCTTCTGTGCCAACTCTTACTGGGAGATGCAAACTG 1147
Db 1109 TGGCAGGTTCCCTGATCCAGATCTTCTGTGCCAACTCTTACTGGGAGATGCAAACTG 1168
Qy 1148 CCACATCTCAGCTCTAAGCAAGCAGGAAACCTTCTGTGGGACTAGCTGTGCTAAA 1207
Db 1169 CCACATCTCAGCTCTAAGCAAGCAGGAAACCTTCTGTGGGACTAGCTGTGCTAAA 1228
Qy 1208 TGGCAAAATGGAATGATACCTTCTGAAATGATCTCCTTCTGAATGAAATGACAAAGCAG 1267
Db 1229 TGGCAAAATGGAATGATACCTTCTGAAATGATCTCCTTCTGAATGAAATGACAAAGCAG 1288
Qy 1268 GTTACTAGTATAGTTTCCCAAACTCTTCCCATCATAGCACATGTAGAAATAATATT 1327
Db 1289 GTTACTAGTATAGTTTCCCAAACTCTTCCCATCATAGCACATGTAGAAATAATATT 1348

Qy 1328 TTTATGGCACACTGGGATATAAACAAGAAATGCTCACTTCTGGAAGCTGCATATGACTA 1387
Db 1349 TTTATGGCACACTGGGATATAAACAAGAAATGCTCACTTCTGGAAGCTGCATATGACTA 1408
Qy 1388 GAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACCTGTGGGAGAGAGGGATCAA 1447
Db 1409 GAGGCTCTTGTGACTGGAGGTAAACAACCTGCCAGTAACCTGTGGGAGAGAGGGATCAA 1468
Qy 1448 TATTTTGCACACCTGTATAGGCCATGACACACAGCCCAAGATGCTCTGCTCACAGTCAG 1507
Db 1469 TATTTTGCACACCTGTATAGGCCATGACACACAGCCCAAGATGCTCTGCTCACAGTCAG 1528
Qy 1508 TATGTTGAAGATCCCTGCTGCTTCCACACGCACTTGTGAGCAAAATAGGAAAT 1567
Db 1529 TATGTTGAAGATCCCTGCTGCTTCCACACGCACTTGTGAGCAAAATAGGAAAT 1588
Qy 1568 GTACCCCTTCGCTTGGAGCAGATGAGCCCTTCCCGAGTGCATGGCTTGGAGAGCAGAA 1627
Db 1589 GTACCCCTTCGCTTGGAGCAGATGAGCCCTTCCCGAGTGCATGGCTTGGAGAGCAGAA 1648
Qy 1628 TGTGGCTGTCATATAAGCACACTCATCCCTTGTCTGGAAATCTTGTGCAAGGCAATAAC 1687
Db 1649 TGTGGCTGTCATATAAGCACACTCATCCCTTGTCTGGAAATCTTGTGCAAGGCAATAAC 1708
Qy 1688 AGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGAGTTGTGGC 1747
Db 1709 AGGCTTAGTAAGTCCAAACACAGATGACAGTGTGTGGTCTCTGTGAGTTGTGGC 1768
Qy 1748 TCTCAGCCATCTAGACACACTCTCAAATGAGTGTGGAAATGTTCTTCTGCAGGGT 1807
Db 1769 TCTCAGCCATCTAGACACACTCTCAAATGAGTGTGGAAATGTTCTTCTGCAGGGT 1828
Qy 1808 CTAGAGACTGCTGGGACACTTTTCTTGGAGTGTACTTTCAGAACCTTATAGGATTTCT 1867
Db 1829 CTAGAGACTGCTGGGACACTTTTCTTGGAGTGTACTTTCAGAACCTTATAGGATTTCT 1888
Qy 1868 TTCTGGCCAGATTTCTTCTGTATCACTCAAAGCAGCTCAGCAGAAAGAGCAGCAATG 1927
Db 1889 TTCTGGCCAGATTTCTTCTGTATCACTCAAAGCAGCTCAGCAGAAAGAGCAGCAATG 1948
Qy 1928 CCCAGTATCCCACTCTCCAAAGAACTGACAGCTTATATTTCTCACACTTCTGGGGA 1987
Db 1949 CCCAGTATCCCACTCTCCAAAGAACTGACAGCTTATATTTCTCACACTTCTGGGGA 2008
Qy 1988 ACTGGGTATTAATCCAAACCATCAAAATAGAGACTTGGAGAGAGCAGAGTCAITTCACAG 2047
Db 2009 ACTGGGTATTAATCCAAACCATCAAAATAGAGACTTGGAGAGAGCAGAGTCAITTCACAG 2068
Qy 2048 AAGCAACTTGGGAGATGATGTCAGATGATAAATGAGTTCATCCAGTTCACAAAGAC 2107
Db 2069 AAGCAACTTGGGAGATGATGTCAGATGATAAATGAGTTCATCCAGTTCACAAAGAC 2128
Qy 2108 TCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTCCGCCACCCCTGGCATGCCCAACAA 2167
Db 2129 TCAGAGAACTAGAGTTTAAAGCTGAGGAGAGTCCGCCACCCCTGGCATGCCCAACAA 2188
Qy 2168 GATCACAGCAGCTTACAGGCAATTAATCTCTCTCAATGAGGAGAAATCAITTCACAA 2227
Db 2189 GATCACAGCAGCTTACAGGCAATTAATCTCTCTCAATGAGGAGAAATCAITTCACAA 2248
Qy 2228 TGAGCAAGAACTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTATA 2287
Db 2249 TGAGCAAGAACTCATATGATCATTTAAGGAAGTGTTCCTTATGTGTAGCAAGTATA 2308
Qy 2288 ATCGGCTAACTCTTAAATCCCAATGAAATGCTCTAGGCTGGAAGCAATGGGCTGCAATT 2347
Db 2309 ATCGGCTAACTCTTAAATCCCAATGAAATGCTCTAGGCTGGAAGCAATGGGCTGCAATT 2368
Qy 2348 AGGAGATTAAGACATCAGTCCCAAGTAAATGAAATCCATAGACTCATCTAGCACCACTAC 2407
Db 2369 AGGAGATTAAGACATCAGTCCCAAGTAAATGAAATCCATAGACTCATCTAGCACCACTAC 2428

2408 CATTAGCATTAGTTAGGAGCTGCAAGGCCCAAGAGTGAAGATGTGATATATGCTGCT 2467
2429 CATTAGCATTAGTTAGGAGCTGCAAGGCCCAAGAGTGAAGATGTGATATATGCTGCT 2488
2468 CTTGTGTAGCTCAGGAGACAAATTCAGACACAGACACTACAGTTAAAGCTGAACTGAGCT 2527
2489 CTTGTGTAGCTCAGGAGACAAATTCAGACACAGACACTACAGTTNNNNNNNNNNNNNT 2548
2528 GCAAGTAATAGCATGAACAGTACAGAAATACCTTATGAGGGGCGAGGCTGAAGCTGGG 2587
2549 GCAAGTAATAGCATGAACAGTACAGAAATACCTTATGAGGGGCGAGGCTGAAGCTGGG 2608
2588 CTTGAAGCATGAGTGAATTTGGATAGAGATGAGAAAGACAGAGGGCTCCAAAGTGAG 2647
2609 CTTGAAGCATGAGTGAATTTGGATAGAGATGAGAAAGACAGAGGGCTCCAAAGTGAG 2668
2648 AGAAGCATGAAATAGCAGAGGGCTGGATCAGTGGGGGTGATTCAGAGCACTCTCCA 2707
2669 AGAAGCATGAAATAGCAGAGGGCTGGATCAGTGGGGGTGATTCAGAGCACTCTCCA 2728
2708 GATGACCATGATGCTCAGAGTCCCTTGCTATGTTGGCAGAGTGTCCAGCCAGATG 2767
2729 GATGACCATGATGCTCAGAGTCCCTTGCTATGTTGGCAGAGTGTCCAGCCAGATG 2788
2768 TGTGCCCCCAGCCCATGCTCATTTACATGTCCTTCAATGCCACCTCAAAAGTACTCT 2827
2789 TGTGCCCCCAGCCCATGCTCATTTACATGTCCTTCAATGCCACCTCAAAAGTACTCT 2848
2828 TCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCACTGCT 2887
2849 TCTGTAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCACTGCT 2908
2888 GTTTTTTCCCTTTGCTGCTCTTATCACTAAACTCATCTCATGAGCTTACAGATAA 2947
2909 GTTTTTTCCCTTTGCTGCTCTTATCACTAAACTCATCTCATGAGCTTACAGATAA 2968
2948 CTAATTAATTTGTTTCTCTCACTACATTTGATGATGAGGATTAACAGATAACGGAAGCC 3007
2969 CTAATTAATTTGTTTCTCTCACTACATTTGATGATGAGGATTAACAGATAACGGAAGCC 3028
3008 GCTGGGGTGTGGCTCAAGCTGTATCCCAACACTTTGGAGGCCAAGCAGCGGATC 3067
3029 GCTGGGGTGTGGCTCAAGCTGTATCCCAACACTTTGGAGGCCAAGCAGCGGATC 3088
3068 ACTGAGGTGAGARTTCGAGATTTCTGGCCCACTGTTGAAACCCCATNTTACTAA 3127
3089 ACCTGAGGTGAGARTTCGAGATTTCTGGCCCACTGTTGAAACCCCATNTTACTAA 3148
3128 AATACGAATTAAGCAGGTGTGGTGGCAGACATCTGTAGTCCAG 3173
3149 AATACGAATTAAGCAGGTGTGGTGGCAGACATCTGTAGTCCAG 3194

RESULT 6
US-10-723-860-1885
; Sequence 1885, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1885
; LENGTH: 1067
; TYPE: DNA

ORGANISM: Homo sapiens
US-10-723-860-1885
Query Match 32.6%; Score 1034; DB 18; Length 1067;
Best Local Similarity 100.0%; Pred. No. 8.8e-309;
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15 CCGTCTTTTCCACAGAAAGGTTAGACCTGCTGAAAGAGATGGCTCAGACACACCTATGGATC 74
34 CCGTCTTTTCCACAGAAAGGTTAGACCTGCTGAAAGAGATGGCTCAGACACACCTATGGATC 93
75 TTGCTCTTTTGGCTCCAAACCTGGCCGGAAGCAGCTGGAAGAGACTCGAAATCTTCACA 134
94 TTGCTCTTTTGGCTCCAAACCTGGCCGGAAGCAGCTGGAAGAGACTCGAAATCTTCACA 153
135 GTGAATGGATTTCTGGGAGAGTCACTCTTCCCTGTAATAATCAAGAAACACGGCAA 194
154 GTGAATGGATTTCTGGGAGAGTCACTCTTCCCTGTAATAATCAAGAAACACGGCAA 213
195 GTTAAATCATTTGCTTGGACTTTCTTAAACATCTGTTGCTTATGTAACACAGGACTCA 254
214 GTTAAATCATTTGCTTGGACTTTCTTAAACATCTGTTGCTTATGTAACACAGGACTCA 273
255 GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATATTATGAACGGATATGCGCTTA 314
274 GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATATTATGAACGGATATGCGCTTA 333
315 GCTCGCACTACAATCTGTCATTTAGCGATCTGAGGATGGAAGACGACAGAGACTACAAA 374
334 GCTCGCACTACAATCTGTCATTTAGCGATCTGAGGATGGAAGACGACAGAGACTACAAA 393
375 GCAGACATAAATACACAGGCTGATCCCTACACACCAAGCGCTTACAACTGCAAAATC 434
394 GCAGACATAAATACACAGGCTGATCCCTACACACCAAGCGCTTACAACTGCAAAATC 453
435 TATGCTGCGCTTGGGAAACCAAAATTAACAGAGTTTAAATGGCATCTGTGACAGACCC 494
454 TATGCTGCGCTTGGGAAACCAAAATTAACAGAGTTTAAATGGCATCTGTGAAACAGCAC 513
495 TGTAAATGTCACACTGATGCTCTGTAGAGAAAGAAAGAAAGATGTGACATACAAATGG 554
514 TGTAAATGTCACACTGATGCTCTGTAGAGAAAGAAAGAAAGATGTGACATACAAATGG 573
555 AGTCCCTCTGGAGAAAGAGGGTAAATGCTTCCAAATCTTCCAGACTCTCTGAGGACCAAG 614
574 AGTCCCTCTGGAGAAAGAGGGTAAATGCTTCCAAATCTTCCAGACTCTCTGAGGACCAAG 633
615 CTGACTTACACGCTGTAAGCCGCAACCTCTGTGACCAACAAATCTGACTCCATCTCTGCC 674
634 CTGACTTACACGCTGTAAGCCGCAACCTCTGTGACCAACAAATCTGACTCCATCTCTGCC 693
675 CGGCAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGGTGTGAGC 734
694 CGGCAGCTCTGTGACAGACATCGCAATGGGCTTCCGTACTCACCACACCGGGTGTGAGC 753
735 GTGCTGGCTATGTTCTTTCTGCTTGTCTCATTTCTGCTTCTGCTGTTTTTGTTCGGTTG 794
754 GTGCTGGCTATGTTCTTTCTGCTTGTCTCATTTCTGCTTCTGCTGTTTTTGTTCGGTTG 813
795 TTCAAGAGAAAGCAAGATGCTCTCAAGAAACCAATATACATATATCATGCTTCA 854
814 TTCAAGAGAAAGCAAGATGCTCTCAAGAAACCAATATACATATATCATGCTTCA 873
855 AGGAACACCCAGCAGCAGAGTCCAGAACTATGATGAAATCTTCCAGTCCAGAGTCTT 914
874 AGGAACACCCAGCAGCAGAGTCCAGAACTATGATGAAATCTTCCAGTCCAGAGTCTT 933
915 CCCTCCAAAGGAGAGCAGGTAACAGAGTATTTCCGAAGTGCAGTTTGTGTAAGATG 974
934 CCCTCCAAAGGAGAGCAGGTAACAGAGTATTTCCGAAGTGCAGTTTGTGTAAGATG 993
975 GGGAAAGCCAGCAGCAGGTAACAGAGTATTTCCGGGACTTCAAGCTATGAATTTGTGATC 1034

Db 994 GGGAAAGCCAGCACACAGACAGTAAACCTCTGGGACTTCAAGCTATGAAATTTGTGATC 1053
QY 1035 TAGGCTGTGGGCT 1048
Db 1054 TAGGCTGTGGGCT 1067

RESULT 7

US-10-436-523-29
; Sequence 29, Application US/10436523
; Publication No. US2003018088A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-523-29

Query Match 32.6%; Score 1033.4; DB 16; Length 1040;
Best Local Similarity 99.9%; Pred. No. 1.3e-308;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CCGTGCTTTTCCACAGAAGTTAGACCTCGTAAAGAGATGGCTCAGCACCACTATGGATC 74
Db 6 CCGTGCTTTTCCACAGAAGTTAGACCTCGTAAAGAGATGGCTCAGCACCACTATGGATC 65
QY 75 TTGCTCTTTTGGCTCGAACCCTGGCGGAGAGCTGGAAAGACTCAGAAATCTTCACA 134
Db 66 TTGCTCTTTTGGCTCGAACCCTGGCGGAGAGCTGGAAAGACTCAGAAATCTTCACA 125
QY 135 GTGAATGGGATTCGGGAGAGTCAGTCACTTTCCCTGTAAATATCAAGAACCCAGCAA 194
Db 126 GTGAATGGGATTCGGGAGAGTCAGTCACTTTCCCTGTAAATATCAAGAACCCAGCAA 185
QY 195 GTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCTTATGTAAACCCAGGAGACTCA 254
Db 186 GTTAAATCATTTGCTTGGACTTCTAAACATCTGTTGCTTATGTAAACCCAGGAGACTCA 245
QY 255 GAAACAGCACCGTAGTTACTGTGACCCACAGAAATTTATGAACGGATACATGCCCTTA 314
Db 246 GAAACAGCACCGTAGTTACTGTGACCCACAGAAATTTATGAACGGATACATGCCCTTA 305
QY 315 GGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGGATGGAAGACCGCAGGAGACTTACAAA 374
Db 306 GGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGGATGGAAGACCGCAGGAGACTTACAAA 365
QY 375 GCAGACATAATPACACAGCTGATCCCTACACCAACCAAGCGGTACAACTCGAAATC 434
Db 366 GCAGACATAATPACACAGCTGATCCCTACACCAACCAAGCGGTACAACTCGAAATC 425
QY 435 TATCGTCGGCTTGGGAAACCAAAATTTACAGAGTTTAAATGGCATCTGTGAACAGACC 494
Db 426 TATCGTCGGCTTGGGAAACCAAAATTTACAGAGTTTAAATGGCATCTGTGAACAGACC 485
QY 495 TGTAAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAAATGG 554
Db 486 TGTAAATGTACACTGACATGCTCTGTAGAGAAAGAAAGAAATGTGACATACAAATGG 545
QY 555 AGTCCCTGGGAGAGAGGTAATGCTCTTCAAACTTTCCAGACTCTCTGAGGACCAAGAG 614
Db 546 AGTCCCTGGGAGAGAGGTAATGCTCTTCAAACTTTCCAGACTCTCTGAGGACCAAGAG 605

QY 615 CTGACTTACAGTCTAGAGCCAGAACCCCTGTCAGCAACAATTTGACTCCATCTCTGCC 674
Db 606 CTGACTTACAGTCTAGAGCCAGAACCCCTGTCAGCAACAATTTGACTCCATCTCTGCC 665
QY 675 CGGAGCTCTCTGAGACATCGCAATGGCTTCCGCTACTCACACACCGGGTTGCTGAGC 734
Db 666 CGGAGCTCTCTGAGACATCGCAATGGCTTCCGCTACTCACACACCGGGTTGCTGAGC 725
QY 735 GTGCTGGCTATGTTCTTTTCTGCTTCTCATCTGTCTTCTGAGTGTGTTTGTTCGGTTG 794
Db 726 GTGCTGGCTATGTTCTTTTCTGCTTCTCATCTGTCTTCTGAGTGTGTTTGTTCGGTTG 785
QY 795 TTCAAGGAACACAGATGCTGCTCAAGAAACCATATACATATATCATGGCTTCA 854
Db 786 TTCAAGGAACACAGATGCTGCTCAAGAAACCATATATACATATATCATGGCTTCA 845
QY 855 AGGAACACCCAGCAGCAGAGTCCAGAAATCTATGATGAAATCCTGCGAGTCAAGGTGCTT 914
Db 846 AGGAACACCCAGCAGCAGAGTCCAGAAATCTATGATGAAATCCTGCGAGTCCAGGTGCTT 905
QY 915 CCCTCCAAAGGAAGAGCCAGTGAACACAGATTTATTCGGAAGTGCAGTTTGTGTAAGATG 974
Db 906 CCCTCCAAAGGAAGAGCCAGTGAACACAGTTTATTCGGAAGTGCAGTTTGTGTAAGATG 965
QY 975 GGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC 1034
Db 966 GGGAAAGCCAGCACACAGGACAGTAAACCTCTCGGACTTCAAGCTATGAAATTTGTGATC 1025
QY 1035 TAGGCTGTGGGCTG 1049
Db 1026 TAGGCTGTGGGCTG 1040

RESULT 8

US-09-809-391-303
; Sequence 303, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 303
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (491)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-303

Query Match 25.6%; Score 813; DB 10; Length 828;
Best Local Similarity 99.2%; Pred. No. 2.3e-240;
Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2146 ACCCTGGCATGCCCCCAACACAGATCACAGCCAGCTTACACAGGCATTAACCTCTCTCA 2205
Db 1 ACCCTGGCATGCCCCCAACACAGATCACAGCCAGCTTACACAGGCATTAACCTCTCTCA 60
QY 2206 ATGAGGAAGAAATCAATTCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGT 2265
Db 61 ATGAGGAAGAAATCAATTCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGT 120
QY 2266 CCCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGC 2325
Db 121 CCCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTAGGC 180
QY 2326 TGGACAGCAATGGGCTGCATTTAGGCAGATAAGACATCAGTCCCGAGTAAATGAATCCAT 2385

181 TGACAGCAATGGCTGCAATTTAGCAGATAAGACATCAGTCCAGTAAGTAAATCAAT 240
2386 AGACTCATCTAGACCAACTACATTAGACACTATGTTAGGAGCTGCAAGGCCCAAGTA 2445
241 AGACTCATCTAGACCAACTACCATTTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTA 300
2446 GAAGATGTCATAATGCTGCTCTTGTGTAGCTCAGGAGACAATTCAGCACAGACACTA 2505
301 GAAGATGTCATAATGCTGCTCTTGTGTAGCTCAGGAGACAATTCAGCACAGACACTA 360
2506 CAGTTAAACCTGAATCGACCTGCAAGTAAATAGCATGAACAGTCAGAAAAATACCTTATG 2565
361 CAGTTAAACCTGAATCGACCTGCAAGTAAATAGCAAGAACAGTCAGAAAAATACCTTATG 420
2566 AGGGGCGAGGCTGAAAGCTGGGCTTGAAGATGGAATGGAATTTGGATAGAGAATGAGGA 2625
421 AGGGGCGAGGCTGAAAGCTGGGCTTGAAGATGGAATGGAATTTGGATAGAGAATGAGGA 480
2626 AGACAGAGGGCTCCCAAGTGAGAGAGCATGAAAAATGAGCGGGCCCTGGATCAAGTGGG 2685
481 AGACAGAGGGCTCCCAAGTGAGAGAGCATGAAAAATGAGCGGGCCCTGGATCAAGTGGG 540
2686 GTGTATTTCAGAGCACCTCCAGATGCACCATGCTCCTCACAGTCCCTTGCCTATGTGT 2745
541 GTGTATTTCAGAGCACCTCCAGATGCACCATGCTCCTCACAGTCCCTTGCCTATGTGT 600
2746 GGAGAGTGTCCAGCAGATGCTGCCGCCACCCCATGTCATTTACATGCTCTTCAAT 2805
601 GGAGAGTGTCCAGCAGATGCTGCCGCCACCCCATGTCATTTACATGCTCTTCAAT 660
2806 GCCCACCCTAAAAGGTACCTCTCTGTAAGCTTTCCCT-GGTATCAGGAATCAAAATTA 2864
661 GCCCACCCTAAAAGGTACCTCTCTGTAAGCTTTCCCTGGGTATCAGGAATCAAAATTA 720
2865 ATCAGGAGTCTTTTCACACTGCTGTTTTTTCCTCTTGTGCTCTTATCACTAAACTCA 2924
721 ATCAGGAGTCTTTTCACACTGCTGTTTTTTCCTCTTGTGCTCTTATCACTAAACTCA 780
2925 TCTCATTCAGCCTTACAGCACTAACTAATTTGTTTCTCTCACTACA 2972
781 TCTCATTCAGCCTTACAGCACTAACTAATTTGTTTCTCTCACTACA 828

RESULT 9

US-09-882-171-303
; Sequence 303, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163

; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22

```

; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,872
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670

; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/049,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match          25.6%; Score 813; DB 10; Length 828;
Best Local Similarity 99.2%; Pred. No. 2.3e-240;
Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Qy 2146 ACCCTGGCATGCCCAACAAACAGATCACAGCCAGCTTACACAGSCATTAATCTCTCA 2205
Db 1 ACCCTGGCATGCCCAACAAACAGATCACAGCCAGCTTACACAGSCATTAATCTCTCA 60

Qy 2206 ATGAGGAGAGATCATTCACAACTGAGCAAGACATTCATATCATCTTTAAGAGAGTGTT 2265
Db 61 ATGAGGAGAGATCATTCACAACTGAGCAAGACATTCATATCATCTTTAAGAGAGTGTT 120

Qy 2266 CCCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGC 2325
Db 121 CCCTTATGTGTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGC 180

Qy 2326 TGAACAGCAATGGGCTGCAATTAGGAGATTAAGACATCAGTCCAGTAATGAATCCAT 2385
Db 181 TGAACAGCAATGGGCTGCAATTAGGAGATTAAGACATCAGTCCAGTAATGAATCCAT 240

Qy 2386 AGACTCATCTAGCACCACTACCACTTAGCCTATGTTAGGAGCTGCAAGGCCCAAGTA 2445
Db 241 AGACTCATCTAGCACCACTACCACTTAGCCTATGTTAGGAGCTGCAAGGCCCAAGTA 300

Qy 2446 GAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAAATTCACAGCACAGACTA 2505
Db 301 GAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAAATTCACAGCACAGACTA 360

Qy 2506 CAGTTAACGCTGAATCGAGCTGCAAGTAATAGATGAACAGTCAAGAAAATACCTTAG 2565
Db 361 CAGTTAACGCTGAATCGAGCTGCAAGTAATAGATGAACAGTCAAGAAAATACCTTAG 420

Qy 2566 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGATGATGAAATTTGATAGAGATGAGGA 2625
Db 421 AGGGGGCAGGGCTGAAGCTGGGCTTGAAGATGATGAAATTTGATAGAGATGAGGA 480

Qy 2626 AGACAGAGGGCTTCAAGTGAAGAGATGAAATGAAGAGGGGCTTGATCAGTGGG 2685
Db 481 AGACAGAGGGCTTCAAGTGAAGAGATGAAATGAAGAGGGGCTTGATCAGTGGG 540

Qy 2686 GTGTATTTCAGAGCAGCTTCCAGATGCACCATGATGCTCAGTCCCTTGCCTATGTGT 2745
Db 541 GTGTATTTCAGAGCAGCTTCCAGATGCACCATGATGCTCAGTCCCTTGCCTATGTGT 600

Qy 2746 GGCAGAGTGTCAGGAGAGATGTGTGCCCCCAGCCCATGCTTACATTTACATGTCTTCAAT 2805
```

```
Db 601 GGCAGAGTCTCCAGCCAGATGTGTGCCCCCACCACATGTCCATTTACATGTCTTCAAT 660
QY 2806 GCCACCTCAAAAGGTACCTCTTCTGTAAGCTTTCCT- GGTATCAGGAATCAAAATTA 2864
Db 661 GCCACCTCAAAAGGYACVCTTCTGTAAGCTTTCCTCTGGTATCAGGAATCAAAATTA 720
QY 2865 ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGCTCTTCTATCACTAAACTCA 2924
Db 721 ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGCTCTTCTATCACTAAACTCA 780
QY 2925 TCTCATTCAGCCTTACAGCATAACTAATTAATTTGTTTTTCTCACTACA 2972
Db 781 TCTCATTCAGCCTTACAGCATAACTAATTAATTTGTTTTTCTCACTACA 828

RESULT 10
US-10-164-861-303
; Sequence 303, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (491)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-303

Query Match 25.6%; Score 813; DB 17; Length 828;
Best Local Similarity 99.2%; Pred. No. 2.3e-240;
Matches 821; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2146 ACCCTGGCATGCCCCCAAAACAGATCACAGCCAGCTTACACAGGCAATTAACCTCTCTCA 2205
Db 1 ACCCTGGCATGCCCCCAAAACAGATCACAGCCAGCTTACACAGGCAATTAACCTCTCTCA 60

QY 2206 ATCAGGAAGATCATTTCACTACACTGAGCAAGATTCATATGATCATTTAAGGAAGTGT 2265
Db 61 ATCAGGAAGATCATTTCACTACACTGAGCAAGATTCATATGATCATTTAAGGAAGTGT 120

QY 2266 CCCTTATGTGTAGCAAGTATATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGC 2325
Db 121 CCCTTATGTGTAGCAAGTATATCGGCTAACTCCTAAATCCCAATGAATAGTCTTAGGC 180

QY 2326 TGGACAGCAATGGCTGCAATTTAGGCAGATTAAGACATCAGTCCCAATGAATCCAT 2385
Db 181 TGGACAGCAATGGCTGCAATTTAGGCAGATTAAGACATCAGTCCCAATGAATCCAT 240

QY 2386 AGACTCATCTAGCACCACTACCATTTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTA 2445
Db 241 AGACTCATCTAGCACCACTACCATTTAGCACTATGTTAGGAGCTGCAAGGCCCAAGTA 300

QY 2446 GAAGATGTGATATGTCTCTTTGTAGCTCAGGAGCAATTTCCAGCACAGACACTA 2505
Db 301 GAAGATGTGATATGTCTCTTTGTAGCTCAGGAGCAATTTCCAGCACAGACACTA 360

QY 2506 CAGTTAACGCTGAACGTGCAAGTAAATAGCATGAACAGTCAGAAAAATACCTTATG 2565
Db 361 CAGTTAACGCTGAACGTGCAAGTAAATAGCATGAACAGTCAGAAAAATACCTTATG 420
```

```
QY 2566 AGGGGCGAGGGCTGAAGCTGGGCCCTTGAAGATGGATGAAATTTGATAGAGAAATGAGGA 2625
Db 421 AGGGGCGAGGGCTGAAGCTGGGCCCTTGAAGATGGATGAAATTTGATAGAGAAATGAGGA 480
QY 2626 AGACAGAGGGCTCCAAAGTGAGAGAGCAATGAAAAATAGCAGGGCCCTGGATCAGTGGG 2685
Db 481 AGACAGAGGGCTCCAAAGTGAGAGAGCAATGAAAAATAGCAGGGCCCTGGATCAGTGGG 540
QY 2686 GTGTATTACAGACACCTCTCCAGATGCACCATGCTCAGAGTCCCTTGGCTATGTGT 2745
Db 541 GTGTATTACAGACACCTCTCCAGATGCACCATGCTCAGAGTCCCTTGGCTATGTGT 600
QY 2746 GGCAGAGTGTCCAGCCAGATGTGTGCCCCCACCACATGTCCATTTACATGTCTTCAAT 2805
Db 601 GGCAGAGTGTCCAGCCAGATGTGTGCCCCCACCACATGTCCATTTACATGTCTTCAAT 660
QY 2806 GCCACCTCAAAAGGTACCTCTTCTGTAAGCTTTCCT- GGTATCAGGAATCAAAATTA 2864
Db 661 GCCACCTCAAAAGGYACVCTTCTGTAAGCTTTCCTCTGGTATCAGGAATCAAAATTA 720
QY 2865 ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGCTCTTCTATCACTAAACTCA 2924
Db 721 ATCAGGATCTTTTACACTGCTGTTTTTCTCTTTGCTCTTCTATCACTAAACTCA 780
QY 2925 TCTCATTCAGCCTTACAGCATAACTAATTAATTTGTTTTTCTCACTACA 2972
Db 781 TCTCATTCAGCCTTACAGCATAACTAATTAATTTGTTTTTCTCACTACA 828

RESULT 11
US-09-918-995-36774
; Sequence 36774, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36774
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36774

Query Match 13.1%; Score 414.2; DB 10; Length 420;
Best Local Similarity 99.3%; Pred. No. 5.6e-117;
Matches 416; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1522 CCTGTGTCGTGGCCCTTCCACACGATCTTGGAGCAATTTAGAAAATGTACCTTCGCTG 1581
Db 2 CGTGTGTCGTGGCCCTTCCACACGATCTTGGAGCAATTTAGAAAATGTACCTTCGCTG 61

QY 1582 AGCAGATGAGCCCTTCCCCGAGTGCATGGCTTGGAGAGCAATTTGGGCTGCATAT 1641
Db 62 AGCAGATGAGCCCTTCCCCGAGTGCATGGCTTGGAGAGCAATTTGGGCTGCATAT 121

QY 1642 AGCAGATGAGCCCTTCCCCGAGTGCATGGCTTGGAGAGCAATTTGGGCTGCATAT 1701
Db 122 AGCAGATGAGCCCTTCCCCGAGTGCATGGCTTGGAGAGCAATTTGGGCTGCATAT 181

QY 1702 CAAACACAGATGAGTGTGTGGGTCTCTGTGAGAGTGTGGCTCTCAGCCATGTAG 1761
Db 182 CAAACACAGATGAGTGTGTGGGTCTCTGTGAGAGTGTGGCTCTCAGCCATGTAG 241

QY 1762 ACACTCTCCAAATGAGTGTGGAAAATGTTCTTCTCAGGGTCTAGAGTGTCTG 1821
```

Db 242 ACACACTCTCCAAATGGAGTGTGGAAATGTTCTTTCTGCAGGGTCTAGAGACTCTCTGG 301
QY 1822 GACACTTTTCTGGAGTGTACTTCAAGACCTTATAGGATTTCTTTCTGGCCAAAGATT 1881
Db 302 GACACTTTTCTGGAGTGTACTTCAAGACCTTATAGGATTTCTTTCTGGCCAAAGATT 361
QY 1882 TCCTTCTGTATCACTCCAGCAGCCTCAGCAGAAAGCAGCCATGCCAGTATTCCTCA 1940
Db 362 TCCTTCTGTATCACTCCAGCAGCCTCAGCAGAAAGCAGCCATGCCAGTATTCCTCA 420

RESULT 12

US-09-783-590-5649
; Sequence 5649. Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5649
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (167)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (206)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (212)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (274)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (334)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (355)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (365)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (368)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (370)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (406)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature

; LOCATION: (420)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (442)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (466)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (468)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (469)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (473)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (483)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (484)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (486)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-5649

Query Match 6.9%; Score 217.6; DB 9; Length 502;
Best Local Similarity 92.5%; Pred. No. 5.3e-56;
Matches 283; Conservative 0; Mismatches 16; Indels 7; Gaps 5;
QY 1200 TGCCTAAATGGACAAATGGATGCATACCCCTTCTCGAAATGACTCCCTTCTCGAAATGAATGA 1259
Db 3 TTCCTAAATGGACAAATGGATGCATACCCCTTCTCGAAATGACTCCCTTCTCGAAATGAATGA 62
QY 1260 CAAAGCAGGTTACCTAGTAGTATGTTTCCCAAACTTCTCCCATCATAGCATAGTAGAAA 1319
Db 63 CAAAGCAGGTTACCTAGTAGTATGTTTCCCAAACTTCTCCCATCATAGCATAGTAGAAA 122
QY 1320 ATAATATTTTATGGCAGCACT-GGGATAAACAAGCAAGATTGCT-CACCTTCTGGAAAGCTG 1377
Db 123 ATAATATTTTATGGCAGCACTGGGGATATAACAAGCAGATTGCTTNCACCTTCTGGNAGCTG 182
QY 1378 CATATGACTAGAGCCTTCTGTG-CTGGAGGTAAACACCTGCCCAAGTAA--CTGTGGG 1434
Db 183 CATATGACTAGAGCCTTCTGTGCTGNACTGGNGGTAAACACCTGCCCAAGTAACTGTGGGA 242
QY 1435 AGAAGGGGATCAATATTTTGCACACCTGTAT--AGGCCATGGCAGCACCAGCCAGATGC 1492
Db 243 GGAAGGGGATCAATATTTTGCACACCTGTATTTGACACCTGTAAATAGGCCATGGGCACACCCAGATGT 302
QY 1493 TCTGCT 1498
Db 303 TCTGGT 308

RESULT 13

US-10-198-846-6370
; Sequence 6370. Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6370
LENGTH: 820
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 640, 642, 643, 644, 658, 668, 675, 687, 697, 725, 726, 727,
LOCATION: 728, 745, 755, 757, 779, 781, 790, 804, 816
OTHER INFORMATION: n = A, T, C or G
US-10-198-846-6370

Query Match 6.7%; Score 212.4; DB 14; Length 820;
Best Local Similarity 96.7%; Pred. No. 2.9e-54;
Matches 238; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY 15 CCGTGCTTTTCCACAGAGTTAGACCTGGAAGAGATGGCTCAGCACCACCTATGGATC 74
DB 388 CCGTGCTTTTCCACAGAGTTAGACCTGGAAGAGATGGCTCAGCACCACCTATGGATC 447
QY 75 TTGCTCCTTTGCTGCAACCTGGCCGGAAGAGCTGGAAGAGACTCAGAAATCTTCACA 134
DB 448 TTGCTCCTTTGCTGCAACCTGGCCGGAAGAGCTGGAAGAGACTCAGAAATCTTCACA 507
QY 135 GTGAATGGGATCTGGGAGAGTCAGTCACCTTTCCCTGTAATATCCAGAACCCAGCGCAA 194
DB 508 GTGAATGGGATCTGGGAGAGTCAGTCACCTTTCCCTGTAATATCCAGAACCCAGCGCAA 567
QY 195 GTTAAATCATCTGCTGGACTCT-AAAACATCTGTT-GCTTATGTAAACACAGGAGACT 252
DB 568 GTTAAATCATCTGCTGGACTTTTAAACACATCTGTTGGCTTATGTAAACAGTAGGAGACT 627
QY 253 CAGAAA 258
DB 628 TAAAAA 633

RESULT 14
US-10-017-161-1579/c
Sequence 1579, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1579
LENGTH: 16815
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(16815)
FEATURE:

NAME/KEY: CDS
LOCATION: (201)..(388)
FEATURE:
NAME/KEY: CDS
LOCATION: (870)..(941)
FEATURE:
NAME/KEY: CDS
LOCATION: (1497)..(1568)
FEATURE:
NAME/KEY: CDS
LOCATION: (1687)..(1956)
FEATURE:
NAME/KEY: CDS
LOCATION: (4564)..(4707)
FEATURE:
NAME/KEY: CDS
LOCATION: (9933)..(9982)
FEATURE:
NAME/KEY: CDS
LOCATION: (16030)..(16267)
FEATURE:
NAME/KEY: CDS
LOCATION: (16483)..(16615)
FEATURE:
NAME/KEY: modified base
LOCATION: (6779)..(6878)
OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1579
Query Match 4.5%; Score 141.2; DB 15; Length 16815;
Best Local Similarity 65.4%; Pred. No. 2.3e-31;
Matches 200; Conservative 3; Mismatches 103; Indels 0; Gaps 0;
QY 2868 AGGGATCTTTTCACACTGCTGTTTTTCTCTCTTTGGTCTCTATCACAATAAACTCATCT 2927
DB 7700 AGCTTTCACTTAAACATTCCTGTTCTTTTACAGTTGAAATTTATAAGAGTTTCCGCC 7641
QY 2928 CATTGAGCCCTTACAGCATAAATAATTTTCTCTCCTCCTACATGTATGTATGTGGGAA 2987
DB 7640 CAGGTGACATGCTCTTGGCCAAAGTGTATCTTTATTTCCAGCAGACTTCTGGTCTTT 7581
QY 2988 TTACAGATAAACGGAAGCKGCTGGGGTGGTGGCTCAGCCCTGTATCCCAACACTTTGG 3047
DB 7580 GTCAAAAGAGAGAGAGGCGGGGTAGTGGCTCATGCTGTATATCCAGCAGACTTTGG 7521
QY 3048 GAGGCCAAGCAGCGGATCCTCAGGTGAGGATTCAGATTTCTGGCCCAACATGG 3107
DB 7520 GAGGCCAAGCAGCGGATCCTCAGGTGAGGATTCAGATTTCTGGCCCAACATGG 7461
QY 3108 TGAACCCCATNTNTACTAAAAATACGAAATTAGCCAGGTGGTGGCAGACATCTGTAG 3167
DB 7460 TGAACCCCTGCTCTACTAAAAATACAAAATTAGCCGCGGTGGTGGCAGACATCTGTAG 7401
QY 3168 TCCAG 3173
DB 7400 TCCAG 7395

RESULT 15
US-10-052-482-184
Sequence 184, Application US/10052482
Publication No. US2004007264A1
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02

```
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 184
; LENGTH: 96592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-482-184

Query Match      4.4%; Score 140; DB 17; Length 96592;
Best Local Similarity 78.9%; Pred. No. 1.7e-30;
Matches 161; Conservative 3; Mismatches 40; Indels 0; Gaps 0;

QY 2970 ACATTGTACATGTGGGAATTACAGATAACGGAAGCKGCTGGGGTGGTGGCTCAGCGCT 3029
Db 25139 ACTTGTATAGAGCAGTATTTGAAATGCAAGTGCCCGGCGTGGTGGCTCAGCGCT 25198

QY 3030 GTAATCCCAACACTTTGGGAGGCCAAGCGAGCGGGATCACCTGAGGTCAGGARTTCGAGA 3089
Db 25199 GTAATCCCAAGCACTTTGGGAGGCCGAGCGCGGATCACCTGAGGTCGGGAGTTTGAGA 25258

QY 3090 TTARTCTGCCCAACATGGTGAAACCCCATNTNTACTAAAAATACGAAATTAGCCAGGTGT 3149
Db 25259 CCAGCCTGACCAACATGGGAGAAACCCCATCTCTACTAAAAATACGAAATTAGCCAGGTGT 25318

QY 3150 GGTGGCACACATCTGTAGTCCAG 3173
Db 25319 GGTGGCAGACACCTGTATATCCAG 25342

Search completed: February 6, 2005, 00:53:42
Job time : 1609 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2005, 11:36:21 ; Search time 9799 Seconds
(without alignments)
12325.536 Million cell updates/sec

Title: US-09-882-171-174
Perfect score: 3173
Sequence: 1 tcagaccacaggtccgtgc.....gcacacatctgtagtcacag 3173

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	987	31.1	987	AY408981	Homo sapi
2	979.6	30.9	987	AY408982	Pan trogl
3	836.6	26.4	916	BQ712229	AGENCOURT
4	671	21.1	890	BQ712137	AGENCOURT
5	621.2	19.6	634	AV716814	AV716814
6	620.2	19.5	1000	BQ710889	AGENCOURT
7	614.4	19.4	666	AW963140	EST375213
8	614	19.4	1074	EG106937	CG02291349
9	606	19.1	608	CV023928	1001 Full
10	585	18.4	598	BP300686	BP300686
11	582	18.3	582	BP303350	BP303350
12	580	18.3	580	BP297015	BP297015
13	579	18.2	590	BU429718	UI-HF-BNO
14	577.8	18.2	581	BP299453	BP299453
15	576.6	18.2	583	BP298646	BP298646
16	573.4	18.1	580	BP300475	BP300475
17	571.8	18.0	581	BP303711	BP303711
18	568	17.9	580	BP297038	BP297038
19	565.6	17.8	652	CB551391	MMSPP0037
20	556	17.5	937	BU198925	DCBCUR08
21	544.4	17.2	603	BP302723	BP302723
22	518.6	16.3	584	BP302120	BP302120
23	514	16.2	535	BP754299	PMO-CT054
24	509.8	16.1	923	AY408983	Mus muscu

25	506.8	16.0	739	6	CB467388	CB467388
26	499.8	15.8	837	5	BP159730	BP159730
27	499.6	15.7	582	5	BP303194	BP303194
28	488.4	15.4	645	6	CA425470	UI-H-DF0-
29	476.6	15.0	613	7	CK903266	id95c06.x
30	460.2	14.5	467	7	CK903267	id95c06.y
31	459.8	14.5	538	2	BE931154	RC1-HY022
32	428	13.5	466	5	BU927996	AGENCOURT
33	396	12.5	788	4	BI151764	602915927
34	394.6	12.4	402	2	AW013969	UI-H-BIO-
35	383.6	12.1	571	6	BY748483	BY748483
36	382	12.0	389	2	AW408076	UI-HF-BMO
37	380.6	12.0	721	6	CB530813	737641 MA
38	365.4	11.5	767	1	AU141507	AU141507
39	353.4	11.1	497	1	AI765654	WI82907.X
40	350.8	11.1	519	4	BM089070	502719 MA
41	348.6	11.0	719	7	CK772231	CK772231
42	344	10.8	540	1	AU159053	AU159053
43	340.4	10.7	677	9	AG090451	AG090451
44	339.2	10.7	651	6	BY724459	BY724459
45	338	10.7	338	5	BX498774	DXF2p779F

ALIGNMENTS

RESULT 1
AY408981
LOCUS
DEFINITION
AY408981 Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408981
VERSION
AY408981.1 GI:39764949
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 987)
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 987)
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..987
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene
1..987
/gene="CD84"
/locus_tag="HCM3405"
ORIGIN
Query Match 31.1%; Score 987; DB 9; Length 987;
Best Local Similarity 100.0%; Pred. No. 3.3e-210;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 ATGCTCAGCACCATCTGATCTCTCTTCTGCTGCAACCTGCCGAGACGCT 110
|||||

```
Db 1 ATGGCTCAGCACCACTATGATCTTGCTCTCTTGGCTGCAAACTGGCGGAGCAGCT 60
QY 111 GGAAGAGCTCAGAAATCTTTCACAGTGAATGGGATCTTGGAGAGTCAGTCACTTTCCCT 170
Db 61 GGAAGAGCTCAGAAATCTTTCACAGTGAATGGGATCTTGGAGAGTCAGTCACTTTCCCT 120
QY 171 GTAATATCAAGAACCCAGGCAAGTTAAATCATTTGCTTGGATCTTAAACATCTGTT 230
Db 121 GTAATATCAAGAACCCAGGCAAGTTAAATCATTTGCTTGGATCTTAAACATCTGTT 180
QY 231 GCTTATGTAACACGAGAGACTCAGAAACAGACCCGTTAGTTACTGTGACCCACAGAAAT 290
Db 181 GCTTATGTAACACGAGAGACTCAGAAACAGACCCGTTAGTTACTGTGACCCACAGAAAT 240
QY 291 TATTATGAACGGATACATGCTTAGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGG 350
Db 241 TATTATGAACGGATACATGCTTAGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGG 300
QY 351 ATGGAAGCGCAGGAGACTACAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 410
Db 301 ATGGAAGCGCAGGAGACTACAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 360
QY 411 ACCAAGCGCTACAACTGCAAAATCTATCGTGGCTTGGGAAACCAAAATTTACACAGCT 470
Db 361 ACCAAGCGCTACAACTGCAAAATCTATCGTGGCTTGGGAAACCAAAATTTACACAGCT 420
QY 471 TTAATGGCATCTGTGAACAGCCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA 530
Db 421 TTAATGGCATCTGTGAACAGCCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA 480
QY 531 GAAAGAAATGTGACATACAAATGGAGTCCCTGGGAGAGAGGTAATGCTTCAAAATC 590
Db 481 GAAAGAAATGTGACATACAAATGGAGTCCCTGGGAGAGAGGTAATGCTTCAAAATC 540
QY 591 TTCCAGACTCTGAGACCAAGAGCTGACTTACCGTGTACAGCCAGAACCCCTGTGACG 650
Db 541 TTCCAGACTCTGAGACCAAGAGCTGACTTACCGTGTACAGCCAGAACCCCTGTGACG 600
QY 651 AACAACTTGACTCCATCTCTGCCGGCAGCTCTGTGAGAGATCGCAATGGGCTTCGTT 710
Db 601 AACAACTTGACTCCATCTCTGCCGGCAGCTCTGTGAGAGATCGCAATGGGCTTCGTT 660
QY 711 ACTCACACACCGGGTGTGAGCGTGTGGGTATGTTCTTCTTCTTCTTCTTCTTCTTCTG 770
Db 661 ACTCACACACCGGGTGTGAGCGTGTGGGTATGTTCTTCTTCTTCTTCTTCTTCTTCTG 720
QY 771 TCTTCAGTGTGTTTGTTCGGTTTGTTCAGAGAGAACAGATGCTGCTTCAAGAGAAACC 830
Db 721 TCTTCAGTGTGTTTGTTCGGTTTGTTCAGAGAGAACAGATGCTGCTTCAAGAGAAACC 780
QY 831 ATATACACATATATCATGCTTCAGGACACCCAGCAGCAGAGTCCAGATCTATGAT 890
Db 781 ATATACACATATATCATGCTTCAGGACACCCAGCAGCAGAGTCCAGATCTATGAT 840
QY 891 GAAATCCTCAGTCCAAAGTGTCTTCCCTCCAAAGGAGAGCCAGTGAACACAGTTTATTC 950
Db 841 GAAATCCTCAGTCCAAAGTGTCTTCCCTCCAAAGGAGAGCCAGTGAACACAGTTTATTC 900
QY 951 GAAGTGCAGTTTGTCTGATTAAGATGGGAAAGCAGCAGACAGATTAACCTCTGGG 1010
Db 901 GAAGTGCAGTTTGTCTGATTAAGATGGGAAAGCAGCAGACAGATTAACCTCTGGG 960
QY 1011 ACTTCAAGCTATGAATTTGTGATCTAG 1037
Db 961 ACTTCAAGCTATGAATTTGTGATCTAG 987
```

```
RESULT 2
AY408982 987 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408982
```

```
AY408982.1 GI:39764950
GSS.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 987)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 987)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..987
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>987
/gene="CD84"
/locus_tag="HCW3405"
gene
ORIGIN
Query Match 30.9%; Score 979.6; DB 9; Length 987;
Best Local Similarity 99.5%; Pred. No. 1.5e-208;
Matches 982; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 51 ATGGCTCAGCACCACTATGATCTTGCTCTTGGCTGCAAACTGGCGGAGCAGCT 110
Db 1 ATGGCTCAGCACCACTATGATCTTGCTCTTGGCTGCAAACTGGCGGAGCAGCT 60
QY 111 GGAAGAGCTCAGAAATCTTTCACAGTGAATGGGATCTTGGAGAGTCAGTCACTTTCCCT 170
Db 61 GGAAGAGCTCAGAAATCTTTCACAGTGAATGGGATCTTGGAGAGTCAGTCACTTTCCCT 120
QY 171 GTAATATCAAGAACCCAGGCAAGTTAAATCATTTGCTTGGATCTTAAACATCTGTT 230
Db 121 GTAATATCAAGAACCCAGGCAAGTTAAATCATTTGCTTGGATCTTAAACATCTGTT 180
QY 231 GCTTATGTAACACGAGAGACTCAGAAACAGACCCGTTAGTTACTGTGACCCACAGAAAT 290
Db 181 GCTTATGTAACACGAGAGACTCAGAAACAGACCCGTTAGTTACTGTGACCCACAGAAAT 240
QY 291 TATTATGAACGGATACATGCTTAGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGG 350
Db 241 TATTATGAACGGATACATGCTTAGTCCGAACTACAATCTGGTCAATTAGCGATCTGAGG 300
QY 351 ATGGAAGCGCAGGAGACTACAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 410
Db 301 ATGGAAGCGCAGGAGACTACAAGCAGACATAAATACACAGGCTGATCCCTACACCACC 360
QY 411 ACCAAGCGCTACAACTGCAAAATCTATCGTGGCTTGGGAAACCAAAATTTACACAGCT 470
Db 361 ACCAAGCGCTACAACTGCAAAATCTATCGTGGCTTGGGAAACCAAAATTTACACAGCT 420
QY 471 TTAATGGCATCTGTGAACAGCCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA 530
Db 421 TTAATGGCATCTGTGAACAGCCTGTAAATGTACACTGACATGCTCTGTAGAGAAAGAA 480
QY 531 GAAAGAAATGTGACATACAAATGGAGTCCCTGGGAGAGAGGTAATGCTTCAAAATC 590
```



```

Db      897 CAAAGCCTAATAGAAATT 915
|||||
B0712137
AGENCOURT 8347554 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279119
5', mRNA sequence.
ACCESSION B0712137
VERSION   B0712137.1 GI:21851036
SOURCE    EST.
ORGANISM  Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2468 row: c column: 24
High quality sequence stop: 490.

FEATURES
Source
1..890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6279119"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 21.1%; Score 671; DB 5; Length 890;
Best Local Similarity 98.2%; Pred. No. 2.2e-139;
Matches 699; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 1976 CACTTCTGGGAACTGGGTATTAATCAACCATCAAAATAGAGACTTGCAGAGCAGA 2035
|||||
Db 13 CACTTCTGGGAACTGGGTATTAATCAACCATCAAAATAGAGACTTGCAGAGCAGA 72
|||||
QY 2036 GTCAATTCCTCCAGAGAACTGGGAGATGATGGTCAGATGATGAATCGGTTCATCCC 2095
|||||
Db 73 GTCAATTCCTCCAGAGAACTGGGAGATGATGGTCAGATGATGAATCGGTTCATCCC 132
|||||
QY 2096 AGTTCCAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCAGAGTCCCGCCACCTTGGCAT 2155
|||||
Db 133 AGTTCCAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCAGAGTCCCGCCACCTTGGCAT 192
|||||
QY 2156 GCCCACAACAGATCAGAGCAGCTTACACAGGCATTAACTTCCTCAATAGGAAAGA 2215
|||||
Db 193 GCCCACAACAGATCAGAGCAGCTTACACAGGCATTAACTTCCTCAATAGGAAAGA 252
|||||
QY 2216 ATCAATTCACACTGAGCAAGACATTCATATGATCATTTTAAGGAAGTTCCTTATGTG 2275
|||||
Db 253 ATCAATTCACACTGAGCAAGACATTCATATGATCATTTTAAGGAAGTTCCTTATGTG 312
|||||
QY 2276 TTAGCAAGTATTAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCA 2335
|||||
Db      313 TTAGCAAGTATTAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCA 372
|||||
QY 2336 TGGGCTGCAATTTAGGCAGATAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCT 2395
|||||
Db 373 TGGGCTGCAATTTAGGCAGATAAGACATCAGTCCAGTAAATGAATCCATAGACTCATCT 432
|||||
QY 2396 AGCACAACATCACTATTAGCACATGTTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGC 2455
|||||
Db 433 AGCACAACATCACTATTAGCACATGTTTAGGAGCTGCAAGGCCCAAGTAGAAGATGTGC 492
|||||
QY 2456 ATAATGTCCTGCTCTGTGTAGCTCAGGAGACAATTCAGCACAGACACTACAGTTAAAGC 2515
|||||
Db 493 ATAATGTCCTGCTCTGTGTAGCTCAGGAGACAATTCAGCACAGACACTACAGTTAAAGC 552
|||||
QY 2516 TGAACCTGAGCTGCAAGTAATAGCATGAACAGTACAGAAAAATACCTTATAGGGGGCAGG 2575
|||||
Db 553 TGAACCTGAGCTGCAAGTAATAGCATGAACAGTACAGAAAAATACCTTATAGGGGGCAGG 611
|||||
QY 2576 GCTGAAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGAAATGAGGAAGACAGAGGG 2635
|||||
Db 612 GCTGAAGCTGGGCTTGAAGGATGGATGAATTTGGATAGAGAAATGAGGAAGACAGAGGG 671
|||||
QY 2636 CCTCCAACTGAGAGAAAGCATGAAAAATGAGCA-GGGGCTCGATCAGTGGGG 2686
|||||
Db 672 CCTCCAGGGGAGAGCATGAAAAATGAGCAGGGGGCTGGATCAGTGGGG 723
|||||

RESULT 5
AV716814 634 bp mRNA linear EST 16-OCT-2000
LOCUS AV716814 DCB Homo sapiens cDNA clone DCBCBC06 5', mRNA sequence.
DEFINITION AV716814
ACCESSION AV716814
VERSION AV716814.1 GI:10813966
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Xu.X., Gu.J., Liu.F., Qu.J., Zhao.M., Li.Y., Huang.Q., Zhou.J.,
Song.H., Gu.Y., Yang.Y., Gao.G., Xiao.H., Li.N., Qian.B., Gao.X.,
Cheng.Z., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M.,
Lu.G., Cheng.Z. and Han.Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Location/Qualifiers
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBCBC06"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
/notes="vector: pTriplex2; Site 1: sfIIA; Site 2: sfIIB"

ORIGIN
Query Match 19.6%; Score 621.2; DB 1; Length 634;
Best Local Similarity 98.3%; Pred. No. 3.1e-128;
Matches 623; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2493 AGCAGACACTACAGTTAACTGCTGAAGTCAAGTCAAGTAAATAGCATGAAGTACAGT 2552
|||||

```

Db 1 ATCACAGACGGTACAGGTAAACGCTGAAGTCAAGTCAAGTAAATAGCATGAACAGTCAAGA 60
Qy 2553 AAAATACCTTATGAGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGAGTAAATTTGGA 2612
Db 61 AAAATACCTTATGAGGGGCGAGGCTGAAGCTGGGCTTGAAGGATGAGTAAATTTGGA 120
Qy 2613 TAGAGATGAGGAAGACAGAGGGCTTCCAAAGTGAGAGAGCATGAAAAATGAGCAGGGGC 2672
Db 121 TAGAGATGAGGAGACAGAGGGCTTCCAAAGTGAGAGAGCATGAAAAATGAGCAGGGGC 180
Qy 2673 CTGGATCAATGAGGGTATTTACAGAGACCTCTCCAGATGACCAATGCTCACAGTCC 2732
Db 181 CTGGATCAATGAGGGTATTTACAGAGACCTCTCCAGATGACCAATGCTCACAGTCC 240
Qy 2733 CTTCCTATGCTGGCAGAGTGTCCAGCAGATGTGCCCCCAGCATGTGCAATTTA 2792
Db 241 CTTCCTATGCTGGCAGAGTGTCCAGCAGATGTGCCCCCAGCATGTGCAATTTA 300
Qy 2793 CATGCTCTCAATGCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCTGGTATCAG 2852
Db 301 CATGCTCTCAATGCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCTGGTATCAG 360
Qy 2853 GAATCAAAATTAATCAGGGATCTTTTACACTGCTGTTTTTCTTTGGTCTTCTAT 2912
Db 361 GAATCAAAATTAATCAGGGATCTTTTACACTGCTGTTTTTCTTTGGTCTTCTAT 420
Qy 2913 CACTAAATCATCTCATTCAGGCTTACAGCATAACTAATTTATTTCTTCTCACTACA 2972
Db 421 CACTAAATCATCTCATTCAGGCTTACAGCATAACTAATTTATTTCTTCTCACTACA 480
Qy 2973 TTGTACATGTTGGAAATTACAGATAAAGCGGAGCGCTGGGCTGCTGCTGCTGTA 3032
Db 481 TTGTACATGTTGGAAATTACAGATAAAGCGGAGCGCTGGGCTGCTGCTGCTGTA 540
Qy 3033 ATCCCAACACTTTGGAGGCAAGCGAGGCGGATCACTGAGTCAAGATTTCGAGTTA 3092
Db 541 ACCCAACACTTTGGAGGCAAGCGAGGCGGATCACTGAGTCAAGATTTCGAGTTA 600
Qy 3093 RTCTGGCAACATGGTGAACCCCATNTACTA 3126
Db 601 GTCTGGCAACATGGTGAACCCCATCTACTA 634

RESULT 6
BQ710889 1000 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT 8501240 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6303101
DEFINITION 5', mRNA sequence.
ACCESSION BQ710889
VERSION BQ710889.1 GI:21849788
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens,
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1000)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2521 row: k column: 06
High quality sequence start: 54
High quality sequence stop: 539.
FEATURES Location/Qualifiers
1..1000 source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6303101"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ScorI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZIP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match	Best Local Similarity	Score	620.2;	DB 5;	Length 1000;	
Matches	692;	Conservative	0;	Mismatches 30;	Indels 5;	Gaps 5;
Qy 1311	ATGTAGAAAATAATATTTTATGGCACACTGGGATAAAACAAGCAAGATTGCTCACTTCTG	1370				
Db 35	ANGAAAATAATATTTTATNGGCACACTGGGGATAAAACAAGCAAGATTGCTCACTTCTG	94				
Qy 1371	GAAGCTGCATATGACTAGAGGCTCTTTGACTGGAGGTAAACAACCTGCCAGTAACCTG	1430				
Db 95	GAAGCTGCATATGACTAGAGGCTCTTTGACTGGAGGTAAACAACCTGCCAGTAACCTG	154				
Qy 1431	TGGGAGAGGGGATCAATATTTTGACACCTCTGTAAGCCATGGCACACCCAGCAAGAT	1490				
Db 155	TGGGAGAGGGGATCAATATTTTGACACCTCTGTAAGCCATGGCACACCCAGCAAGAT	214				
Qy 1491	GCTCTGCTCACAGTACAGTATGTGAAAGATCCCTGGTGGCTGSCCTTCCACGCACTTT	1550				
Db 215	GCTCTGCTCACAGTACAGTATGTGAAAGATCCCTGGTGGCTGSCCTTCCACGCACTTT	274				
Qy 1551	GAGCAAAATGAGAAAATGACCTTCCTGCTGAGGAGATGACAGCCCTTCCCCGAGTGCA	1610				
Db 275	GAGCAAAATGAGAAAATGACCTTCCTGCTGAGGAGATGACAGCCCTTCCCCGAGTGCA	334				
Qy 1611	TGGCTTGGAGAGCAGAAATGTGGGCTGCATATAGCACACTCATCTCTTGTCTGGGAATC	1670				
Db 335	TGGCTTGGAGAGCAGAAATGTGGGCTGCATATAGCACACTCATCTCTTGTCTGGGAATC	394				
Qy 1671	TTTGTGCAGGGCAATACAGGCTTAGTAAGTCCAAACAACAGATGACAGTGTGTGGGTC	1730				
Db 395	TTTGTGCAGGGCAATACAGGCTTAGTAAGTCCAAACAACAGATGACAGTGTGTGGGTC	454				
Qy 1731	TCTGTCAAGATTGTGCTCTCAGCCATGTAGACACTCTCCAAATGGAGTGTGGAAA	1790				
Db 455	TCTGTCAAGATTGTGCTCTCAGCCATGTAGACACTCTCCAAATGGAGTGTGGAAA	514				
Qy 1791	TGTTCTTTCTGACGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTCTACTTCAGAA	1850				
Db 515	TGTTCTTTCTGACGGCTTAGAGACTGTGGGACACTTTTCTTGGAGTGTCTACTTCAGAA	574				
Qy 1851	GCCTTATAGGA-TTTTCTTTCTGCGCAAGA-TTTTCTTTCTGTATCATCTCCAAG-CAGCCT	1907				
Db 575	GCCTTATAGGA-TTTTCTTTCTGCGCAAGA-TTTTCTTTCTGTATCATCTCCAAG-CAGCCT	634				
Qy 1908	CAGCAGAAGAGCAGCCATGCCAGTATTCCTCACTCTCCAAAGGAAGTAACCCAGCTTAT	1967				
Db 635	CAGCAGAAGAGCAGCCATGCCAGTATTCCTCACTCTCCAAAGGAAGTAACCCAGCTTAT	694				
Qy 1968	ATTCTTCACACTTCTGGGG-AACTGGGTATAATCCCAACCA-TCAAAATAGAGACCTTGC	2025				
Db 695	ATTCTTCACACTTCTGGGG-AACTGGGTATAATCCCAACCA-TCAAAATAGAGACCTTGC	754				
Qy 2026	AAGAAGC 2032					
Db 755	CAGAAAC 761					

```
RESULT 7
AW963140          666 bp mRNA linear EST 01-JUN-2000
LOCUS
DEFINITION
EST375213 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW963140
VERSION
AW963140.1 GI:8152976
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 666)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
TITLE
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL
Unpublished (2000)
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 184
Seq primer: Reverse.
FEATURES
source
1..666
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/notes="Vector: pBluescriptSKm"
ORIGIN
Query Match 19.4%; Score 614.4; DB 2; Length 666;
Best Local Similarity 95.2%; Pred. No. 1e-126;
Matches 633; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1770 TCCAAATGAGTGTGGAAATGTTCTTCTCAGGGTCTAGAGACTGTGGACACTTT 1829
DB 1 TCCAAATGAGTGTGGAAATGTTCTTCTCAGGGTCTAGAGACTGTGGACACTTT 60
QY 1830 TCTTGAGTGCTACTTCAGAGCTTATAGGATTTCTTCTGCGCAAGATTTCTCTCG 1889
DB 61 TCTTGAGTGCTACTTCAGAGCTTATAGGATTTCTTCTGCGCAAGATTTCTCTCG 120
QY 1890 TATCACTCCAAGCAGCTCAGCAGAGAGAGAGCCATGCCAGTATTCCTCACTTCCAAA 1949
DB 121 TATCACTCCAAGCAGCTCAGCAGAGAGAGAGCCATGCCAGTATTCCTCACTTCCAAA 180
QY 1950 AGGAAGTACCAAGCTTATATTTCTCACACTTCTGGGAACTGGGTATATCAACATCA 2009
DB 181 AGGAAGTACCAAGCTTATATTTCTCACACTTCTGGGAACTGGGTATATCAACATCA 240
QY 2010 AATAGAAGACCTTGCAGAGCAGAGTCAATTCCTCAGAGAGAACTTGGGAGATGATGT 2069
DB 241 AATAGAAGACCTTGCAGAGCAGAGTCAATTCCTCAGAGAGAACTTGGGAGATGATGT 300
QY 2070 GCAGATGATGAACCTGGGTTCATCCAGTTCCTCAAGACTCAGAGAACTAGATTTAAGCT 2129
DB 301 GCAGATGATGAACCTGGGTTCATCCAGTTCCTCAAGACTCAGAGAACTAGATTTAAGCT 360
QY 2130 GAGGAGAGTGGCCACCTGGCATGCCCAACCAACAGATCACCAGCCAGCTTACAGAG 2189
DB 361 GAGGAGAGTGGCCACCTGGCATGCCCAACCAACAGATCACCAGCCAGCTTACAGAG 420
QY 2190 GCATTAACTCTCTCAATGAGGAAGATCATTCACAACTGAGCAGACATTCATATGATC 2249
DB 421 GCATTAACTCTCTCAATGAGGAAGATCATTCACAACTGAGCAGACATTCATATGATC 480
QY 2250 ATTAAAGGAAGTGTTCCTTTATGTAGCAAGTATATATCGGCTAACTCCTTAATCCCA 2309
DB |||||
```

```
DB 481 ANTTAAAGAGAGTGTTCCTCTATGTGTAGCAAGTATATCGGTAACTCCTTAAATCCA 540
QY 2310 ATGATAGTCTCTAGCTCGACAGCAATGGCTGCAATTAGGCAGATAAGACATCAGTCC 2369
DB 541 AAGAATAGTCTCTAAGCTGGACAGGATGGGCTTGCATTATGCAGATTAAAGCATCTAATC 600
QY 2370 CAGTAAATGAATCCATAGACTCATCTAGCAACCACTTACCATTTAGCAGCTATGTTAGAGCT 2429
DB 601 CAGTAAATGAATCCATAGACTCATCTAGCACTTTTACCCTCCCTTTAGCCCTTATGTTAGAGCT 660
QY 2430 GCAAG 2434
DB 661 GCAAG 665

RESULT 8
BG106937
LOCUS
DEFINITION
602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
mRNA sequence.
ACCESSION
BG106937
VERSION
BG106937.1 GI:12600783
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1074)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10068 row: b column: 14
High quality sequence stop: 638.
FEATURES
source
1..1074
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4385965"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
/notes="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 19.4%; Score 614; DB 4; Length 1074;
Best Local Similarity 87.4%; Pred. No. 1.3e-126;
Matches 764; Conservative 0; Mismatches 100; Indels 10; Gaps 8;
QY 23 TTCCACAGAGCTTAGACCTCGAAGAGATGGCTCAGCA-CCACCTATGGATCTTGCTCC 81
DB 22 TCCGACAGAGCTTAGACCTCGAAGAGATGGCTCAGCAGCCACTATGGATCTTGCTCC 81
QY 82 TTTGCTCTCAAACTGGCCGGAAGCAGCTGGAAAGACTCAGAAATCTTCACAGTGAATG 141
DB 82 TTTGCTCTCAAACTGGCCGGAAGCAGCTGGAAAGACTCAGAAATCTTCACAGTGAATG 141
QY 142 GGATTTCTGGGAGTCACTCACTTTCCTGTAAATATCCAGAACCCAGCGAAGTTAAA 201
DB 142 GGATTTCTGGGAGTCACTCACTTTCCTGTAAATATCCAGAACCCAGCGAAGTTAAA 201
```



```
QY 591 TTCCAGACTCCCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGAACCCCTGTCCAG 650
Db 541 TTCCAGACTCCCTGAGGACCAAGAGCTGACTTACAGTGTACAGCCAGAACCCCTGTCCAG 600
QY 651 AACAAAT 656
Db 601 AACAAAT 606

RESULT 10
BP300686 598 bp mRNA linear EST 17-SEP-2004
LOCUS BP300686 Sugano cDNA library, macrophage Homo sapiens cDNA clone
DEFINITION MPE01728, mRNA sequence.
ACCESSION BP300686
VERSION BP300686.1 GI:52229646
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 598)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
Location/Qualifiers
1..598
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MPE01728"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

ORIGIN
Query Match 18.4%; Score 585; DB 5; Length 598;
Best Local Similarity 99.8%; Pred. No. 48-120; Indels 1; Gaps 1;
Matches 596; Conservative 0; Mismatches 0;

QY 1079 CACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCCAACTCTTACTGGGAGAT 1138
Db 1 CACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCCAACTCTTACTGGGAGAT 60
QY 1139 TGCAAACTGCCACATCTCAGCTGTGAAGCAAAAGCAGGAACCTTCTGCTGGGCATAGCTT 1198
Db 61 TGCAAACTGCCACATCTCAGCTGTGAAGCAAAAGCAGGAACCTTCTGCTGGGCATAGCTT 120
QY 1199 GTGCCCTAAATGACAATGGATGCATACCTCTTCTGAAATGACTCCCTTCTGAATGAATG 1258
Db 121 GTGCCCTAAATGACAATGGATGCATACCTCTTCTGAAATGACTCCCTTCTGAATGAATG 180
QY 1259 ACAAGACAGGTTACCTAGTATAGTTTTCCTCAAACTCTTCCCATCATAGCACATGTAGAA 1318
Db 181 ACAAGACAGGTTACCTAGTATAGTTTTCCTCAAACTCTTCCCATCATAGCACATGTAGAA 240
QY 1319 AATAATATTTTATGGCAGCTGGGATAAAGCAAGCAAGTTCTCCTCTGGAAGCTGC 1378
Db 241 AATAATATTTTATGGCAGCTGGGATAAAGCAAGCAAGTTCTCCTCTGGAAGCTGC 300
QY 1379 ATATGACTAGAGGCTCTTGTGACTGGAGGTAAACCAACCTGCCCCAGTAAGTCTGGGAGAA 1438
Db 301 ATATGACTAGAGGCTCTTGTGACTGGAGGTAAACCAACCTGCCCCAGTAAGTCTGGGAGAA 360
QY 1439 GGGGATCAATATTTTGACACCTGTAATAGGCCATGGGACACACGACCAAGATGCTCTGCT 1498
Db 361 GGGGATCAATATTTTGACACCTGTAATAGGCCATGGGACACACGACCAAGATGCTCTGCT 420
```

```
QY 1499 CACAGTCACTATGTGTGAAGATCCCTGTGCTGGCCTTACACCGCATCTTGAGCAAT 1558
Db 421 CACAGTCACTATGTGTGAAGATCCCTGTGCTGGCCTTACACCGCATCTTGAGCAAT 480
QY 1559 TAGGAAAATGTACCCCTTCGCTTGGAGCAGATGCAGCCCTTCCCCGAGTGCATGCTTGG 1618
Db 481 TAGGAAAATGTACCCCTTCGCTTGGAGCAGATGCAGCCCTTCCCCGAGTGCATGCTTGG 540
QY 1619 AGAGCAGAATGTGGG-CTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTG 1674
Db 541 AGAGCAGAATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTG 597

RESULT 11
BP303350 582 bp mRNA linear EST 17-SEP-2004
LOCUS BP303350 Sugano cDNA library, macrophage Homo sapiens cDNA clone
DEFINITION MPE08190, mRNA sequence.
ACCESSION BP303350
VERSION BP303350.1 GI:52232310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MPE08190"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

ORIGIN
Query Match 18.3%; Score 582; DB 5; Length 582;
Best Local Similarity 100.0%; Pred. No. 1.9e-119; Indels 0; Gaps 0;
Matches 582; Conservative 0; Mismatches 0;

QY 204 ATTGCTTGGACTCTTAAACATCTGTGCTTATGTAAACACGAGAGACTCAGAACAGCA 263
Db 1 ATTGCTTGGACTCTTAAACATCTGTGCTTATGTAAACACGAGAGACTCAGAACAGCA 60
QY 264 CCCGTAGTCTAGTCACCCACAGAAATTTATTATGAACGGATACATGCTTAGTCTCCGAC 323
Db 61 CCCGTAGTCTAGTCACCCACAGAAATTTATTATGAACGGATACATGCTTAGTCTCCGAC 120
QY 324 TACAATCTGTCATTAGCGATCTGAGGATGGAAGACGCGAGAGACTACAAAGCAGACATA 383
Db 121 TACAATCTGTCATTAGCGATCTGAGGATGGAAGACGCGAGAGACTACAAAGCAGACATA 180
QY 384 AATACACAGGCTGATCCCTACACACACGAGGCTTACACCTGCAATCTATGTCGG 443
Db 181 AATACACAGGCTGATCCCTACACACACGAGGCTTACAACTGCAATCTATGTCGG 240
QY 444 CTGCGAAACCAAAATTTACACAGAGTTTAAATGCATCTGTGAACAGCACCTGTAATGTC 503
Db 241 CTGCGAAACCAAAATTTACACAGAGTTTAAATGCATCTGTGAACAGCACCTGTAATGTC 300
QY 504 ACATGACATCTCTGTAGAGAAAGAAAGATGTGACATACAATTTGAGTCCCTG 563
```


This Page Blank (uspto)